

Yi Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3731036/publications.pdf>

Version: 2024-02-01

211
papers

64,275
citations

1238

110
h-index

1755

212
g-index

223
all docs

223
docs citations

223
times ranked

53813
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of Histone H3 Lysine 27 Methylation in Polycomb-Group Silencing. <i>Science</i> , 2002, 298, 1039-1043.	12.6	3,294
2	Tet Proteins Can Convert 5-Methylcytosine to 5-Formylcytosine and 5-Carboxylcytosine. <i>Science</i> , 2011, 333, 1300-1303.	12.6	2,898
3	Double Nicking by RNA-Guided CRISPR Cas9 for Enhanced Genome Editing Specificity. <i>Cell</i> , 2013, 154, 1380-1389.	28.9	2,862
4	Oncometabolite 2-Hydroxyglutarate Is a Competitive Inhibitor of α -Ketoglutarate-Dependent Dioxygenases. <i>Cancer Cell</i> , 2011, 19, 17-30.	16.8	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.	27.8	2,224
6	Histone demethylation by a family of JmjC domain-containing proteins. <i>Nature</i> , 2006, 439, 811-816.	27.8	1,846
7	The diverse functions of histone lysine methylation. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 838-849.	37.0	1,781
8	Role of histone H2A ubiquitination in Polycomb silencing. <i>Nature</i> , 2004, 431, 873-878.	27.8	1,502
9	TET enzymes, TDG and the dynamics of DNA demethylation. <i>Nature</i> , 2013, 502, 472-479.	27.8	1,323
10	TET-mediated active DNA demethylation: mechanism, function and beyond. <i>Nature Reviews Genetics</i> , 2017, 18, 517-534.	16.3	1,109
11	Role of Histone H3 Lysine 27 Methylation in X Inactivation. <i>Science</i> , 2003, 300, 131-135.	12.6	1,098
12	JmjC-domain-containing proteins and histone demethylation. <i>Nature Reviews Genetics</i> , 2006, 7, 715-727.	16.3	1,096
13	Active DNA demethylation: many roads lead to Rome. <i>Nature Reviews Molecular Cell Biology</i> , 2010, 11, 607-620.	37.0	937
14	Reversing DNA Methylation: Mechanisms, Genomics, and Biological Functions. <i>Cell</i> , 2014, 156, 45-68.	28.9	914
15	New Nomenclature for Chromatin-Modifying Enzymes. <i>Cell</i> , 2007, 131, 633-636.	28.9	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.	3.3	795
17	MBD2 is a transcriptional repressor belonging to the MeCP1 histone deacetylase complex. <i>Nature Genetics</i> , 1999, 23, 58-61.	21.4	783
18	Role of Bmi-1 and Ring1A in H2A Ubiquitylation and Hox Gene Silencing. <i>Molecular Cell</i> , 2005, 20, 845-854.	9.7	766

