

Crosstalk among Histone Modifications

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Defining specificity of transcription factor regulatory activities. <i>Journal of Cell Science</i> , 2009, 122, 4027-4034.	2.0	22
2	From Zygote to Implantation: Morphological and Molecular Dynamics during Embryo Development in the Pig. <i>Reproduction in Domestic Animals</i> , 2009, 44, 39-49.	1.4	94
3	Histone acetyl transferases as emerging drug targets. <i>Drug Discovery Today</i> , 2009, 14, 942-948.	6.4	283
4	The dynamic epigenetic program in male germ cells: Its role in spermatogenesis, testis cancer, and its response to the environment. <i>Microscopy Research and Technique</i> , 2009, 72, 603-619.	2.2	96
5	Recent advances in understanding the structure and function of general transcription factor TFIID. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 2123-2134.	5.4	74
6	Theoretical framework for the histone modification network: modifications in the unstructured histone tails form a robust scale-free network. <i>Genes To Cells</i> , 2009, 14, 789-806.	1.2	15
7	CDK9 directs H2B monoubiquitination and controls replication-independent histone mRNA 3' end processing. <i>EMBO Reports</i> , 2009, 10, 894-900.	4.5	142
8	Insights into SAGA function during gene expression. <i>EMBO Reports</i> , 2009, 10, 843-850.	4.5	140
9	Histone Crosstalk between H3S10ph and H4K16ac Generates a Histone Code that Mediates Transcription Elongation. <i>Cell</i> , 2009, 138, 1122-1136.	28.9	360
10	Polytene chromosome squash methods for studying transcription and epigenetic chromatin modification in <i>Drosophila</i> using antibodies. <i>Methods</i> , 2009, 48, 387-397.	3.8	45
11	Comprehensive Mapping of Post-Translational Modifications on Synaptic, Nuclear, and Histone Proteins in the Adult Mouse Brain. <i>Journal of Proteome Research</i> , 2009, 8, 4966-4982.	3.7	133
12	Epigenetic changes during disease progression in a murine model of human chronic lymphocytic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13433-13438.	7.1	79
13	Reading chromatin. <i>Epigenetics</i> , 2010, 5, 573-577.	2.7	34
14	The significance, development and progress of high-throughput combinatorial histone code analysis. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 3983-4000.	5.4	90
15	The impact of histone post-translational modifications on developmental gene regulation. <i>Amino Acids</i> , 2010, 39, 1087-1105.	2.7	24
16	Application of machine learning methods to histone methylation ChIP-Seq data reveals H4R3me2 globally represses gene expression. <i>BMC Bioinformatics</i> , 2010, 11, 396.	2.6	74
17	Role of HDAC1 in senescence, aging, and cancer. <i>Experimental Gerontology</i> , 2010, 45, 279-285.	2.8	74
18	The prevalence of epigenetic mechanisms in the regulation of cognitive functions and behaviour. <i>Current Opinion in Neurobiology</i> , 2010, 20, 441-449.	4.2	35

#	ARTICLE	IF	CITATIONS
19	Posttranslational modifications of NF- κ B: Another layer of regulation for NF- κ B signaling pathway. Cellular Signalling, 2010, 22, 1282-1290.	3.6	285
20	Epigenetics to proteomics: From yeast to brain. Proteomics, 2010, 10, 749-770.	2.2	9
21	Mixed lineage leukemia: histone H3 lysine 4 methyltransferases from yeast to human. FEBS Journal, 2010, 277, 1805-1821.	4.7	53
22	KIAA1718 is a histone demethylase that erases repressive histone methyl marks. Genes To Cells, 2010, 15, 867-873.	1.2	24
23	A cathepsin L-like proteinase is involved in moulting and metamorphosis in <i>Helicoverpa armigera</i> . Insect Molecular Biology, 2010, 19, 99-111.	2.0	67
24	Enzymatic and structural insights for substrate specificity of a family of jumonji histone lysine demethylases. Nature Structural and Molecular Biology, 2010, 17, 38-43.	8.2	351
25	BRCA1 affects global DNA methylation through regulation of DNMT1. Cell Research, 2010, 20, 1201-1215.	12.0	92
26	Environmental epigenetics. Heredity, 2010, 105, 105-112.	2.6	468
27	Soft skills turned into hard facts: nucleosome remodelling at developmental switches. Heredity, 2010, 105, 71-79.	2.6	10
28	Deconstructing repression: evolving models of co-repressor action. Nature Reviews Genetics, 2010, 11, 109-123.	16.3	466
29	A case study in cross-talk: the histone lysine methyltransferases G9a and GLP. Nucleic Acids Research, 2010, 38, 3503-3511.	14.5	56
30	Novel <i>trans</i> -Tail Regulation of H2B Ubiquitylation and H3K4 Methylation by the N Terminus of Histone H2A. Molecular and Cellular Biology, 2010, 30, 3635-3645.	2.3	43
31	Nuclear Role of WASp in the Pathogenesis of Dysregulated T _H 1 Immunity in Human Wiskott-Aldrich Syndrome. Science Translational Medicine, 2010, 2, 37ra44.	12.4	109
32	PHF8 Targets Histone Methylation and RNA Polymerase II To Activate Transcription. Molecular and Cellular Biology, 2010, 30, 3286-3298.	2.3	98
33	Pitx2-dependent Occupancy by Histone Deacetylases Is Associated with T-box Gene Regulation in Mammalian Abdominal Tissue. Journal of Biological Chemistry, 2010, 285, 11129-11142.	3.4	20
34	KDM8, a H3K36me2 histone demethylase that acts in the cyclin A1 coding region to regulate cancer cell proliferation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9671-9676.	7.1	164
35	Functional Interplay between Acetylation and Methylation of the RelA Subunit of NF- κ B. Molecular and Cellular Biology, 2010, 30, 2170-2180.	2.3	115
36	Drosophila p53 Is Required to Increase the Levels of the dKDM4B Demethylase after UV-induced DNA Damage to Demethylate Histone H3 Lysine 9. Journal of Biological Chemistry, 2010, 285, 31370-31379.	3.4	38

