

# Yi Zhang

## List of Publications by Year in descending order

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211  
papers

64,275  
citations

1461

110  
h-index

2018

212  
g-index

223  
all docs

223  
docs citations

223  
times ranked

59404  
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of Histone H3 Lysine 27 Methylation in Polycomb-Group Silencing. <i>Science</i> , 2002, 298, 1039-1043.	6.0	3,294
2	Tet Proteins Can Convert 5-Methylcytosine to 5-Formylcytosine and 5-Carboxylcytosine. <i>Science</i> , 2011, 333, 1300-1303.	6.0	2,898
3	Double Nicking by RNA-Guided CRISPR Cas9 for Enhanced Genome Editing Specificity. <i>Cell</i> , 2013, 154, 1380-1389.	13.5	2,862
4	Oncometabolite 2-Hydroxyglutarate Is a Competitive Inhibitor of $\alpha$ -Ketoglutarate-Dependent Dioxygenases. <i>Cancer Cell</i> , 2011, 19, 17-30.	7.7	2,340
5	Role of Tet proteins in 5mC to 5hmC conversion, ES-cell self-renewal and inner cell mass specification. <i>Nature</i> , 2010, 466, 1129-1133.	13.7	2,224
6	Histone demethylation by a family of JmjC domain-containing proteins. <i>Nature</i> , 2006, 439, 811-816.	13.7	1,846
7	The diverse functions of histone lysine methylation. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 838-849.	16.1	1,781
8	Role of histone H2A ubiquitination in Polycomb silencing. <i>Nature</i> , 2004, 431, 873-878.	13.7	1,502
9	TET enzymes, TDG and the dynamics of DNA demethylation. <i>Nature</i> , 2013, 502, 472-479.	13.7	1,323
10	TET-mediated active DNA demethylation: mechanism, function and beyond. <i>Nature Reviews Genetics</i> , 2017, 18, 517-534.	7.7	1,109
11	Role of Histone H3 Lysine 27 Methylation in X Inactivation. <i>Science</i> , 2003, 300, 131-135.	6.0	1,098
12	JmjC-domain-containing proteins and histone demethylation. <i>Nature Reviews Genetics</i> , 2006, 7, 715-727.	7.7	1,096
13	Active DNA demethylation: many roads lead to Rome. <i>Nature Reviews Molecular Cell Biology</i> , 2010, 11, 607-620.	16.1	937
14	Reversing DNA Methylation: Mechanisms, Genomics, and Biological Functions. <i>Cell</i> , 2014, 156, 45-68.	13.5	914
15	New Nomenclature for Chromatin-Modifying Enzymes. <i>Cell</i> , 2007, 131, 633-636.	13.5	849
16	The functions of E(Z)/EZH2-mediated methylation of lysine 27 in histone H3. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 155-164.	1.5	795
17	MBD2 is a transcriptional repressor belonging to the MeCP1 histone deacetylase complex. <i>Nature Genetics</i> , 1999, 23, 58-61.	9.4	783
18	Role of Bmi-1 and Ring1A in H2A Ubiquitylation and Hox Gene Silencing. <i>Molecular Cell</i> , 2005, 20, 845-854.	4.5	766

