

Yi Zhang

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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.

206
papers

53,235
citations

103
h-index

223
g-index

223
ext. papers

59,659
ext. citations

19.1
avg, IF

7.93
L-index

#	Paper	IF	Citations
206	Role of histone H3 lysine 27 methylation in Polycomb-group silencing. <i>Science</i> , 2002 , 298, 1039-43	33.3	2794
205	Tet proteins can convert 5-methylcytosine to 5-formylcytosine and 5-carboxylcytosine. <i>Science</i> , 2011 , 333, 1300-3	33.3	2426
204	Double nicking by RNA-guided CRISPR Cas9 for enhanced genome editing specificity. <i>Cell</i> , 2013 , 154, 1380-9	56.2	2348
203	Oncometabolite 2-hydroxyglutarate is a competitive inhibitor of Eketoglutarate-dependent dioxygenases. <i>Cancer Cell</i> , 2011 , 19, 17-30	24.3	1919
202	Role of Tet proteins in 5mC to 5hmC conversion, ES-cell self-renewal and inner cell mass specification. <i>Nature</i> , 2010 , 466, 1129-33	50.4	1915
201	The diverse functions of histone lysine methylation. <i>Nature Reviews Molecular Cell Biology</i> , 2005 , 6, 838-48.7	48.7	1566
200	Histone demethylation by a family of JmjC domain-containing proteins. <i>Nature</i> , 2006 , 439, 811-6	50.4	1553
199	Role of histone H2A ubiquitination in Polycomb silencing. <i>Nature</i> , 2004 , 431, 873-8	50.4	1264
198	TET enzymes, TDG and the dynamics of DNA demethylation. <i>Nature</i> , 2013 , 502, 472-9	50.4	1026
197	Role of histone H3 lysine 27 methylation in X inactivation. <i>Science</i> , 2003 , 300, 131-5	33.3	978
196	JmjC-domain-containing proteins and histone demethylation. <i>Nature Reviews Genetics</i> , 2006 , 7, 715-27	30.1	940
195	Active DNA demethylation: many roads lead to Rome. <i>Nature Reviews Molecular Cell Biology</i> , 2010 , 11, 607-20	48.7	840
194	New nomenclature for chromatin-modifying enzymes. <i>Cell</i> , 2007 , 131, 633-6	56.2	745
193	Reversing DNA methylation: mechanisms, genomics, and biological functions. <i>Cell</i> , 2014 , 156, 45-68	56.2	738
192	The functions of E(Z)/EZH2-mediated methylation of lysine 27 in histone H3. <i>Current Opinion in Genetics and Development</i> , 2004 , 14, 155-64	4.9	711
191	TET-mediated active DNA demethylation: mechanism, function and beyond. <i>Nature Reviews Genetics</i> , 2017 , 18, 517-534	30.1	698
190	MBD2 is a transcriptional repressor belonging to the MeCP1 histone deacetylase complex. <i>Nature Genetics</i> , 1999 , 23, 58-61	36.3	692