#	ARTICLE	IF	CITATIONS
37	p300-mediated Acetylation of Histone H3 Lysine 56 Functions in DNA Damage Response in Mammals. <i>Journal of Biological Chemistry</i> , 2010, 285, 28553-28564.	3.4	151
38	Quantitative Mass Spectrometry of Histones H3.2 and H3.3 in Suz12-deficient Mouse Embryonic Stem Cells Reveals Distinct, Dynamic Post-translational Modifications at Lys-27 and Lys-36. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 838-850.	3.8	121
39	Nuclear Pore Proteins Nup153 and Megator Define Transcriptionally Active Regions in the <i>Drosophila</i> Genome. <i>PLoS Genetics</i> , 2010, 6, e1000846.	3.5	218
40	The Epigenetic Landscape of Latent Kaposi Sarcoma-Associated Herpesvirus Genomes. <i>PLoS Pathogens</i> , 2010, 6, e1000935.	4.7	227
41	Epigenetics in the unicellular parasite <i>Entamoeba histolytica</i> . <i>Future Microbiology</i> , 2010, 5, 1875-1884.	2.0	10
42	Epigenetic therapy: targeting histones and their modifications in human disease. <i>Future Medicinal Chemistry</i> , 2010, 2, 543-548.	2.3	11
43	The human sperm epigenome and its potential role in embryonic development. <i>Molecular Human Reproduction</i> , 2010, 16, 37-47.	2.8	204
44	Coordinated Chromatin Control: Structural and Functional Linkage of DNA and Histone Methylation. <i>Biochemistry</i> , 2010, 49, 2999-3008.	2.5	199
45	Transcriptional Activity Affects the H3K4me3 Level and Distribution in the Coding Region. <i>Molecular and Cellular Biology</i> , 2010, 30, 2933-2946.	2.3	38
46	Control of β -herpesvirus IE gene expression by HCF-1 coupled chromatin modification activities. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 257-265.	1.9	77
47	Protein lysine acetylation in cellular function and its role in cancer manifestation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 702-716.	1.9	45
48	Regulation of antigen receptor gene assembly by genetic "epigenetic crosstalk. <i>Seminars in Immunology</i> , 2010, 22, 313-322.	5.6	24
49	Interplay Between Different Epigenetic Modifications and Mechanisms. <i>Advances in Genetics</i> , 2010, 70, 101-141.	1.8	128
50	RFX1 regulates CD70 and CD11a expression in lupus T cells by recruiting the histone methyltransferase SUV39H1. <i>Arthritis Research and Therapy</i> , 2010, 12, R227.	3.5	75
51	Quantitative proteomics reveals direct and indirect alterations in the histone code following methyltransferase knockdown. <i>Molecular BioSystems</i> , 2010, 6, 1719.	2.9	36
52	Keeping it in the family: diverse histone recognition by conserved structural folds. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2010, 45, 488-505.	5.2	96
53	Inhibition of LSD1 sensitizes glioblastoma cells to histone deacetylase inhibitors. <i>Neuro-Oncology</i> , 2011, 13, 894-903.	1.2	122
54	Signals and Combinatorial Functions of Histone Modifications. <i>Annual Review of Biochemistry</i> , 2011, 80, 473-499.	11.1	429

#	ARTICLE	IF	CITATIONS
55	Introduction“Epiphanies in Epigenetics. Progress in Molecular Biology and Translational Science, 2011, 101, 1-21.	1.7	18
56	Molecular and Functional Models in Neuropsychiatry. Current Topics in Behavioral Neurosciences, 2011, , .	1.7	3
57	Epigenetics and Disease. , 2011, , .		5
58	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets. Genome Biology, 2011, 12, R15.	9.6	118
59	Role for Dpy-30 in ES Cell-Fate Specification by Regulation of H3K4 Methylation within Bivalent Domains. Cell, 2011, 144, 513-525.	28.9	282
60	Mechanisms for the Inheritance of Chromatin States. Cell, 2011, 146, 510-518.	28.9	207
61	Regulation of secondary metabolism by chromatin structure and epigenetic codes. Fungal Genetics and Biology, 2011, 48, 62-69.	2.1	217
62	Kinase Consensus Sequences: A Breeding Ground for Crosstalk. ACS Chemical Biology, 2011, 6, 881-892.	3.4	89
63	WAC, a Functional Partner of RNF20/40, Regulates Histone H2B Ubiquitination and Gene Transcription. Molecular Cell, 2011, 41, 384-397.	9.7	128
64	When Signaling Kinases Meet Histones and Histone Modifiers in the Nucleus. Molecular Cell, 2011, 42, 274-284.	9.7	131
65	The RING Finger Protein MSL2 in the MOF Complex Is an E3“Ubiquitin Ligase for H2B K34 and Is Involved in Crosstalk with H3 K4 and K79 Methylation. Molecular Cell, 2011, 43, 132-144.	9.7	131
66	Combinatorial Readout of Dual Histone Modifications by Paired Chromatin-associated Modules. Journal of Biological Chemistry, 2011, 286, 18363-18368.	3.4	57
67	Are corepressors always repressors?. Endocrinology Studies, 2011, 1, 8.	0.2	0
68	Epigenetic control of IRF1 responses in HIV-exposed seronegative versus HIV-susceptible individuals. Blood, 2011, 117, 2649-2657.	1.4	37
69	Control of nuclear receptor function by local chromatin structure. FEBS Journal, 2011, 278, 2211-2230.	4.7	35
70	Structure and function of active chromatin and DNase I hypersensitive sites. FEBS Journal, 2011, 278, 2182-2210.	4.7	110
71	Integrative epigenomic mapping defines four main chromatin states in Arabidopsis. EMBO Journal, 2011, 30, 1928-1938.	7.8	600
72	Chromatin regulation and genome maintenance by mammalian SIRT6. Trends in Biochemical Sciences, 2011, 36, 39-46.	7.5	136