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19	Regulation of histone methylation by demethylination and demethylation. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 307-318.	16.1	764
20	Methylation of H3-Lysine 79 Is Mediated by a New Family of HMTases without a SET Domain. <i>Current Biology</i> , 2002, 12, 1052-1058.	1.8	748
21	The Dermatomyositis-Specific Autoantigen Mi2 Is a Component of a Complex Containing Histone Deacetylase and Nucleosome Remodeling Activities. <i>Cell</i> , 1998, 95, 279-289.	13.5	745
22	hDOT1L Links Histone Methylation to Leukemogenesis. <i>Cell</i> , 2005, 121, 167-178.	13.5	737
23	JHDM2A, a JmjC-Containing H3K9 Demethylase, Facilitates Transcription Activation by Androgen Receptor. <i>Cell</i> , 2006, 125, 483-495.	13.5	737
24	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.	4.5	733
25	DNA Methylation in Mammals. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a019133-a019133.	2.3	717
26	Methylation of Histone H4 at Arginine 3 Facilitating Transcriptional Activation by Nuclear Hormone Receptor. <i>Science</i> , 2001, 293, 853-857.	6.0	673
27	Lysine Glutarylation Is a Protein Posttranslational Modification Regulated by SIRT5. <i>Cell Metabolism</i> , 2014, 19, 605-617.	7.2	647
28	The First Identification of Lysine Malonylation Substrates and Its Regulatory Enzyme. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012658.	2.5	598
29	C9a-mediated irreversible epigenetic inactivation of Oct-3/4 during early embryogenesis. <i>Nature Cell Biology</i> , 2006, 8, 188-194.	4.6	581
30	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. <i>Nature</i> , 2011, 473, 389-393.	13.7	581
31	Structural basis for specific binding of Polycomb chromodomain to histone H3 methylated at Lys 27. <i>Genes and Development</i> , 2003, 17, 1823-1828.	2.7	567
32	Mechanisms and functions of Tet protein-mediated 5-methylcytosine oxidation. <i>Genes and Development</i> , 2011, 25, 2436-2452.	2.7	565
33	The transcriptional repressor JHDM3A demethylates trimethyl histone H3 lysine <sup>9</sup> and lysine <sup>36</sup> . <i>Nature</i> , 2006, 442, 312-316.	13.7	563
34	Histone Deacetylases and SAP18, a Novel Polypeptide, Are Components of a Human Sin3 Complex. <i>Cell</i> , 1997, 89, 357-364.	13.5	548
35	Dnmt3a-Dependent Nonpromoter DNA Methylation Facilitates Transcription of Neurogenic Genes. <i>Science</i> , 2010, 329, 444-448.	6.0	544
36	Hierarchical Recruitment of Polycomb Group Silencing Complexes. <i>Molecular Cell</i> , 2004, 14, 637-646.	4.5	513

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37	The diverse functions of Dot1 and H3K79 methylation. <i>Genes and Development</i> , 2011, 25, 1345-1358.	2.7	492
38	Bre1, an E3 Ubiquitin Ligase Required for Recruitment and Substrate Selection of Rad6 at a Promoter. <i>Molecular Cell</i> , 2003, 11, 267-274.	4.5	489
39	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, 679-684.	2.7	488
40	Purification and Functional Characterization of a Histone H3-Lysine 4-Specific Methyltransferase. <i>Molecular Cell</i> , 2001, 8, 1207-1217.	4.5	472
41	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, 1518-1527.	2.7	471
42	Single-Cell RNA-Seq Reveals Hypothalamic Cell Diversity. <i>Cell Reports</i> , 2017, 18, 3227-3241.	2.9	458
43	Histone H3 and H4 Ubiquitylation by the CUL4-DDB-ROC1 Ubiquitin Ligase Facilitates Cellular Response to DNA Damage. <i>Molecular Cell</i> , 2006, 22, 383-394.	4.5	447
44	Genome-wide Analysis Reveals TET- and TDG-Dependent 5-Methylcytosine Oxidation Dynamics. <i>Cell</i> , 2013, 153, 692-706.	13.5	440
45	Tudor, MBT and chromo domains gauge the degree of lysine methylation. <i>EMBO Reports</i> , 2006, 7, 397-403.	2.0	438
46	Replication-Dependent Loss of 5-Hydroxymethylcytosine in Mouse Preimplantation Embryos. <i>Science</i> , 2011, 334, 194-194.	6.0	435
47	PLU-1 Is an H3K4 Demethylase Involved in Transcriptional Repression and Breast Cancer Cell Proliferation. <i>Molecular Cell</i> , 2007, 25, 801-812.	4.5	431
48	Recognition of Histone H3 Lysine-4 Methylation by the Double Tudor Domain of JMJD2A. <i>Science</i> , 2006, 312, 748-751.	6.0	406
49	Role of Jhdm2a in regulating metabolic gene expression and obesity resistance. <i>Nature</i> , 2009, 458, 757-761.	13.7	402
50	The Retinoblastoma Binding Protein RBP2 Is an H3K4 Demethylase. <i>Cell</i> , 2007, 128, 889-900.	13.5	399
51	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, 1296-1300.	9.4	386
52	Embryonic Development following Somatic Cell Nuclear Transfer Impeded by Persisting Histone Methylation. <i>Cell</i> , 2014, 159, 884-895.	13.5	382
53	Transcriptional regulation by histone ubiquitination and deubiquitination. <i>Genes and Development</i> , 2003, 17, 2733-2740.	2.7	369
54	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, 34655-34657.	1.6	365