189	The dermatomyositis-specific autoantigen Mi2 is a component of a complex containing histone deacetylase and nucleosome remodeling activities. <i>Cell</i> , 1998 , 95, 279-89	56.2	688
188	Role of Bmi-1 and Ring1A in H2A ubiquitylation and Hox gene silencing. <i>Molecular Cell</i> , 2005 , 20, 845-54	17.6	679
187	JHDM2A, a JmjC-containing H3K9 demethylase, facilitates transcription activation by androgen receptor. <i>Cell</i> , 2006 , 125, 483-95	56.2	659
186	Regulation of histone methylation by demethylination and demethylation. <i>Nature Reviews Molecular Cell Biology</i> , 2007 , 8, 307-18	48.7	657
185	Methylation of H3-lysine 79 is mediated by a new family of HMTases without a SET domain. <i>Current Biology</i> , 2002 , 12, 1052-8	6.3	644
184	hDOT1L links histone methylation to leukemogenesis. <i>Cell</i> , 2005 , 121, 167-78	56.2	640
183	SUZ12 is required for both the histone methyltransferase activity and the silencing function of the EED-EZH2 complex. <i>Molecular Cell</i> , 2004 , 15, 57-67	17.6	628
182	Methylation of histone H4 at arginine 3 facilitating transcriptional activation by nuclear hormone receptor. <i>Science</i> , 2001 , 293, 853-7	33.3	603
181	G9a-mediated irreversible epigenetic inactivation of Oct-3/4 during early embryogenesis. <i>Nature Cell Biology</i> , 2006 , 8, 188-94	23.4	527
180	The transcriptional repressor JHDM3A demethylates trimethyl histone H3 lysine 9 and lysine 36. <i>Nature</i> , 2006 , 442, 312-6	50.4	513
179	Histone deacetylases and SAP18, a novel polypeptide, are components of a human Sin3 complex. <i>Cell</i> , 1997 , 89, 357-64	56.2	500
178	Lysine glutarylation is a protein posttranslational modification regulated by SIRT5. <i>Cell Metabolism</i> , 2014 , 19, 605-17	24.6	496
177	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , 2011 , 473, 389-93	50.4	496
176	DNA methylation in mammals. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014 , 6, a019133	10.2	492
175	Structural basis for specific binding of Polycomb chromodomain to histone H3 methylated at Lys 27. <i>Genes and Development</i> , 2003 , 17, 1823-8	12.6	488
174	Mechanisms and functions of Tet protein-mediated 5-methylcytosine oxidation. <i>Genes and Development</i> , 2011 , 25, 2436-52	12.6	487
173	The first identification of lysine malonylation substrates and its regulatory enzyme. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.012658	7.6	482
172	Dnmt3a-dependent nonpromoter DNA methylation facilitates transcription of neurogenic genes. <i>Science</i> , 2010 , 329, 444-8	33.3	480

171	Genome-wide analysis of 5-hydroxymethylcytosine distribution reveals its dual function in transcriptional regulation in mouse embryonic stem cells. <i>Genes and Development</i> , 2011 , 25, 679-84	12.6	431
170	Hierarchical recruitment of polycomb group silencing complexes. <i>Molecular Cell</i> , 2004 , 14, 637-46	17.6	431
169	Purification and functional characterization of a histone H3-lysine 4-specific methyltransferase. <i>Molecular Cell</i> , 2001 , 8, 1207-17	17.6	422
168	The diverse functions of Dot1 and H3K79 methylation. <i>Genes and Development</i> , 2011 , 25, 1345-58	12.6	401
167	Histone H3 and H4 ubiquitylation by the CUL4-DDB-ROC1 ubiquitin ligase facilitates cellular response to DNA damage. <i>Molecular Cell</i> , 2006 , 22, 383-94	17.6	400
166	Bre1, an E3 ubiquitin ligase required for recruitment and substrate selection of Rad6 at a promoter. <i>Molecular Cell</i> , 2003 , 11, 267-74	17.6	400
165	Lysine methylation within the globular domain of histone H3 by Dot1 is important for telomeric silencing and Sir protein association. <i>Genes and Development</i> , 2002 , 16, 1518-27	12.6	396
164	Tudor, MBT and chromo domains gauge the degree of lysine methylation. <i>EMBO Reports</i> , 2006 , 7, 397-403	35	394
163	Genome-wide analysis reveals TET- and TDG-dependent 5-methylcytosine oxidation dynamics. <i>Cell</i> , 2013 , 153, 692-706	56.2	390
162	PLU-1 is an H3K4 demethylase involved in transcriptional repression and breast cancer cell proliferation. <i>Molecular Cell</i> , 2007 , 25, 801-12	17.6	387
161	Replication-dependent loss of 5-hydroxymethylcytosine in mouse preimplantation embryos. <i>Science</i> , 2011 , 334, 194	33.3	384
160	Recognition of histone H3 lysine-4 methylation by the double tudor domain of JMJD2A. <i>Science</i> , 2006 , 312, 748-51	33.3	364
159	Role of Jhdm2a in regulating metabolic gene expression and obesity resistance. <i>Nature</i> , 2009 , 458, 757-61	61.4	353
158	Imprinting along the Kcnq1 domain on mouse chromosome 7 involves repressive histone methylation and recruitment of Polycomb group complexes. <i>Nature Genetics</i> , 2004 , 36, 1296-300	36.3	351
157	The retinoblastoma binding protein RBP2 is an H3K4 demethylase. <i>Cell</i> , 2007 , 128, 889-900	56.2	343
156	Histone demethylase JHDM2A is critical for Tnp1 and Prm1 transcription and spermatogenesis. <i>Nature</i> , 2007 , 450, 119-23	50.4	312
155	Ubiquitination of histone H2B by Rad6 is required for efficient Dot1-mediated methylation of histone H3 lysine 79. <i>Journal of Biological Chemistry</i> , 2002 , 277, 34655-7	5.4	311
154	Transcriptional regulation by histone ubiquitination and deubiquitination. <i>Genes and Development</i> , 2003 , 17, 2733-40	12.6	307