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73	Nuclear receptor coregulators merge transcriptional coregulation with epigenetic regulation. Trends in Biochemical Sciences, 2011, 36, 272-281.	7.5	91
74	Histone demethylases in chromatin cross-talks. Biology of the Cell, 2011, 103, 381-401.	2.0	38
75	Transcriptional and epigenetic networks in haematological malignancy. FEBS Letters, 2011, 585, 2100-2111.	2.8	32
76	Animal Models of Epigenetic Regulation in Neuropsychiatric Disorders. Current Topics in Behavioral Neurosciences, 2011, 7, 281-322.	1.7	10
77	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. Molecular and Cellular Proteomics, 2011, 10, M111.013284.	3.8	754
78	Effect of trichostatin A and 5-Aza-2'-deoxycytidine on transgene reactivation and epigenetic modification in transgenic pig fibroblast cells. Molecular and Cellular Biochemistry, 2011, 355, 157-165.	3.1	16
79	The struggle for life of the genome's selfish architects. Biology Direct, 2011, 6, 19.	4.6	198
80	Dot1 binding induces chromatin rearrangements by histone methylation-dependent and -independent mechanisms. Epigenetics and Chromatin, 2011, 4, 2.	3.9	28
81	Mechanism(s) of SWI/SNF-Induced Nucleosome Mobilization. ChemBioChem, 2011, 12, 196-204.	2.6	41
82	Chromatin Modification in Zebrafish Development. Methods in Cell Biology, 2011, 104, 401-428.	1.1	6
83	Histone H3 Lysine 4 Hypermethylation Prevents Aberrant Nucleosome Remodeling at the <i>PHO5</i> Promoter. Molecular and Cellular Biology, 2011, 31, 3171-3181.	2.3	45
84	Phosphorylation of histone H3(T118) alters nucleosome dynamics and remodeling. Nucleic Acids Research, 2011, 39, 6465-6474.	14.5	63
85	The Histone Modifications Governing TFF1 Transcription Mediated by Estrogen Receptor. Journal of Biological Chemistry, 2011, 286, 13925-13936.	3.4	51
86	Insulin resistance and epigenetic regulation: insights from human studies and prospects for future research. Biomolecular Concepts, 2011, 2, 445-457.	2.2	2
87	Identification of Histone Mutants That Are Defective for Transcription-Coupled Nucleosome Occupancy. Molecular and Cellular Biology, 2011, 31, 3557-3568.	2.3	32
88	Epigenetic switch involved in activation of pioneer factor FOXA1-dependent enhancers. Genome Research, 2011, 21, 555-565.	5.5	196
89	GCN5 Regulates the Superoxide-Generating System in Leukocytes Via Controlling gp91-phox Gene Expression. Journal of Immunology, 2011, 186, 3015-3022.	0.8	39
90	Epigenomic Reorganization of the Clustered Hox Genes in Embryonic Stem Cells Induced by Retinoic Acid. Journal of Biological Chemistry, 2011, 286, 3250-3260.	3.4	86

#	ARTICLE	IF	CITATIONS
91	Patterns of Histone H3 Lysine 27 Monomethylation and Erythroid Cell Type-specific Gene Expression. <i>Journal of Biological Chemistry</i> , 2011, 286, 39457-39465.	3.4	22
92	The histone H3K36 demethylase Rph1/KDM4 regulates the expression of the photoreactivation gene PHR1. <i>Nucleic Acids Research</i> , 2011, 39, 4151-4165.	14.5	31
94	Plant homeodomain fingers form a helping hand for transcription. <i>Epigenetics</i> , 2011, 6, 4-8.	2.7	52
95	Systematic Dissection of Roles for Chromatin Regulators in a Yeast Stress Response. <i>PLoS Biology</i> , 2012, 10, e1001369.	5.6	162
96	Functional Antagonism between Sas3 and Gcn5 Acetyltransferases and ISWI Chromatin Remodelers. <i>PLoS Genetics</i> , 2012, 8, e1002994.	3.5	26
97	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, 18505-18510.	7.1	52
98	Maintenance of gene silencing by the coordinate action of the H3K9 methyltransferase G9a/KMT1C and the H3K4 demethylase Jarid1a/KDM5A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18845-18850.	7.1	83
99	The ubiquitin hydrolase USP22 contributes to 3' end processing of JAK-STAT inducible genes. <i>FASEB Journal</i> , 2012, 26, 842-854.	0.5	33
100	ARABIDOPSIS TRITHORAX-RELATED3/SET DOMAIN GROUP2 is Required for the Winter-Annual Habit of <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2012, 53, 834-846.	3.1	58
101	Synergistic repression of the embryonic programme by SET DOMAIN GROUP 8 and EMBRYONIC FLOWER 2 in <i>Arabidopsis</i> seedlings. <i>Journal of Experimental Botany</i> , 2012, 63, 1391-1404.	4.8	71
102	Environmental chemical exposures and human epigenetics. <i>International Journal of Epidemiology</i> , 2012, 41, 79-105.	1.9	377
103	PKM2 Phosphorylates Histone H3 and Promotes Gene Transcription and Tumorigenesis. <i>Cell</i> , 2012, 150, 685-696.	28.9	635
104	Male Germline Control of Transposable Elements1. <i>Biology of Reproduction</i> , 2012, 86, 162, 1-14.	2.7	44
105	Histone modification profiles characterize function-specific gene regulation. <i>Journal of Theoretical Biology</i> , 2012, 310, 132-142.	1.7	12
106	mRNA export and gene expression: The SAGA-TREX-2 connection. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 555-565.	1.9	71
107	Histone modification pattern evolution after yeast gene duplication. <i>BMC Evolutionary Biology</i> , 2012, 12, 111.	3.2	9
108	Yeast Genetic Structures and Functions. , 2012, , 73-125.		2
109	Chromatin Computation. <i>PLoS ONE</i> , 2012, 7, e35703.	2.5	16