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55	Structure of the Catalytic Domain of Human DOT1L, a Non-SET Domain Nucleosomal Histone Methyltransferase. <i>Cell</i> , 2003, 112, 711-723.	13.5	363
56	Histone demethylase JHDM2A is critical for Tnp1 and Prm1 transcription and spermatogenesis. <i>Nature</i> , 2007, 450, 119-123.	13.7	350
57	Maternal H3K27me3 controls DNA methylation-independent imprinting. <i>Nature</i> , 2017, 547, 419-424.	13.7	349
58	Genetic and Epigenetic Variations in iPSCs: Potential Causes and Implications for Application. <i>Cell Stem Cell</i> , 2013, 13, 149-159.	5.2	326
59	The Histone H3K79 Methyltransferase Dot1L Is Essential for Mammalian Development and Heterochromatin Structure. <i>PLoS Genetics</i> , 2008, 4, e1000190.	1.5	317
60	Generation of Insulin-secreting Islet-like Clusters from Human Skin Fibroblasts. <i>Journal of Biological Chemistry</i> , 2008, 283, 31601-31607.	1.6	313
61	Cancer mediates effector T cell dysfunction by targeting microRNAs and EZH2 via glycolysis restriction. <i>Nature Immunology</i> , 2016, 17, 95-103.	7.0	310
62	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. <i>Nature</i> , 2015, 528, 142-146.	13.7	303
63	mAM Facilitates Conversion by ESET of Dimethyl to Trimethyl Lysine 9 of Histone H3 to Cause Transcriptional Repression. <i>Molecular Cell</i> , 2003, 12, 475-487.	4.5	300
64	Purification and Functional Characterization of SET8, a Nucleosomal Histone H4-Lysine 20-Specific Methyltransferase. <i>Current Biology</i> , 2002, 12, 1086-1099.	1.8	299
65	pRB family proteins are required for H3K27 trimethylation and Polycomb repression complexes binding to and silencing p16INK4a tumor suppressor gene. <i>Genes and Development</i> , 2007, 21, 49-54.	2.7	292
66	Kdm2b maintains murine embryonic stem cell status by recruiting PRC1 complex to CpG islands of developmental genes. <i>Nature Cell Biology</i> , 2013, 15, 373-384.	4.6	292
67	Mechanism and Function of Oxidative Reversal of DNA and RNA Methylation. <i>Annual Review of Biochemistry</i> , 2014, 83, 585-614.	5.0	289
68	The H3K36 demethylase Jhdm1b/Kdm2b regulates cell proliferation and senescence through p15Ink4b. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1169-1175.	3.6	287
69	AID/APOBEC deaminases disfavor modified cytosines implicated in DNA demethylation. <i>Nature Chemical Biology</i> , 2012, 8, 751-758.	3.9	274
70	SAP30, a Novel Protein Conserved between Human and Yeast, Is a Component of a Histone Deacetylase Complex. <i>Molecular Cell</i> , 1998, 1, 1021-1031.	4.5	268
71	A role for the elongator complex in zygotic paternal genome demethylation. <i>Nature</i> , 2010, 463, 554-558.	13.7	258
72	Tet1 controls meiosis by regulating meiotic gene expression. <i>Nature</i> , 2012, 492, 443-447.	13.7	255