153	Structure of the catalytic domain of human DOT1L, a non-SET domain nucleosomal histone methyltransferase. <i>Cell</i> , 2003 , 112, 711-23	56.2	303
152	Generation of insulin-secreting islet-like clusters from human skin fibroblasts. <i>Journal of Biological Chemistry</i> , 2008 , 283, 31601-7	5.4	278
151	Single-Cell RNA-Seq Reveals Hypothalamic Cell Diversity. <i>Cell Reports</i> , 2017 , 18, 3227-3241	10.6	271
150	Embryonic development following somatic cell nuclear transfer impeded by persisting histone methylation. <i>Cell</i> , 2014 , 159, 884-95	56.2	271
149	mAM facilitates conversion by ESET of dimethyl to trimethyl lysine 9 of histone H3 to cause transcriptional repression. <i>Molecular Cell</i> , 2003 , 12, 475-87	17.6	268
148	Genetic and epigenetic variations in iPSCs: potential causes and implications for application. <i>Cell Stem Cell</i> , 2013 , 13, 149-59	18	263
147	The histone H3K79 methyltransferase Dot1L is essential for mammalian development and heterochromatin structure. <i>PLoS Genetics</i> , 2008 , 4, e1000190	6	262
146	Purification and functional characterization of SET8, a nucleosomal histone H4-lysine 20-specific methyltransferase. <i>Current Biology</i> , 2002 , 12, 1086-99	6.3	262
145	pRB family proteins are required for H3K27 trimethylation and Polycomb repression complexes binding to and silencing p16INK4alpha tumor suppressor gene. <i>Genes and Development</i> , 2007 , 21, 49-54	12.6	250
144	The H3K36 demethylase Jhdm1b/Kdm2b regulates cell proliferation and senescence through p15(Ink4b). <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 1169-75	17.6	246
143	SAP30, a novel protein conserved between human and yeast, is a component of a histone deacetylase complex. <i>Molecular Cell</i> , 1998 , 1, 1021-31	17.6	245
142	Mechanism and function of oxidative reversal of DNA and RNA methylation. <i>Annual Review of Biochemistry</i> , 2014 , 83, 585-614	29.1	243
141	AID/APOBEC deaminases disfavor modified cytosines implicated in DNA demethylation. <i>Nature Chemical Biology</i> , 2012 , 8, 751-8	11.7	238
140	A role for the elongator complex in zygotic paternal genome demethylation. <i>Nature</i> , 2010 , 463, 554-8	50.4	236
139	Cancer mediates effector T cell dysfunction by targeting microRNAs and EZH2 via glycolysis restriction. <i>Nature Immunology</i> , 2016 , 17, 95-103	19.1	234
138	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. <i>Nature</i> , 2015 , 528, 142-6	50.4	228
137	Kdm2b maintains murine embryonic stem cell status by recruiting PRC1 complex to CpG islands of developmental genes. <i>Nature Cell Biology</i> , 2013 , 15, 373-84	23.4	225
136	Generation and replication-dependent dilution of 5fC and 5caC during mouse preimplantation development. <i>Cell Research</i> , 2011 , 21, 1670-6	24.7	220