#	ARTICLE	IF	CITATIONS
110	Dynamic alterations in the paternal epigenetic landscape following fertilization. <i>Frontiers in Genetics</i> , 2012, 3, 143.	2.3	51
111	C9a/GLP Histone Lysine Dimethyltransferase Complex Activity in the Hippocampus and the Entorhinal Cortex Is Required for Gene Activation and Silencing during Memory Consolidation. <i>Journal of Neuroscience</i> , 2012, 32, 5440-5453.	3.6	205
112	Histone modification in <i>Drosophila</i> . <i>Briefings in Functional Genomics</i> , 2012, 11, 319-331.	2.7	36
113	Redox signaling and histone acetylation in acute pancreatitis. <i>Free Radical Biology and Medicine</i> , 2012, 52, 819-837.	2.9	67
114	Histone demethylation and steroid receptor function in cancer. <i>Molecular and Cellular Endocrinology</i> , 2012, 348, 12-20.	3.2	13
115	Epigenetic regulation of transcription by RNA polymerase III. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 1015-1025.	1.9	13
116	Histone modifications in the male germ line of <i>Drosophila</i> . <i>BMC Developmental Biology</i> , 2013, 13, 7.	2.1	21
117	Transcriptional and epigenetic signatures of zygotic genome activation during early <i>drosophila</i> embryogenesis. <i>BMC Genomics</i> , 2013, 14, 226.	2.8	13
118	Applicability of Histone Deacetylase Inhibition for the Treatment of Spinal Muscular Atrophy. <i>Neurotherapeutics</i> , 2013, 10, 677-687.	4.4	12
119	Precision Mapping of Coexisting Modifications in Histone H3 Tails from Embryonic Stem Cells by ETD-MS/MS. <i>Analytical Chemistry</i> , 2013, 85, 8232-8239.	6.5	70
120	A Cul4 E3 Ubiquitin Ligase Regulates Histone Hand-Off during Nucleosome Assembly. <i>Cell</i> , 2013, 155, 817-829.	28.9	116
121	Retinoids induce stem cell differentiation via epigenetic changes. <i>Seminars in Cell and Developmental Biology</i> , 2013, 24, 701-705.	5.0	70
122	Homeotic Gene Regulation: A Paradigm for Epigenetic Mechanisms Underlying Organismal Development. <i>Sub-Cellular Biochemistry</i> , 2013, 61, 177-207.	2.4	1
123	Toxicogenomic approaches for understanding molecular mechanisms of heavy metal mutagenicity and carcinogenicity. <i>International Journal of Hygiene and Environmental Health</i> , 2013, 216, 587-598.	4.3	162
124	H2A.Z-dependent crosstalk between enhancer and promoter regulates Cyclin D1 expression. <i>Oncogene</i> , 2013, 32, 4243-4251.	5.9	44
125	Modulation of Epigenetic Targets for Anticancer Therapy: Clinicopathological Relevance, Structural Data and Drug Discovery Perspectives. <i>Current Pharmaceutical Design</i> , 2013, 19, 578-613.	1.9	69
126	Repressive Epigenetic Changes at the <i>mGlu2</i> Promoter in Frontal Cortex of 5-HT _{2A} Knockout Mice. <i>Molecular Pharmacology</i> , 2013, 83, 1166-1175.	2.3	33
127	Crosstalk between NSL Histone Acetyltransferase and MLL/SET Complexes: NSL Complex Functions in Promoting Histone H3K4 Di-Methylation Activity by MLL/SET Complexes. <i>PLoS Genetics</i> , 2013, 9, e1003940.	3.5	44

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128	Bimodal quantitative relationships between histone modifications for X-linked and autosomal loci. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6949-6954.	7.1	9
129	Convergent Chemical Synthesis of Histone H2B Protein for the Site-specific Ubiquitination at Lys34. Angewandte Chemie - International Edition, 2013, 52, 8059-8063.	13.8	119
132	Mechanisms of Environmental and Occupational Carcinogenesis. , 2014, , 33-48.		0
133	Transcription of the Geminin gene is regulated by a negative-feedback loop. Molecular Biology of the Cell, 2014, 25, 1374-1383.	2.1	4
134	Recruitment of PfSET2 by RNA Polymerase II to Variant Antigen Encoding Loci Contributes to Antigenic Variation in P. falciparum. PLoS Pathogens, 2014, 10, e1003854.	4.7	65
135	Nuclear receptors and chromatin: an inducible couple. Journal of Molecular Endocrinology, 2014, 52, R137-R149.	2.5	36
136	Foodinformatics. , 2014, , .		15
137	DNMTs as potential therapeutic targets in high-risk pediatric embryonal brain tumors. Expert Opinion on Therapeutic Targets, 2014, 18, 1103-1107.	3.4	12
138	Physical and Functional Interactions between the Histone H3K4 Demethylase KDM5A and the Nucleosome Remodeling and Deacetylase (NuRD) Complex. Journal of Biological Chemistry, 2014, 289, 28956-28970.	3.4	67
139	The transcriptional co-repressor TLE3 suppresses basal signaling on a subset of estrogen receptor $\hat{+}$ target genes. Nucleic Acids Research, 2014, 42, 11339-11348.	14.5	26
140	Arginine methylation of hnRNPK negatively modulates apoptosis upon DNA damage through local regulation of phosphorylation. Nucleic Acids Research, 2014, 42, 9908-9924.	14.5	46
141	A nucleosomal approach to inferring causal relationships of histone modifications. BMC Genomics, 2014, 15, S7.	2.8	3
143	Deciphering the epigenetic code of T lymphocytes. Immunological Reviews, 2014, 261, 50-61.	6.0	15
145	Bioinformatic and Proteomic Analysis of Bulk Histones Reveals PTM Crosstalk and Chromatin Features. Journal of Proteome Research, 2014, 13, 3330-3337.	3.7	15
146	dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav052-bav052.	3.0	13
149	Enzymatic cleavage of histone H3: a new consideration when measuring histone modifications in human samples. Clinical Epigenetics, 2015, 7, 7.	4.1	19
150	Cadmium affects mitotically inherited histone modification pathways in mouse embryonic stem cells. Toxicology in Vitro, 2015, 30, 583-592.	2.4	8
151	Nanoparticles in food. Epigenetic changes induced by nanomaterials and possible impact on health. Food and Chemical Toxicology, 2015, 77, 64-73.	3.6	116