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73	Establishing Chromatin Regulatory Landscape during Mouse Preimplantation Development. <i>Cell</i> , 2016, 165, 1375-1388.	13.5	254
74	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, 13956-13961.	3.3	248
75	Generation and replication-dependent dilution of 5fC and 5caC during mouse preimplantation development. <i>Cell Research</i> , 2011, 21, 1670-1676.	5.7	244
76	DOT1L, the H3K79 methyltransferase, is required for MLL-AF9-mediated leukemogenesis. <i>Blood</i> , 2011, 117, 6912-6922.	0.6	234
77	Molecular cloning of ESET, a novel histone H3-specific methyltransferase that interacts with ERG transcription factor. <i>Oncogene</i> , 2002, 21, 148-152.	2.6	228
78	Role of Tet proteins in enhancer activity and telomere elongation. <i>Genes and Development</i> , 2014, 28, 2103-2119.	2.7	226
79	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, 52812-52815.	1.6	221
80	NAT, a Human Complex Containing Srb Polypeptides that Functions as a Negative Regulator of Activated Transcription. <i>Molecular Cell</i> , 1998, 2, 213-222.	4.5	210
81	Somatic Cell Nuclear Transfer Reprogramming: Mechanisms and Applications. <i>Cell Stem Cell</i> , 2018, 23, 471-485.	5.2	207
82	Mechanisms of epigenetic inheritance. <i>Current Opinion in Cell Biology</i> , 2007, 19, 266-272.	2.6	199
83	Role of Tet1 in erasure of genomic imprinting. <i>Nature</i> , 2013, 504, 460-464.	13.7	199
84	Structure of a Bmi-1-Ring1B Polycomb Group Ubiquitin Ligase Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 20643-20649.	1.6	197
85	KDM2b/JHDM1b, an H3K36me2-specific demethylase, is required for initiation and maintenance of acute myeloid leukemia. <i>Blood</i> , 2011, 117, 3869-3880.	0.6	195
86	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.	5.2	191
87	Role of Mammalian DNA Methyltransferases in Development. <i>Annual Review of Biochemistry</i> , 2020, 89, 135-158.	5.0	182
88	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, 2918-2932.	1.1	177
89	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, 1639-1643.	1.8	169
90	Leukaemic transformation by CALM-AF10 involves upregulation of Hoxa5 by hDOT1L. <i>Nature Cell Biology</i> , 2006, 8, 1017-1024.	4.6	166

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91	Kdm2b promotes induced pluripotent stem cell generation by facilitating gene activation early in reprogramming. <i>Nature Cell Biology</i> , 2012, 14, 457-466.	4.6	166
92	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, 7120-7125.	3.3	165
93	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.	5.2	158
94	Role of hPHF1 in H3K27 Methylation and Hox Gene Silencing. <i>Molecular and Cellular Biology</i> , 2008, 28, 1862-1872.	1.1	157
95	Embryonic stem cell and induced pluripotent stem cell: an epigenetic perspective. <i>Cell Research</i> , 2013, 23, 49-69.	5.7	152
96	Dynamics of 5-methylcytosine and 5-hydroxymethylcytosine during germ cell reprogramming. <i>Cell Research</i> , 2013, 23, 329-339.	5.7	152
97	A modular network model of aging. <i>Molecular Systems Biology</i> , 2007, 3, 147.	3.2	151
98	An Extensive Network of TET2-Targeting MicroRNAs Regulates Malignant Hematopoiesis. <i>Cell Reports</i> , 2013, 5, 471-481.	2.9	139
99	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. <i>Nature Biotechnology</i> , 2014, 32, 1231-1240.	9.4	139
100	Loss of DUX causes minor defects in zygotic genome activation and is compatible with mouse development. <i>Nature Genetics</i> , 2019, 51, 947-951.	9.4	138
101	Nucleosome assembly is required for nuclear pore complex assembly in mouse zygotes. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 609-616.	3.6	137
102	Histone H3K27me3 demethylases KDM6A and KDM6B modulate definitive endoderm differentiation from human ESCs by regulating WNT signaling pathway. <i>Cell Research</i> , 2013, 23, 122-130.	5.7	134
103	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, 7374-7383.	1.6	130
104	DOT1L regulates dystrophin expression and is critical for cardiac function. <i>Genes and Development</i> , 2011, 25, 263-274.	2.7	129
105	The lncRNA DEANR1 Facilitates Human Endoderm Differentiation by Activating FOXA2 Expression. <i>Cell Reports</i> , 2015, 11, 137-148.	2.9	127
106	5-Hydroxymethylcytosine: generation, fate, and genomic distribution. <i>Current Opinion in Cell Biology</i> , 2013, 25, 289-296.	2.6	126
107	Butyrate Promotes Induced Pluripotent Stem Cell Generation. <i>Journal of Biological Chemistry</i> , 2010, 285, 25516-25521.	1.6	123
108	Tet1 and 5-hydroxymethylation. <i>Cell Cycle</i> , 2011, 10, 2428-2436.	1.3	121