135	Maternal H3K27me3 controls DNA methylation-independent imprinting. <i>Nature</i> , 2017 , 547, 419-424	50.4	217
134	Tet1 controls meiosis by regulating meiotic gene expression. <i>Nature</i> , 2012 , 492, 443-7	50.4	207
133	NAT, a human complex containing Srb polypeptides that functions as a negative regulator of activated transcription. <i>Molecular Cell</i> , 1998 , 2, 213-22	17.6	201
132	Molecular cloning of ESET, a novel histone H3-specific methyltransferase that interacts with ERG transcription factor. <i>Oncogene</i> , 2002 , 21, 148-52	9.2	201
131	DOT1L, the H3K79 methyltransferase, is required for MLL-AF9-mediated leukemogenesis. <i>Blood</i> , 2011 , 117, 6912-22	2.2	195
130	Crystal structure of human histone lysine-specific demethylase 1 (LSD1). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 13956-61	11.5	193
129	Ring1b-mediated H2A ubiquitination associates with inactive X chromosomes and is involved in initiation of X inactivation. <i>Journal of Biological Chemistry</i> , 2004 , 279, 52812-5	5.4	192
128	Role of Tet proteins in enhancer activity and telomere elongation. <i>Genes and Development</i> , 2014 , 28, 2103-19	12.6	176
127	Structure of a Bmi-1-Ring1B polycomb group ubiquitin ligase complex. <i>Journal of Biological Chemistry</i> , 2006 , 281, 20643-9	5.4	173
126	Role of Tet1 in erasure of genomic imprinting. <i>Nature</i> , 2013 , 504, 460-4	50.4	164
125	Mechanisms of epigenetic inheritance. <i>Current Opinion in Cell Biology</i> , 2007 , 19, 266-72	9	164
124	RBP1 recruits the mSIN3-histone deacetylase complex to the pocket of retinoblastoma tumor suppressor family proteins found in limited discrete regions of the nucleus at growth arrest. <i>Molecular and Cellular Biology</i> , 2001 , 21, 2918-32	4.8	162
123	Tet3 and DNA replication mediate demethylation of both the maternal and paternal genomes in mouse zygotes. <i>Cell Stem Cell</i> , 2014 , 15, 459-471	18	161
122	Establishing Chromatin Regulatory Landscape during Mouse Preimplantation Development. <i>Cell</i> , 2016 , 165, 1375-1388	56.2	158
121	KDM2b/JHDM1b, an H3K36me2-specific demethylase, is required for initiation and maintenance of acute myeloid leukemia. <i>Blood</i> , 2011 , 117, 3869-80	2.2	157
120	Leukaemic transformation by CALM-AF10 involves upregulation of Hoxa5 by hDOT1L. <i>Nature Cell Biology</i> , 2006 , 8, 1017-24	23.4	153
119	Neocortical Tet3-mediated accumulation of 5-hydroxymethylcytosine promotes rapid behavioral adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 7120-5	11.5	145
118	Role of hPHF1 in H3K27 methylation and Hox gene silencing. <i>Molecular and Cellular Biology</i> , 2008 , 28, 1862-72	4.8	139