#	ARTICLE	IF	CITATIONS
19	Regulation of histone methylation by demethylination and demethylation. Nature Reviews Molecular Cell Biology, 2007, 8, 307-318.	37.0	764
20	Methylation of H3-Lysine 79 Is Mediated by a New Family of HMTases without a SET Domain. Current Biology, 2002, 12, 1052-1058.	3.9	748
21	The Dermatomyositis-Specific Autoantigen Mi2 Is a Component of a Complex Containing Histone Deacetylase and Nucleosome Remodeling Activities. Cell, 1998, 95, 279-289.	28.9	745
22	hDOT1L Links Histone Methylation to Leukemogenesis. Cell, 2005, 121, 167-178.	28.9	737
23	JHDM2A, a JmjC-Containing H3K9 Demethylase, Facilitates Transcription Activation by Androgen Receptor. Cell, 2006, 125, 483-495.	28.9	737
24	SUZ12 Is Required for Both the Histone Methyltransferase Activity and the Silencing Function of the EED-EZH2 Complex. Molecular Cell, 2004, 15, 57-67.	9.7	733
25	DNA Methylation in Mammals. Cold Spring Harbor Perspectives in Biology, 2014, 6, a019133-a019133.	5.5	717
26	Methylation of Histone H4 at Arginine 3 Facilitating Transcriptional Activation by Nuclear Hormone Receptor. Science, 2001, 293, 853-857.	12.6	673
27	Lysine Glutarylation Is a Protein Posttranslational Modification Regulated by SIRT5. Cell Metabolism, 2014, 19, 605-617.	16.2	647
28	The First Identification of Lysine Malonylation Substrates and Its Regulatory Enzyme. Molecular and Cellular Proteomics, 2011, 10, M111.012658.	3.8	598
29	C9a-mediated irreversible epigenetic inactivation of Oct-3/4 during early embryogenesis. Nature Cell Biology, 2006, 8, 188-194.	10.3	581
30	Dual functions of Tet1 in transcriptional regulation in mouse embryonic stem cells. Nature, 2011, 473, 389-393.	27.8	581
31	Structural basis for specific binding of Polycomb chromodomain to histone H3 methylated at Lys 27. Genes and Development, 2003, 17, 1823-1828.	5.9	567
32	Mechanisms and functions of Tet protein-mediated 5-methylcytosine oxidation. Genes and Development, 2011, 25, 2436-2452.	5.9	565
33	The transcriptional repressor JHDM3A demethylates trimethyl histone H3 lysine 9 and lysine 36. Nature, 2006, 442, 312-316.	27.8	563
34	Histone Deacetylases and SAP18, a Novel Polypeptide, Are Components of a Human Sin3 Complex. Cell, 1997, 89, 357-364.	28.9	548
35	Dnmt3a-Dependent Nonpromoter DNA Methylation Facilitates Transcription of Neurogenic Genes. Science, 2010, 329, 444-448.	12.6	544
36	Hierarchical Recruitment of Polycomb Group Silencing Complexes. Molecular Cell, 2004, 14, 637-646.	9.7	513

#	ARTICLE	IF	CITATIONS
37	The diverse functions of Dot1 and H3K79 methylation. <i>Genes and Development</i> , 2011, 25, 1345-1358.	5.9	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.	9.7	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.	5.9	488
40	Purification and Functional Characterization of a Histone H3-Lysine 4-Specific Methyltransferase. <i>Molecular Cell</i> , 2001, 8, 1207-1217.	9.7	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.	5.9	471
42	Single-Cell RNA-Seq Reveals Hypothalamic Cell Diversity. <i>Cell Reports</i> , 2017, 18, 3227-3241.	6.4	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.	9.7	447
44	Genome-wide Analysis Reveals TET- and TDG-Dependent 5-Methylcytosine Oxidation Dynamics. <i>Cell</i> , 2013, 153, 692-706.	28.9	440
45	Tudor, MBT and chromo domains gauge the degree of lysine methylation. <i>EMBO Reports</i> , 2006, 7, 397-403.	4.5	438
46	Replication-Dependent Loss of 5-Hydroxymethylcytosine in Mouse Preimplantation Embryos. <i>Science</i> , 2011, 334, 194-194.	12.6	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.	9.7	431
48	Recognition of Histone H3 Lysine-4 Methylation by the Double Tudor Domain of JMJD2A. <i>Science</i> , 2006, 312, 748-751.	12.6	406
49	Role of Jhdm2a in regulating metabolic gene expression and obesity resistance. <i>Nature</i> , 2009, 458, 757-761.	27.8	402
50	The Retinoblastoma Binding Protein RBP2 Is an H3K4 Demethylase. <i>Cell</i> , 2007, 128, 889-900.	28.9	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.	21.4	386
52	Embryonic Development following Somatic Cell Nuclear Transfer Impeded by Persisting Histone Methylation. <i>Cell</i> , 2014, 159, 884-895.	28.9	382
53	Transcriptional regulation by histone ubiquitination and deubiquitination. <i>Genes and Development</i> , 2003, 17, 2733-2740.	5.9	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.	3.4	365