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152	Retinoic acid receptors: From molecular mechanisms to cancer therapy. <i>Molecular Aspects of Medicine</i> , 2015, 41, 1-115.	6.4	284
153	Resistance to Targeted ABC Transporters in Cancer. <i>Resistance To Targeted Anti-cancer Therapeutics</i> , 2015, , .	0.1	3
154	<scp>MPP</scp> 8 and <scp>SIRT</scp> 1 crosstalk in Eâ€cadherin gene silencing and epithelialâ€mesenchymal transition. <i>EMBO Reports</i> , 2015, 16, 689-699.	4.5	48
155	Computer-aided Molecular Design of Compounds Targeting Histone Modifying Enzymes. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 358-365.	4.1	19
156	High-Resolution Chromatin Dynamics during a Yeast Stress Response. <i>Molecular Cell</i> , 2015, 58, 371-386.	9.7	183
157	Modeling the relationship of epigenetic modifications to transcription factor binding. <i>Nucleic Acids Research</i> , 2015, 43, 3873-3885.	14.5	86
158	H3K23me2 is a new heterochromatic mark in <i>Caenorhabditis elegans</i>. <i>Nucleic Acids Research</i> , 2015, 43, gkv1063.	14.5	37
159	Nucleosome competition reveals processive acetylation by the SAGA HAT module. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5461-70.	7.1	55
160	Histone proteolysis: A proposal for categorization into â€clippingâ€™™ and â€degradationâ€™™. <i>BioEssays</i> , 2015, 37, 70-79.	2.5	58
161	Histone Posttranslational Modifications of CD4+ T Cell in Autoimmune Diseases. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1547.	4.1	21
162	Epigenetic regulation of epithelialâ€mesenchymal transition. <i>Cellular and Molecular Life Sciences</i> , 2016, 73, 4493-4515.	5.4	97
163	Evidence that ubiquitylated H2B corrals hDot1L on the nucleosomal surface to induce H3K79 methylation. <i>Nature Communications</i> , 2016, 7, 10589.	12.8	59
164	Histone Modifications and Cancer. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a019521.	5.5	626
165	The epigenome: the next substrate for engineering. <i>Genome Biology</i> , 2016, 17, 183.	8.8	44
166	Molecular modeling of structural and functional variance in the SAGA deubiquitinating module caused by Sgf73 Y57A mutation. <i>RSC Advances</i> , 2016, 6, 74991-75001.	3.6	1
167	A brief histone in time: understanding the combinatorial functions of histone PTMs in the nucleosome context. <i>Biochemistry and Cell Biology</i> , 2016, 94, 33-42.	2.0	15
168	Role of co-regulators in metabolic and transcriptional actions of thyroid hormone. <i>Journal of Molecular Endocrinology</i> , 2016, 56, R73-R97.	2.5	29
169	Epigeneticsâ€™™a potential mediator between air pollution and preterm birth. <i>Environmental Epigenetics</i> , 2016, 2, dvv008.	1.8	27

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170	Histone modifications in DNA damage response. <i>Science China Life Sciences</i> , 2016, 59, 257-270.	4.9	39
171	Profiling post-translational modifications of histones in neural differentiation of embryonic stem cells using liquid chromatography-mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1017-1018, 36-44.	2.3	5
172	Multiplex detection of histone-modifying enzymes by total internal reflection fluorescence-based single-molecule detection. <i>Chemical Communications</i> , 2016, 52, 1218-1221.	4.1	50
173	The roles of cross-talk epigenetic patterns in <i>Arabidopsis thaliana</i> . <i>Briefings in Functional Genomics</i> , 2016, 15, 278-287.	2.7	31
174	Epigenetic interplay at the β -globin locus. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017, 1860, 393-404.	1.9	12
175	CRL4DCAF8 Ubiquitin Ligase Targets Histone H3K79 and Promotes H3K9 Methylation in the Liver. <i>Cell Reports</i> , 2017, 18, 1499-1511.	6.4	24
176	Arsenic activates the expression of 3β -HSD in mouse Leydig cells through repression of histone H3K9 methylation. <i>Toxicology and Applied Pharmacology</i> , 2017, 326, 7-14.	2.8	48
177	Histone variant H3.3 orchestrates neural stem cell differentiation in the developing brain. <i>Cell Death and Differentiation</i> , 2017, 24, 1548-1563.	11.2	51
178	Retrieving Quantitative Information of Histone PTMs by Mass Spectrometry. <i>Methods in Enzymology</i> , 2017, 586, 165-191.	1.0	6
179	Histone ubiquitination in the DNA damage response. <i>DNA Repair</i> , 2017, 56, 92-101.	2.8	167
180	Molecular structures guide the engineering of chromatin. <i>Nucleic Acids Research</i> , 2017, 45, 7555-7570.	14.5	17
181	Sexually Dimorphic Epigenetic Regulation of Brain-Derived Neurotrophic Factor in Fetal Brain in the Valproic Acid Model of Autism Spectrum Disorder. <i>Developmental Neuroscience</i> , 2017, 39, 507-518.	2.0	19
182	Comprehensive profiling of lysine ubiquitome reveals diverse functions of lysine ubiquitination in common wheat. <i>Scientific Reports</i> , 2017, 7, 13601.	3.3	31
183	The role of epigenetics in lysosomal storage disorders: Uncharted territory. <i>Molecular Genetics and Metabolism</i> , 2017, 122, 10-18.	1.1	41
185	Ambient Air Pollution and Biomarkers of Health Effect. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1017, 59-102.	1.6	39
186	An Assay Based on SAMDI Mass Spectrometry for Profiling Protein Interaction Domains. <i>Journal of the American Chemical Society</i> , 2017, 139, 10320-10327.	13.7	16
187	Histone peptide microarray screen of chromo and Tudor domains defines new histone lysine methylation interactions. <i>Epigenetics and Chromatin</i> , 2017, 10, 12.	3.9	47
188	Chronic MeHg exposure modifies the histone H3K4me3 epigenetic landscape in <i>Caenorhabditis elegans</i> . <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2017, 191, 109-116.	2.6	19