117	Kdm2b promotes induced pluripotent stem cell generation by facilitating gene activation early in reprogramming. <i>Nature Cell Biology</i> , 2012 , 14, 457-66	23.4	137
116	A modular network model of aging. <i>Molecular Systems Biology</i> , 2007 , 3, 147	12.2	134
115	Embryonic stem cell and induced pluripotent stem cell: an epigenetic perspective. <i>Cell Research</i> , 2013 , 23, 49-69	24.7	127
114	The MES-2/MES-3/MES-6 complex and regulation of histone H3 methylation in <i>C. elegans</i> . <i>Current Biology</i> , 2004 , 14, 1639-43	6.3	127
113	Dynamics of 5-methylcytosine and 5-hydroxymethylcytosine during germ cell reprogramming. <i>Cell Research</i> , 2013 , 23, 329-39	24.7	125
112	Somatic Cell Nuclear Transfer Reprogramming: Mechanisms and Applications. <i>Cell Stem Cell</i> , 2018 , 23, 471-485	18	120
111	Histone Demethylase Expression Enhances Human Somatic Cell Nuclear Transfer Efficiency and Promotes Derivation of Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2015 , 17, 758-766	18	119
110	Tet1 and 5-hydroxymethylation: a genome-wide view in mouse embryonic stem cells. <i>Cell Cycle</i> , 2011 , 10, 2428-36	4.7	113
109	Nickel ions inhibit histone demethylase JMJD1A and DNA repair enzyme ABH2 by replacing the ferrous iron in the catalytic centers. <i>Journal of Biological Chemistry</i> , 2010 , 285, 7374-83	5.4	113
108	Butyrate promotes induced pluripotent stem cell generation. <i>Journal of Biological Chemistry</i> , 2010 , 285, 25516-21	5.4	111
107	An extensive network of TET2-targeting MicroRNAs regulates malignant hematopoiesis. <i>Cell Reports</i> , 2013 , 5, 471-81	10.6	109
106	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. <i>Nature Biotechnology</i> , 2014 , 32, 1231-40	44.5	107
105	Nucleosome assembly is required for nuclear pore complex assembly in mouse zygotes. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 609-16	17.6	107
104	5-Hydroxymethylcytosine: generation, fate, and genomic distribution. <i>Current Opinion in Cell Biology</i> , 2013 , 25, 289-96	9	107
103	The lncRNA DEANR1 facilitates human endoderm differentiation by activating FOXA2 expression. <i>Cell Reports</i> , 2015 , 11, 137-48	10.6	102
102	DOT1L regulates dystrophin expression and is critical for cardiac function. <i>Genes and Development</i> , 2011 , 25, 263-74	12.6	102
101	Histone H3K27me3 demethylases KDM6A and KDM6B modulate definitive endoderm differentiation from human ESCs by regulating WNT signaling pathway. <i>Cell Research</i> , 2013 , 23, 122-30	24.7	100
100	Role of H3K27 methylation in the regulation of lncRNA expression. <i>Cell Research</i> , 2010 , 20, 1109-16	24.7	97

99	MES-4: an autosome-associated histone methyltransferase that participates in silencing the X chromosomes in the <i>C. elegans</i> germ line. <i>Development (Cambridge)</i> , 2006 , 133, 3907-17	6.6	97
98	Cyclin-dependent kinase 1 (CDK1)-mediated phosphorylation of enhancer of zeste 2 (Ezh2) regulates its stability. <i>Journal of Biological Chemistry</i> , 2011 , 286, 28511-9	5.4	95
97	The trithorax-group protein Lid is a histone H3 trimethyl-Lys4 demethylase. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 341-3	17.6	91
96	Yeast Jhd2p is a histone H3 Lys4 trimethyl demethylase. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 243-5	17.6	90
95	JmjC enzyme KDM2A is a regulator of rRNA transcription in response to starvation. <i>EMBO Journal</i> , 2010 , 29, 1510-22	13	84
94	Cell cycle and p53 gate the direct conversion of human fibroblasts to dopaminergic neurons. <i>Nature Communications</i> , 2015 , 6, 10100	17.4	82
93	Substrate preferences of the EZH2 histone methyltransferase complex. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8365-70	5.4	82
92	The histone methyltransferase Set7/9 promotes myoblast differentiation and myofibril assembly. <i>Journal of Cell Biology</i> , 2011 , 194, 551-65	7.3	81
91	Loss of DUX causes minor defects in zygotic genome activation and is compatible with mouse development. <i>Nature Genetics</i> , 2019 , 51, 947-951	36.3	76
90	Genomic imprinting of by maternal H3K27me3. <i>Genes and Development</i> , 2017 , 31, 1927-1932	12.6	73
89	Demethylation of histone H3K36 and H3K9 by Rph1: a vestige of an H3K9 methylation system in <i>Saccharomyces cerevisiae</i> ?. <i>Molecular and Cellular Biology</i> , 2007 , 27, 3951-61	4.8	69
88	Inhibition of excess nodal signaling during mouse gastrulation by the transcriptional corepressor DRAP1. <i>Science</i> , 2002 , 298, 1996-9	33.3	69
87	Regulation of TET protein stability by calpains. <i>Cell Reports</i> , 2014 , 6, 278-84	10.6	68
86	Validation-based insertional mutagenesis identifies lysine demethylase FBXL11 as a negative regulator of NFkappaB. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 16339-44	11.5	68
85	Loss of H3K27me3 Imprinting in Somatic Cell Nuclear Transfer Embryos Disrupts Post-Implantation Development. <i>Cell Stem Cell</i> , 2018 , 23, 343-354.e5	18	65
84	Identification and functional characterization of the p66/p68 components of the MeCP1 complex. <i>Molecular and Cellular Biology</i> , 2002 , 22, 536-46	4.8	64
83	Histone demethylase JHDM2A is involved in male infertility and obesity. <i>Journal of Andrology</i> , 2010 , 31, 75-8		63
82	UBR2 mediates transcriptional silencing during spermatogenesis via histone ubiquitination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 1912-7	11.5	61