#	ARTICLE	IF	CITATIONS
55	Structure of the Catalytic Domain of Human DOT1L, a Non-SET Domain Nucleosomal Histone Methyltransferase. <i>Cell</i> , 2003, 112, 711-723.	28.9	363
56	Histone demethylase JHDM2A is critical for Tnp1 and Prm1 transcription and spermatogenesis. <i>Nature</i> , 2007, 450, 119-123.	27.8	350
57	Maternal H3K27me3 controls DNA methylation-independent imprinting. <i>Nature</i> , 2017, 547, 419-424.	27.8	349
58	Genetic and Epigenetic Variations in iPSCs: Potential Causes and Implications for Application. <i>Cell Stem Cell</i> , 2013, 13, 149-159.	11.1	326
59	The Histone H3K79 Methyltransferase Dot1L Is Essential for Mammalian Development and Heterochromatin Structure. <i>PLoS Genetics</i> , 2008, 4, e1000190.	3.5	317
60	Generation of Insulin-secreting Islet-like Clusters from Human Skin Fibroblasts. <i>Journal of Biological Chemistry</i> , 2008, 283, 31601-31607.	3.4	313
61	Cancer mediates effector T cell dysfunction by targeting microRNAs and EZH2 via glycolysis restriction. <i>Nature Immunology</i> , 2016, 17, 95-103.	14.5	310
62	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. <i>Nature</i> , 2015, 528, 142-146.	27.8	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.	9.7	300
64	Purification and Functional Characterization of SET8, a Nucleosomal Histone H4-Lysine 20-Specific Methyltransferase. <i>Current Biology</i> , 2002, 12, 1086-1099.	3.9	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.	5.9	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.	10.3	292
67	Mechanism and Function of Oxidative Reversal of DNA and RNA Methylation. <i>Annual Review of Biochemistry</i> , 2014, 83, 585-614.	11.1	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.	8.2	287
69	AID/APOBEC deaminases disfavor modified cytosines implicated in DNA demethylation. <i>Nature Chemical Biology</i> , 2012, 8, 751-758.	8.0	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.	9.7	268
71	A role for the elongator complex in zygotic paternal genome demethylation. <i>Nature</i> , 2010, 463, 554-558.	27.8	258
72	Tet1 controls meiosis by regulating meiotic gene expression. <i>Nature</i> , 2012, 492, 443-447.	27.8	255

#	ARTICLE	IF	CITATIONS
73	Establishing Chromatin Regulatory Landscape during Mouse Preimplantation Development. <i>Cell</i> , 2016, 165, 1375-1388.	28.9	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.	7.1	248
75	Generation and replication-dependent dilution of 5fC and 5caC during mouse preimplantation development. <i>Cell Research</i> , 2011, 21, 1670-1676.	12.0	244
76	DOT1L, the H3K79 methyltransferase, is required for MLL-AF9-mediated leukemogenesis. <i>Blood</i> , 2011, 117, 6912-6922.	1.4	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.	5.9	228
78	Role of Tet proteins in enhancer activity and telomere elongation. <i>Genes and Development</i> , 2014, 28, 2103-2119.	5.9	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.	3.4	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.	9.7	210
81	Somatic Cell Nuclear Transfer Reprogramming: Mechanisms and Applications. <i>Cell Stem Cell</i> , 2018, 23, 471-485.	11.1	207
82	Mechanisms of epigenetic inheritance. <i>Current Opinion in Cell Biology</i> , 2007, 19, 266-272.	5.4	199
83	Role of Tet1 in erasure of genomic imprinting. <i>Nature</i> , 2013, 504, 460-464.	27.8	199
84	Structure of a Bmi-1-Ring1B Polycomb Group Ubiquitin Ligase Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 20643-20649.	3.4	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.	1.4	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.	11.1	191
87	Role of Mammalian DNA Methyltransferases in Development. <i>Annual Review of Biochemistry</i> , 2020, 89, 135-158.	11.1	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.	2.3	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.	3.9	169
90	Leukaemic transformation by CALM-AF10 involves upregulation of Hoxa5 by hDOT1L. <i>Nature Cell Biology</i> , 2006, 8, 1017-1024.	10.3	166