#	ARTICLE	IF	CITATIONS
189	KSHV encoded ORF59 modulates histone arginine methylation of the viral genome to promote viral reactivation. PLoS Pathogens, 2017, 13, e1006482.	4.7	25
190	T Cell Receptor and Cytokine Signaling Can Function at Different Stages to Establish and Maintain Transcriptional Memory and Enable T Helper Cell Differentiation. Frontiers in Immunology, 2017, 8, 204.	4.8	25
191	The Histone Modification Code in the Pathogenesis of Autoimmune Diseases. Mediators of Inflammation, 2017, 2017, 1-12.	3.0	70
192	Release, Characterization, and Safety of Nanoencapsulated Food Ingredients. , 2017, , 401-453.		17
193	Co-occurring protein phosphorylation are functionally associated. PLoS Computational Biology, 2017, 13, e1005502.	3.2	26
194	Down-Regulation of H3K4me3 by MM-102 Facilitates Epigenetic Reprogramming of Porcine Somatic Cell Nuclear Transfer Embryos. Cellular Physiology and Biochemistry, 2018, 45, 1529-1540.	1.6	46
195	An Integrated Approach Based on a DNA Self-Assembly Technique for Characterization of Crosstalk among Combinatorial Histone Modifications. Analytical Chemistry, 2018, 90, 3692-3696.	6.5	12
196	The SAGA/TREX-2 subunit Sus1 binds widely to transcribed genes and affects mRNA turnover globally. Epigenetics and Chromatin, 2018, 11, 13.	3.9	19
197	RNF20 controls astrocytic differentiation through epigenetic regulation of STAT3 in the developing brain. Cell Death and Differentiation, 2018, 25, 294-306.	11.2	15
198	Die Rolle von Histonmethylierungen in der Entwicklung des zentralen Nervensystems und bei Neuralrohrdefekten. Neuroforum, 2018, 24, 111-120.	0.3	0
199	Structure-guided development of YEATS domain inhibitors by targeting π - π stacking. Nature Chemical Biology, 2018, 14, 1140-1149.	8.0	76
200	Histone methylations in the developing central nervous system and in neural tube defects. Neuroforum, 2018, 24, A85-A94.	0.3	0
201	Total Chemical Synthesis of Modified Histones. Frontiers in Chemistry, 2018, 6, 19.	3.6	26
202	Chromatin and Metabolism. Annual Review of Biochemistry, 2018, 87, 27-49.	11.1	37
203	Histone Deacetylase 3 Governs Perinatal Cerebral Development via Neural Stem and Progenitor Cells. IScience, 2019, 20, 148-167.	4.1	17
204	Epigenetics: Dissecting Gene Expression Alteration in PDAC. , 2019, , .		1
205	Yeast epigenetics: the inheritance of histone modification states. Bioscience Reports, 2019, 39, .	2.4	28
206	Coordinate activation of a target gene by KDM1C histone demethylase and OTLD1 histone deubiquitinase in Arabidopsis. Epigenetics, 2019, 14, 602-610.	2.7	10

#	ARTICLE	IF	CITATIONS
207	Structural Basis of Dot1L Stimulation by Histone H2B Lysine 120 Ubiquitination. <i>Molecular Cell</i> , 2019, 74, 1010-1019.e6.	9.7	115
208	Mechanism of Cross-talk between H2B Ubiquitination and H3 Methylation by Dot1L. <i>Cell</i> , 2019, 176, 1490-1501.e12.	28.9	177
209	HDA9-PWR-HOS15 Is a Core Histone Deacetylase Complex Regulating Transcription and Development. <i>Plant Physiology</i> , 2019, 180, 342-355.	4.8	52
210	Methylmercury Epigenetics. <i>Toxics</i> , 2019, 7, 56.	3.7	25
211	Transgenerational Inheritance of Environmentally Induced Epigenetic Alterations during Mammalian Development. <i>Cells</i> , 2019, 8, 1559.	4.1	66
212	TCellXTalk facilitates the detection of co-modified peptides for the study of protein post-translational modification cross-talk in T cells. <i>Bioinformatics</i> , 2019, 35, 1404-1413.	4.1	1
213	Histone demethylase KDM3A is required for enhancer activation of hippo target genes in colorectal cancer. <i>Nucleic Acids Research</i> , 2019, 47, 2349-2364.	14.5	47
214	Intrinsic protein disorder and protein modifications in the processing of biological signals. <i>Current Opinion in Structural Biology</i> , 2020, 60, 1-6.	5.7	13
215	The expression of histone methyltransferases and distribution of selected histone methylations in testes of yak and cattle-yak hybrid. <i>Theriogenology</i> , 2020, 144, 164-173.	2.1	17
216	H4S1ph, an alternative epigenetic marker for sperm maturity. <i>Andrologia</i> , 2020, 52, e13352.	2.1	2
217	The mechanisms of action of chromatin remodelers and implications in development and disease. <i>Biochemical Pharmacology</i> , 2020, 180, 114200.	4.4	18
218	Circadian Rhythms in Environmental Health Sciences. <i>Current Environmental Health Reports</i> , 2020, 7, 272-281.	6.7	9
219	Transgenerational epigenetic reprogramming of early embryos: a mechanistic model. <i>Environmental Epigenetics</i> , 2020, 6, dvaa009.	1.8	14
220	Avocado: a multi-scale deep tensor factorization method learns a latent representation of the human epigenome. <i>Genome Biology</i> , 2020, 21, 81.	8.8	77
221	Epigenetic mechanisms in the regulation of lymphocyte differentiation. , 2020, , 77-116.		3
222	Both combinatorial K4me0-K36me3 marks on sister histone H3s of a nucleosome are required for Dnmt3a-Dnmt3L mediated de novo DNA methylation. <i>Journal of Genetics and Genomics</i> , 2020, 47, 105-114.	3.9	4
223	circEgg regulates histone H3K9me3 by sponging bmo-miR-3391 and encoding circEgg-P122 protein in the silkworm, <i>Bombyx mori</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2020, 124, 103430.	2.7	20
224	Protein arginine deiminase 4 antagonizes methylglyoxal-induced histone glycation. <i>Nature Communications</i> , 2020, 11, 3241.	12.8	39