81	The H3K4 demethylase lid associates with and inhibits histone deacetylase Rpd3. <i>Molecular and Cellular Biology</i> , 2009 , 29, 1401-10	4.8	56
80	Inhibition of histone methylation arrests ongoing graft-versus-host disease in mice by selectively inducing apoptosis of alloreactive effector T cells. <i>Blood</i> , 2012 , 119, 1274-82	2.2	54
79	AOF1 is a histone H3K4 demethylase possessing demethylase activity-independent repression function. <i>Cell Research</i> , 2010 , 20, 276-87	24.7	54
78	Role of Mammalian DNA Methyltransferases in Development. <i>Annual Review of Biochemistry</i> , 2020 , 89, 135-158	29.1	54
77	Essential role of DOT1L in maintaining normal adult hematopoiesis. <i>Cell Research</i> , 2011 , 21, 1370-3	24.7	53
76	Dynamic regulation of histone H3 methylated at lysine 79 within a tissue-specific chromatin domain. <i>Journal of Biological Chemistry</i> , 2003 , 278, 18346-52	5.4	53
75	Global reduction of the epigenetic H3K79 methylation mark and increased chromosomal instability in CALM-AF10-positive leukemias. <i>Blood</i> , 2009 , 114, 651-8	2.2	51
74	Genome-wide uH2A localization analysis highlights Bmi1-dependent deposition of the mark at repressed genes. <i>PLoS Genetics</i> , 2009 , 5, e1000506	6	48
73	Charting oxidized methylcytosines at base resolution. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 656-61	17.6	47
72	Maternal knockout causes loss of H3K27me3 imprinting and random X inactivation in the extraembryonic cells. <i>Genes and Development</i> , 2018 , 32, 1525-1536	12.6	47
71	WNT3 is a biomarker capable of predicting the definitive endoderm differentiation potential of hESCs. <i>Stem Cell Reports</i> , 2013 , 1, 46-52	8	44
70	Inactivation of NuRD component Mta2 causes abnormal T cell activation and lupus-like autoimmune disease in mice. <i>Journal of Biological Chemistry</i> , 2008 , 283, 13825-33	5.4	43
69	A universal competitive fluorescence polarization activity assay for S-adenosylmethionine utilizing methyltransferases. <i>Analytical Biochemistry</i> , 2008 , 373, 296-306	3.1	42
68	Cell totipotency: molecular features, induction, and maintenance. <i>National Science Review</i> , 2015 , 2, 217-225	4.1	41
67	Transcriptional activation of transposable elements in mouse zygotes is independent of Tet3-mediated 5-methylcytosine oxidation. <i>Cell Research</i> , 2012 , 22, 1640-9	24.7	40
66	Ikbkap/Elp1 deficiency causes male infertility by disrupting meiotic progression. <i>PLoS Genetics</i> , 2013 , 9, e1003516	6	40
65	Mechanisms of epigenetic memory and addiction. <i>EMBO Journal</i> , 2014 , 33, 1091-103	13	39
64	Double Nicking by RNA-Guided CRISPR Cas9 for Enhanced Genome Editing Specificity. <i>Cell</i> , 2013 , 155, 479-480	56.2	39