#	ARTICLE	IF	CITATIONS
91	Kdm2b promotes induced pluripotent stem cell generation by facilitating gene activation early in reprogramming. <i>Nature Cell Biology</i> , 2012, 14, 457-466.	10.3	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.	7.1	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.	11.1	158
94	Role of hPHF1 in H3K27 Methylation and Hox Gene Silencing. <i>Molecular and Cellular Biology</i> , 2008, 28, 1862-1872.	2.3	157
95	Embryonic stem cell and induced pluripotent stem cell: an epigenetic perspective. <i>Cell Research</i> , 2013, 23, 49-69.	12.0	152
96	Dynamics of 5-methylcytosine and 5-hydroxymethylcytosine during germ cell reprogramming. <i>Cell Research</i> , 2013, 23, 329-339.	12.0	152
97	A modular network model of aging. <i>Molecular Systems Biology</i> , 2007, 3, 147.	7.2	151
98	An Extensive Network of TET2-Targeting MicroRNAs Regulates Malignant Hematopoiesis. <i>Cell Reports</i> , 2013, 5, 471-481.	6.4	139
99	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. <i>Nature Biotechnology</i> , 2014, 32, 1231-1240.	17.5	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.	21.4	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.	8.2	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.	12.0	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.	3.4	130
104	DOT1L regulates dystrophin expression and is critical for cardiac function. <i>Genes and Development</i> , 2011, 25, 263-274.	5.9	129
105	The lncRNA DEANR1 Facilitates Human Endoderm Differentiation by Activating FOXA2 Expression. <i>Cell Reports</i> , 2015, 11, 137-148.	6.4	127
106	5-Hydroxymethylcytosine: generation, fate, and genomic distribution. <i>Current Opinion in Cell Biology</i> , 2013, 25, 289-296.	5.4	126
107	Butyrate Promotes Induced Pluripotent Stem Cell Generation. <i>Journal of Biological Chemistry</i> , 2010, 285, 25516-25521.	3.4	123
108	Tet1 and 5-hydroxymethylation. <i>Cell Cycle</i> , 2011, 10, 2428-2436.	2.6	121

#	ARTICLE	IF	CITATIONS
109	eccDNAs are apoptotic products with high innate immunostimulatory activity. <i>Nature</i> , 2021, 599, 308-314.	27.8	121
110	Role of H3K27 methylation in the regulation of lncRNA expression. <i>Cell Research</i> , 2010, 20, 1109-1116.	12.0	120
111	Genomic imprinting of <i>Xist</i> by maternal H3K27me3. <i>Genes and Development</i> , 2017, 31, 1927-1932.	5.9	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.	3.4	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.	2.5	111
114	Yeast Jhd2p is a histone H3 Lys4 trimethyl demethylase. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 243-245.	8.2	111
115	Cell cycle and p53 gate the direct conversion of human fibroblasts to dopaminergic neurons. <i>Nature Communications</i> , 2015, 6, 10100.	12.8	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.	11.1	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.	8.2	100
118	Cell type-specific transcriptional programs in mouse prefrontal cortex during adolescence and addiction. <i>Nature Communications</i> , 2019, 10, 4169.	12.8	100
119	The histone methyltransferase Set7/9 promotes myoblast differentiation and myofibril assembly. <i>Journal of Cell Biology</i> , 2011, 194, 551-565.	5.2	99
120	JmjC enzyme KDM2A is a regulator of rRNA transcription in response to starvation. <i>EMBO Journal</i> , 2010, 29, 1510-1522.	7.8	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.	5.9	93
122	Regulation of TET Protein Stability by Calpains. <i>Cell Reports</i> , 2014, 6, 278-284.	6.4	92
123	Substrate Preferences of the EZH2 Histone Methyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 8365-8370.	3.4	91
124	Decoding molecular and cellular heterogeneity of mouse nucleus accumbens. <i>Nature Neuroscience</i> , 2021, 24, 1757-1771.	14.8	87
125	Allelic H3K27me3 to allelic DNA methylation switch maintains noncanonical imprinting in extraembryonic cells. <i>Science Advances</i> , 2019, 5, eaay7246.	10.3	83
126	Distinct dynamics and functions of H2AK119ub1 and H3K27me3 in mouse preimplantation embryos. <i>Nature Genetics</i> , 2021, 53, 551-563.	21.4	83