#	ARTICLE	IF	CITATIONS
225	PRMT5-mediated histone arginine methylation antagonizes transcriptional repression by polycomb complex PRC2. <i>Nucleic Acids Research</i> , 2020, 48, 2956-2968.	14.5	38
226	Multiple Site-Specific One-Pot Synthesis of Two Proteins by the Bio-Orthogonal Flexizyme System. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 37.	4.1	3
227	Inhibition of HDAC6 by tubastatin A disrupts mouse oocyte meiosis via regulating histone modifications and mRNA expression. <i>Journal of Cellular Physiology</i> , 2020, 235, 7030-7042.	4.1	13
228	Dynamic changes of histone acetylation and methylation in bovine oocytes, zygotes, and preimplantation embryos. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2020, 334, 245-256.	1.3	10
229	Regulatory mechanisms governing chromatin organization and function. <i>Current Opinion in Cell Biology</i> , 2021, 70, 10-17.	5.4	27
230	Emerging histone glutamine modifications mediated gene expression in cell differentiation and the VTA reward pathway. <i>Gene</i> , 2021, 768, 145323.	2.2	5
231	Regulation of Gene Expression. , 2021, , 157-201.		0
232	Succinylation of H3K122 destabilizes nucleosomes and enhances transcription. <i>EMBO Reports</i> , 2021, 22, e51009.	4.5	36
233	Epigenetics of Alzheimer's Disease. <i>Biomolecules</i> , 2021, 11, 195.	4.0	74
234	Regulation of the Dot1 histone H3K79 methyltransferase by histone H4K16 acetylation. <i>Science</i> , 2021, 371, .	12.6	70
235	Histone modification dynamics at H3K27 are associated with altered transcription of in planta induced genes in <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , 2021, 17, e1009376.	3.5	56
236	Magnetic induction inspires a schematic theory for crosstalk-driven relaxation dynamics in cells. <i>Physical Review E</i> , 2021, 103, 042417.	2.1	0
237	Roles of lysine-specific demethylase 1 (LSD1) in homeostasis and diseases. <i>Journal of Biomedical Science</i> , 2021, 28, 41.	7.0	48
238	Reassembling protein complexes after controlled disassembly by top-down mass spectrometry in native mode. <i>International Journal of Mass Spectrometry</i> , 2021, 465, 116591.	1.5	8
239	Do Epigenetic Timers Control Petal Development?. <i>Frontiers in Plant Science</i> , 2021, 12, 709360.	3.6	4
240	Nucleotide Metabolism Behind Epigenetics. <i>Frontiers in Endocrinology</i> , 2021, 12, 731648.	3.5	8
241	Investigating crosstalk between H3K27 acetylation and H3K4 trimethylation in CRISPR/dCas-based epigenome editing and gene activation. <i>Scientific Reports</i> , 2021, 11, 15912.	3.3	29
242	Integrative Chemical Biology Approaches to Deciphering the Histone Code: A Problem-Driven Journey. <i>Accounts of Chemical Research</i> , 2021, 54, 3734-3747.	15.6	17