63	Tudor staphylococcal nuclease (Tudor-SN) participates in small ribonucleoprotein (snRNP) assembly via interacting with symmetrically dimethylated Sm proteins. <i>Journal of Biological Chemistry</i> , 2012 , 287, 18130-41	5.4	39
62	A rapid and versatile tool for genomic engineering in <i>Lactococcus lactis</i> . <i>Microbial Cell Factories</i> , 2019 , 18, 22	6.4	38
61	Minireview: role of protein methylation and demethylation in nuclear hormone signaling. <i>Molecular Endocrinology</i> , 2009 , 23, 1323-34		38
60	Cell type-specific transcriptional programs in mouse prefrontal cortex during adolescence and addiction. <i>Nature Communications</i> , 2019 , 10, 4169	17.4	36
59	Myc and Dnmt1 impede the pluripotent to totipotent state transition in embryonic stem cells. <i>Nature Cell Biology</i> , 2019 , 21, 835-844	23.4	36
58	Allelic H3K27me3 to allelic DNA methylation switch maintains noncanonical imprinting in extraembryonic cells. <i>Science Advances</i> , 2019 , 5, eaay7246	14.3	35
57	Simultaneous mapping of active DNA demethylation and sister chromatid exchange in single cells. <i>Genes and Development</i> , 2017 , 31, 511-523	12.6	34
56	Cold-inducible RNA-binding protein CIRP/hnRNP A18 regulates telomerase activity in a temperature-dependent manner. <i>Nucleic Acids Research</i> , 2016 , 44, 761-75	20.1	34
55	Enzymatic analysis of Tet proteins: key enzymes in the metabolism of DNA methylation. <i>Methods in Enzymology</i> , 2012 , 512, 93-105	1.7	33
54	Haploinsufficiency, but not defective paternal 5mC oxidation, accounts for the developmental defects of maternal Tet3 knockouts. <i>Cell Reports</i> , 2015 , 10, 463-70	10.6	32
53	Loss of HDAC-Mediated Repression and Gain of NF- κ B Activation Underlie Cytokine Induction in ARID1A- and PIK3CA-Mutation-Driven Ovarian Cancer. <i>Cell Reports</i> , 2016 , 17, 275-288	10.6	31
52	Cloning and characterization of extended hammerheads from a diverse set of caudate amphibians. <i>Gene</i> , 1996 , 172, 183-90	3.8	30
51	Purification of histone demethylases from HeLa cells. <i>Methods</i> , 2006 , 40, 318-26	4.6	29
50	The Role of N-Acetyltransferase 10 Protein in DNA Methylation and Genomic Imprinting. <i>Molecular Cell</i> , 2017 , 68, 89-103.e7	17.6	28
49	Maternal H3K27me3-dependent autosomal and X chromosome imprinting. <i>Nature Reviews Genetics</i> , 2020 , 21, 555-571	30.1	28
48	Histone methyltransferase and histone methylation in inflammatory T-cell responses. <i>Immunotherapy</i> , 2013 , 5, 989-1004	3.8	27
47	Developmental regulation of Suz 12 localization. <i>Chromosoma</i> , 2005 , 114, 183-92	2.8	27
46	Aberrant upregulation of 14-3-3 β and EZH2 expression serves as an inferior prognostic biomarker for hepatocellular carcinoma. <i>PLoS ONE</i> , 2014 , 9, e107251	3.7	25

45	The <i>Saccharomyces cerevisiae</i> histone demethylase Jhd1 fine-tunes the distribution of H3K36me2. <i>Molecular and Cellular Biology</i> , 2007 , 27, 5055-65	4.8	25
44	Purification of histone methyltransferases from HeLa cells. <i>Methods in Enzymology</i> , 2004 , 377, 213-26	1.7	25
43	Transcription of satellite 2 DNA from the newt is driven by a snRNA type of promoter. <i>Nucleic Acids Research</i> , 1994 , 22, 4697-704	20.1	25
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41	The <i>C. elegans</i> methionine aminopeptidase 2 analog map-2 is required for germ cell proliferation. <i>FEBS Letters</i> , 2004 , 576, 245-50	3.8	24
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