#	ARTICLE	IF	CITATIONS
127	Myc and Dnmt1 impede the pluripotent to totipotent state transition in embryonic stem cells. <i>Nature Cell Biology</i> , 2019, 21, 835-844.	10.3	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.	2.3	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.	7.1	76
130	Validation-based insertional mutagenesis identifies lysine demethylase FBXL11 as a negative regulator of NF- κ B. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16339-16344.	7.1	74
131	Inhibition of Excess Nodal Signaling During Mouse Gastrulation by the Transcriptional Corepressor DRAP1. <i>Science</i> , 2002, 298, 1996-1999.	12.6	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.	1.4	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.	2.3	69
135	The H3K4 Demethylase Lid Associates with and Inhibits Histone Deacetylase Rpd3. <i>Molecular and Cellular Biology</i> , 2009, 29, 1401-1410.	2.3	68
136	Cell totipotency: molecular features, induction, and maintenance. <i>National Science Review</i> , 2015, 2, 217-225.	9.5	66
137	AOF1 is a histone H3K4 demethylase possessing demethylase activity-independent repression function. <i>Cell Research</i> , 2010, 20, 276-287.	12.0	62
138	Charting oxidized methylcytosines at base resolution. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 656-661.	8.2	62
139	A rapid and versatile tool for genomic engineering in <i>Lactococcus lactis</i> . <i>Microbial Cell Factories</i> , 2019, 18, 22.	4.0	62
140	Global reduction of the epigenetic H3K79 methylation mark and increased chromosomal instability in CALM-AF10 α -positive leukemias. <i>Blood</i> , 2009, 114, 651-658.	1.4	59
141	Genome-Wide uH2A Localization Analysis Highlights Bmi1-Dependent Deposition of the Mark at Repressed Genes. <i>PLoS Genetics</i> , 2009, 5, e1000506.	3.5	58
142	Essential role of DOT1L in maintaining normal adult hematopoiesis. <i>Cell Research</i> , 2011, 21, 1370-1373.	12.0	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.	3.4	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.	3.4	56

#	ARTICLE	IF	CITATIONS
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.	3.4	53
146	Maternal H3K27me3-dependent autosomal and X chromosome imprinting. <i>Nature Reviews Genetics</i> , 2020, 21, 555-571.	16.3	53
147	Profiling and functional characterization of maternal mRNA translation during mouse maternal-to-zygotic transition. <i>Science Advances</i> , 2022, 8, eabj3967.	10.3	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.	4.8	50
149	A universal competitive fluorescence polarization activity assay for S-adenosylmethionine utilizing methyltransferases. <i>Analytical Biochemistry</i> , 2008, 373, 296-306.	2.4	48
150	Mechanisms of epigenetic memory and addiction. <i>EMBO Journal</i> , 2014, 33, 1091-1103.	7.8	48
151	Maternal-biased H3K27me3 correlates with paternal-specific gene expression in the human morula. <i>Genes and Development</i> , 2019, 33, 382-387.	5.9	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.	12.0	45
153	Double Nicking by RNA-Guided CRISPR Cas9 for Enhanced Genome Editing Specificity. <i>Cell</i> , 2013, 155, 479-480.	28.9	45
154	lbbkap/Elp1 Deficiency Causes Male Infertility by Disrupting Meiotic Progression. <i>PLoS Genetics</i> , 2013, 9, e1003516.	3.5	45
155	Simultaneous mapping of active DNA demethylation and sister chromatid exchange in single cells. <i>Genes and Development</i> , 2017, 31, 511-523.	5.9	45
156	Cold-inducible RNA-binding protein CIRP/hnRNP A18 regulates telomerase activity in a temperature-dependent manner. <i>Nucleic Acids Research</i> , 2016, 44, 761-775.	14.5	44
157	A transcriptional roadmap for 2C-like "to" pluripotent state transition. <i>Science Advances</i> , 2020, 6, eaay5181.	10.3	44
158	Minireview: Role of Protein Methylation and Demethylation in Nuclear Hormone Signaling. <i>Molecular Endocrinology</i> , 2009, 23, 1323-1334.	3.7	41
159	Haploinsufficiency, but Not Defective Paternal 5mC Oxidation, Accounts for the Developmental Defects of Maternal Tet3 Knockouts. <i>Cell Reports</i> , 2015, 10, 463-470.	6.4	38
160	A novel antiviral lncRNA, EDAL, shields a T309 O-GlcNAcylation site to promote EZH2 lysosomal degradation. <i>Genome Biology</i> , 2020, 21, 228.	8.8	38
161	Enzymatic Analysis of Tet Proteins: Key Enzymes in the Metabolism of DNA Methylation. <i>Methods in Enzymology</i> , 2012, 512, 93-105.	1.0	37
162	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.	6.4	37