#	ARTICLE	IF	CITATIONS
243	Histone lysine modifying enzymes and their critical roles in DNA double-strand break repair. DNA Repair, 2021, 107, 103206.	2.8	6
245	Activation of p21 by HDAC Inhibitors Requires Acetylation of H2A.Z. PLoS ONE, 2013, 8, e54102.	2.5	41
246	Cleavage of Histone 3 by Cathepsin D in the Involuting Mammary Gland. PLoS ONE, 2014, 9, e103230.	2.5	26
247	The transcription factor c-Fos coordinates with histone lysine-specific demethylase 2A to activate the expression of <i>cyclooxygenase-2</i> . Oncotarget, 2015, 6, 34704-34717.	1.8	8
248	Epigenetic Regulation of EMT: The Snail Story. Current Pharmaceutical Design, 2014, 20, 1698-1705.	1.9	116
249	Histone Cleavage as a Mechanism for Epigenetic Regulation: Current Insights and Perspectives. Current Molecular Medicine, 2014, 14, 1164-1172.	1.3	39
252	Mechanisms of Chemoresistance in Human Ovarian Cancer at a Glance. Gynecology & Obstetrics (Sunnyvale, Calif), 2012, 02, .	0.1	10
253	The role of maintenance proteins in the preservation of epithelial cell identity during mammary gland remodeling and breast cancer initiation. Chinese Journal of Cancer, 2014, 33, 51-67.	4.9	8
254	A synthetic biology approach to probing nucleosome symmetry. ELife, 2017, 6, .	6.0	16
255	Dynamics of Histone Lysine Methylation: Structures of Methyl Writers and Erasers. , 2011, 67, 107-124.		40
256	Poly(ADP-Ribosyl)ation of Chromosomal Proteins, Epigenetic Regulation and Human Genomic Integrity in Health and Disease. , 2011, , 411-424.		0
257	Histone Phosphorylation and Chromatin Dynamics. , 2014, , 341-354.		0
258	The Epigenetic Regulatory Machinery. Epigenetics and Human Health, 2014, , 1-11.	0.2	0
259	Molecular Approaches to Explore Natural and Food-Compound Modulators in Cancer Epigenetics and Metabolism. , 2014, , 131-149.		0
260	Drugs Affecting Epigenetic Modifications of ABC Transporters for Drug Resistance. Resistance To Targeted Anti-cancer Therapeutics, 2015, , 273-297.	0.1	0
264	Genetics, Epigenetics, and Environmental Interactions. , 2020, , 21-38.		0
268	Chemical methods for studying the crosstalk between histone H2B ubiquitylation and H3 methylation. Journal of Peptide Science, 2022, 28, e3381.	1.4	1
269	Promiscuous Domains in Eukaryotes and HAT Proteins in FUNGI Have Followed Different Evolutionary Paths. Journal of Molecular Evolution, 2022, 90, 124-138.	1.8	0

#	ARTICLE	IF	CITATIONS
270	Epigenetics of pregnancy: looking beyond the DNA code. <i>Journal of Assisted Reproduction and Genetics</i> , 2022, 39, 801-816.	2.5	25
271	The Non-Specific Lethal (NSL) Histone Acetyltransferase Complex Transcriptionally Regulates Yin Yang 1-Mediated Cell Proliferation in Human Cells. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3801.	4.1	2
273	Cross-Talk Between Histone Methyltransferases and Demethylases Regulate REST Transcription During Neurogenesis. <i>Frontiers in Oncology</i> , 2022, 12, .	2.8	2
277	Beyond Moco Biosynthesisâ€•Moonlighting Roles of MoaE and MOCS2. <i>Molecules</i> , 2022, 27, 3733.	3.8	1
278	Expression and prognostic significance of chromatin modulators EHMT2/G9a and KDM2b in acute myeloid leukemia. <i>Journal of Cellular Biochemistry</i> , 2022, 123, 1340-1355.	2.6	2
279	H2B Lys34 Ubiquitination Induces Nucleosome Distortion to Stimulate Dot1L Activity. <i>Nature Chemical Biology</i> , 2022, 18, 972-980.	8.0	38
280	PHF20 is crucial for epigenetic control of starvation-induced autophagy through enhancer activation. <i>Nucleic Acids Research</i> , 2022, 50, 7856-7872.	14.5	6
281	The role of histone modifications: from neurodevelopment to neurodiseases. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, .	17.1	63
282	Genetic modification, intercellular communication, and epigenetic regulation in plants: An outlook. <i>Biochemical and Biophysical Research Communications</i> , 2022, 633, 92-95.	2.1	0
283	<scp>SHP</scp>â€1 dephosphorylates histone <scp>H2B</scp> to facilitate its ubiquitination during transcription. <i>EMBO Journal</i> , 2022, 41, .	7.8	2
284	An interplay between BRD4 and G9a regulates skeletal myogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	3.7	1
285	Epigenetic regulation of B cells and its role in autoimmune pathogenesis. , 2022, 19, 1215-1234.		15
286	Histone modifications and DNA methylation act cooperatively in regulating symbiosis genes in the sea anemone <i>Aiptasia</i> . <i>BMC Biology</i> , 2022, 20, .	3.8	3
289	Inhibitors targeting epigenetic modifications in cancer. , 2023, , 287-324.		0
292	Dysregulation of histone modifications in bone marrow mesenchymal stem cells during skeletal ageing: roles and therapeutic prospects. <i>Stem Cell Research and Therapy</i> , 2023, 14, .	5.5	1
293	Context-defined cancer co-dependency mapping identifies a functional interplay between PRC2 and MLL-MEN1 complex in lymphoma. <i>Nature Communications</i> , 2023, 14, .	12.8	5
294	Fundamental insights into the correlation between chromosome configuration and transcription. <i>Physical Biology</i> , 2023, 20, 051002.	1.8	2
295	A global view of the human post-translational modification landscape. <i>Biochemical Journal</i> , 2023, 480, 1241-1265.	3.7	8

#	ARTICLE	IF	CITATIONS
296	The BAH domain: A versatile histone modification reader. , 2024, , 13-30.		0
297	Domain architecture and protein–protein interactions regulate KDM5A recruitment to the chromatin. Epigenetics, 2023, 18, .	2.7	1
298	Inducible Expression of the Restriction Enzyme Uncovered Genome-Wide Distribution and Dynamic Behavior of Histones H4K16ac and H2A.Z at DNA Double-Strand Breaks in Arabidopsis. Plant and Cell Physiology, 0, , .	3.1	1
299	Chromatin balances cell redox and energy homeostasis. Epigenetics and Chromatin, 2023, 16, .	3.9	0
300	HDAC6 decreases H4K16 and α -tubulin acetylation during porcine oocyte maturation. Cell Cycle, 2023, 22, 2057-2069.	2.6	0
301	Single-cell joint profiling of multiple epigenetic proteins and gene transcription. Science Advances, 2024, 10, .	10.3	0
302	Single-cell omics in tracing cellular heterogeneity of drug-induced liver injury: Technological landscape and prospective application. , 2024, , .		0
303	Histone modification–dependent production of peptide hormones facilitates acquisition of pluripotency during leaf-to-callus transition in Arabidopsis. New Phytologist, 2024, 242, 1068-1083.	7.3	0