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109	eccDNAs are apoptotic products with high innate immunostimulatory activity. <i>Nature</i> , 2021, 599, 308-314.	13.7	121
110	Role of H3K27 methylation in the regulation of lncRNA expression. <i>Cell Research</i> , 2010, 20, 1109-1116.	5.7	120
111	Genomic imprinting of <i>Xist</i> by maternal H3K27me3. <i>Genes and Development</i> , 2017, 31, 1927-1932.	2.7	118
112	Cyclin-dependent Kinase 1 (CDK1)-mediated Phosphorylation of Enhancer of Zeste 2 (Ezh2) Regulates Its Stability. <i>Journal of Biological Chemistry</i> , 2011, 286, 28511-28519.	1.6	117
113	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, 3907-3917.	1.2	111
114	Yeast Jhd2p is a histone H3 Lys4 trimethyl demethylase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 243-245.	3.6	111
115	Cell cycle and p53 gate the direct conversion of human fibroblasts to dopaminergic neurons. <i>Nature Communications</i> , 2015, 6, 10100.	5.8	108
116	Loss of H3K27me3 Imprinting in Somatic Cell Nuclear Transfer Embryos Disrupts Post-Implantation Development. <i>Cell Stem Cell</i> , 2018, 23, 343-354.e5.	5.2	105
117	The trithorax-group protein Lid is a histone H3 trimethyl-Lys4 demethylase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 341-343.	3.6	100
118	Cell type-specific transcriptional programs in mouse prefrontal cortex during adolescence and addiction. <i>Nature Communications</i> , 2019, 10, 4169.	5.8	100
119	The histone methyltransferase Set7/9 promotes myoblast differentiation and myofibril assembly. <i>Journal of Cell Biology</i> , 2011, 194, 551-565.	2.3	99
120	JmjC enzyme KDM2A is a regulator of rRNA transcription in response to starvation. <i>EMBO Journal</i> , 2010, 29, 1510-1522.	3.5	98
121	Maternal <i>Eed</i> knockout causes loss of H3K27me3 imprinting and random X inactivation in the extraembryonic cells. <i>Genes and Development</i> , 2018, 32, 1525-1536.	2.7	93
122	Regulation of TET Protein Stability by Calpains. <i>Cell Reports</i> , 2014, 6, 278-284.	2.9	92
123	Substrate Preferences of the EZH2 Histone Methyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 8365-8370.	1.6	91
124	Decoding molecular and cellular heterogeneity of mouse nucleus accumbens. <i>Nature Neuroscience</i> , 2021, 24, 1757-1771.	7.1	87
125	Allelic H3K27me3 to allelic DNA methylation switch maintains noncanonical imprinting in extraembryonic cells. <i>Science Advances</i> , 2019, 5, eaay7246.	4.7	83
126	Distinct dynamics and functions of H2AK119ub1 and H3K27me3 in mouse preimplantation embryos. <i>Nature Genetics</i> , 2021, 53, 551-563.	9.4	83