#	ARTICLE	IF	CITATIONS
163	The Role of N-lysine acetyltransferase 10 Protein in DNA Methylation and Genomic Imprinting. <i>Molecular Cell</i> , 2017, 68, 89-103.e7.	9.7	36
164	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. <i>Cell Reports</i> , 2017, 21, 455-466.	6.4	36
165	Cloning and characterization of extended hammerheads from a diverse set of caudate amphibians. <i>Gene</i> , 1996, 172, 183-190.	2.2	34
166	It takes a PHD to interpret histone methylation. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 572-574.	8.2	34
167	Two-phase differential expression analysis for single cell RNA-seq. <i>Bioinformatics</i> , 2018, 34, 3340-3348.	4.1	34
168	The <i>Saccharomyces cerevisiae</i> Histone Demethylase Jhd1 Fine-Tunes the Distribution of H3K36me2. <i>Molecular and Cellular Biology</i> , 2007, 27, 5055-5065.	2.3	32
169	Histone methyltransferase and histone methylation in inflammatory T-cell responses. <i>Immunotherapy</i> , 2013, 5, 989-1004.	2.0	32
170	Epigenetic regulation of mouse preimplantation embryo development. <i>Current Opinion in Genetics and Development</i> , 2020, 64, 13-20.	3.3	32
171	Hsp90 inhibition destabilizes Ezh2 protein in alloreactive T cells and reduces graft-versus-host disease in mice. <i>Blood</i> , 2017, 129, 2737-2748.	1.4	31
172	Purification of histone demethylases from HeLa cells. <i>Methods</i> , 2006, 40, 318-326.	3.8	30
173	Base-resolution profiling of active DNA demethylation using MAB-seq and caMAB-seq. <i>Nature Protocols</i> , 2016, 11, 1081-1100.	12.0	30
174	Reprogramming of Chromatin Accessibility in Somatic Cell Nuclear Transfer Is DNA Replication Independent. <i>Cell Reports</i> , 2018, 23, 1939-1947.	6.4	30
175	KDM3A histone demethylase functions as an essential factor for activation of JAK2-STAT3 signaling pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11766-11771.	7.1	29
176	Purification of Histone Methyltransferases from HeLa Cells. <i>Methods in Enzymology</i> , 2003, 377, 213-226.	1.0	28
177	Developmental regulation of Suz12 localization. <i>Chromosoma</i> , 2005, 114, 183-192.	2.2	28
178	MTA2/NuRD Regulates B Cell Development and Cooperates with OCA-B in Controlling the Pre-B to Immature B Cell Transition. <i>Cell Reports</i> , 2019, 28, 472-485.e5.	6.4	28
179	Aberrant Upregulation of 14-3-3 σ and EZH2 Expression Serves as an Inferior Prognostic Biomarker for Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2014, 9, e107251.	2.5	27
180	Transcription of satellite 2 DNA from the newt is driven by a snRNA type of promoter. <i>Nucleic Acids Research</i> , 1994, 22, 4697-4704.	14.5	26