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127	Myc and Dnmt1 impede the pluripotent to totipotent state transition in embryonic stem cells. <i>Nature Cell Biology</i> , 2019, 21, 835-844.	4.6	82
128	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, 3951-3961.	1.1	79
129	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, 1912-1917.	3.3	76
130	Validation-based insertional mutagenesis identifies lysine demethylase FBXL11 as a negative regulator of NF $\kappa$ B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16339-16344.	3.3	74
131	Inhibition of Excess Nodal Signaling During Mouse Gastrulation by the Transcriptional Corepressor DRAP1. <i>Science</i> , 2002, 298, 1996-1999.	6.0	73
132	Histone Demethylase JHDM2A Is Involved in Male Infertility and Obesity. <i>Journal of Andrology</i> , 2010, 31, 75-78.	2.0	73
133	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, 1274-1282.	0.6	70
134	Identification and Functional Characterization of the p66/p68 Components of the MeCP1 Complex. <i>Molecular and Cellular Biology</i> , 2002, 22, 536-546.	1.1	69
135	The H3K4 Demethylase Lid Associates with and Inhibits Histone Deacetylase Rpd3. <i>Molecular and Cellular Biology</i> , 2009, 29, 1401-1410.	1.1	68
136	Cell totipotency: molecular features, induction, and maintenance. <i>National Science Review</i> , 2015, 2, 217-225.	4.6	66
137	AOF1 is a histone H3K4 demethylase possessing demethylase activity-independent repression function. <i>Cell Research</i> , 2010, 20, 276-287.	5.7	62
138	Charting oxidized methylcytosines at base resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 656-661.	3.6	62
139	A rapid and versatile tool for genomic engineering in <i>Lactococcus lactis</i> . <i>Microbial Cell Factories</i> , 2019, 18, 22.	1.9	62
140	Global reduction of the epigenetic H3K79 methylation mark and increased chromosomal instability in CALM-AF10 $\Delta$ positive leukemias. <i>Blood</i> , 2009, 114, 651-658.	0.6	59
141	Genome-Wide uH2A Localization Analysis Highlights Bmi1-Dependent Deposition of the Mark at Repressed Genes. <i>PLoS Genetics</i> , 2009, 5, e1000506.	1.5	58
142	Essential role of DOT1L in maintaining normal adult hematopoiesis. <i>Cell Research</i> , 2011, 21, 1370-1373.	5.7	58
143	Dynamic Regulation of Histone H3 Methylated at Lysine 79 within a Tissue-specific Chromatin Domain. <i>Journal of Biological Chemistry</i> , 2003, 278, 18346-18352.	1.6	57
144	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, 13825-13833.	1.6	56

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145	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, 18130-18141.	1.6	53
146	Maternal H3K27me3-dependent autosomal and X chromosome imprinting. <i>Nature Reviews Genetics</i> , 2020, 21, 555-571.	7.7	53
147	Profiling and functional characterization of maternal mRNA translation during mouse maternal-to-zygotic transition. <i>Science Advances</i> , 2022, 8, eabj3967.	4.7	52
148	WNT3 Is a Biomarker Capable of Predicting the Definitive Endoderm Differentiation Potential of hESCs. <i>Stem Cell Reports</i> , 2013, 1, 46-52.	2.3	50
149	A universal competitive fluorescence polarization activity assay for S-adenosylmethionine utilizing methyltransferases. <i>Analytical Biochemistry</i> , 2008, 373, 296-306.	1.1	48
150	Mechanisms of epigenetic memory and addiction. <i>EMBO Journal</i> , 2014, 33, 1091-1103.	3.5	48
151	Maternal-biased H3K27me3 correlates with paternal-specific gene expression in the human morula. <i>Genes and Development</i> , 2019, 33, 382-387.	2.7	47
152	Transcriptional activation of transposable elements in mouse zygotes is independent of Tet3-mediated 5-methylcytosine oxidation. <i>Cell Research</i> , 2012, 22, 1640-1649.	5.7	45
153	Double Nicking by RNA-Guided CRISPR Cas9 for Enhanced Genome Editing Specificity. <i>Cell</i> , 2013, 155, 479-480.	13.5	45
154	lbbkap/Elp1 Deficiency Causes Male Infertility by Disrupting Meiotic Progression. <i>PLoS Genetics</i> , 2013, 9, e1003516.	1.5	45
155	Simultaneous mapping of active DNA demethylation and sister chromatid exchange in single cells. <i>Genes and Development</i> , 2017, 31, 511-523.	2.7	45
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