#	ARTICLE	IF	CITATIONS
181	TheC. elegansmethionine aminopeptidase 2 analogmap-2is required for germ cell proliferation. FEBS Letters, 2004, 576, 245-250.	2.8	26
182	No exception to reversibility. Nature, 2004, 431, 637-638.	27.8	23
183	The chromatin remodeler Snf2h is essential for oocyte meiotic cell cycle progression. Genes and Development, 2020, 34, 166-178.	5.9	21
184	Silencing the EZH2 gene by RNA interference reverses the drug resistance of human hepatic multidrug-resistant cancer cells to 5-Fu. Life Sciences, 2013, 92, 896-902.	4.3	20
185	RNAi-mediated EZH2 depletion decreases MDR1 expression and sensitizes multidrug-resistant hepatocellular carcinoma cells to chemotherapy. Oncology Reports, 2013, 29, 1037-1042.	2.6	19
186	AHCYL1 senses SAH to inhibit autophagy through interaction with PIK3C3 in an MTORC1-independent manner. Autophagy, 2022, 18, 309-319.	9.1	17
187	DPPA2 and DPPA4 are dispensable for mouse zygotic genome activation and pre-implantation development. Development (Cambridge), 2021, 148, .	2.5	17
188	Essential role of PR-domain protein MDS1-EVI1 in MLL-AF9 leukemia. Blood, 2013, 122, 2888-2892.	1.4	16
189	Cell type-specific mechanism of Setd1a heterozygosity in schizophrenia pathogenesis. Science Advances, 2022, 8, eabm1077.	10.3	16
190	Sp1 and ETS family transcription factors regulate the mouse Mta2 gene expression. Gene, 2001, 268, 77-85.	2.2	15
191	Identification of Motifs That Are Conserved in 12 Drosophila Species and Regulate Midline Glia vs. Neuron Expression. Genetics, 2008, 178, 787-799.	2.9	15
192	Loss of Slc38a4 imprinting is a major cause of mouse placenta hyperplasia in somatic cell nuclear transferred embryos at late gestation. Cell Reports, 2022, 38, 110407.	6.4	15
193	Hypo-CpG methylation controls PTEN expression and cell apoptosis in irradiated lung. Free Radical Research, 2016, 50, 875-886.	3.3	14
194	Telbivudine treatment corrects HBV-induced epigenetic alterations in liver cells of patients with chronic hepatitis B. Carcinogenesis, 2014, 35, 53-61.	2.8	13
195	Analysis of developmental imprinting dynamics in primates using SNP-free methods to identify imprinting defects in cloned placenta. Developmental Cell, 2021, 56, 2826-2840.e7.	7.0	12
196	Recent progress in the epigenetics and chromatin field. Cell Research, 2011, 21, 373-374.	12.0	11
197	Early Embryos Reprogram DNA Methylation in Two Steps. Cell Stem Cell, 2012, 10, 487-489.	11.1	11
198	Methylation of Histone H3K79 by Dot1L Requires Multiple Contacts with the Ubiquitinated Nucleosome. Molecular Cell, 2019, 74, 862-863.	9.7	11

#	ARTICLE	IF	CITATIONS
199	The dynamics of polycomb group proteins in early embryonic nervous system in mouse and human. International Journal of Developmental Neuroscience, 2013, 31, 487-495.	1.6	9
200	The role of the PZP domain of AF10 in acute leukemia driven by AF10 translocations. Nature Communications, 2021, 12, 4130.	12.8	8
201	Histone H3 Arg2 methylation provides alternative directions for COMPASS. Nature Structural and Molecular Biology, 2007, 14, 1058-1060.	8.2	7
202	Janus Kinase 2: An Epigenetic 'Writer' that Activates Leukemogenic Genes. Journal of Molecular Cell Biology, 2010, 2, 231-233.	3.3	7
203	Intracerebral Distribution of the Oncometabolite d-2-Hydroxyglutarate in Mice Bearing Mutant Isocitrate Dehydrogenase Brain Tumors: Implications for Tumorigenesis. Frontiers in Oncology, 2016, 6, 211.	2.8	7
204	Impaired KDM2B-mediated PRC1 recruitment to chromatin causes defective neural stem cell self-renewal and ASD/ID-like behaviors. IScience, 2022, 25, 103742.	4.1	7
205	BET-bromodomain and EZH2 inhibitor-treated chronic GVHD mice have blunted germinal centers with distinct transcriptomes. Blood, 2022, 139, 2983-2997.	1.4	6
206	Everything is E(Z): linking histone methylation to B cell development. Nature Immunology, 2003, 4, 101-103.	14.5	5
207	Mastermind Mutations Generate a Unique Constellation of Midline Cells within the Drosophila CNS. PLoS ONE, 2011, 6, e26197.	2.5	5
208	Chemical answers to epigenetic crosstalk. Nature Chemical Biology, 2008, 4, 335-337.	8.0	4
209	In vivo nuclear capture and molecular profiling identifies Gmeb1 as a transcriptional regulator essential for dopamine neuron function. Nature Communications, 2019, 10, 2508.	12.8	3
210	hDOT1L Links Histone Methylation to Leukemogenesis. Cell, 2005, 121, 809.	28.9	2
211	TARSII and CARSII: Two approaches for SNP-independent identification of germline differentially methylated regions in mammals. STAR Protocols, 2022, 3, 101240.	1.2	0