

Axel Imhof

List of Publications by Year in descending order

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Version: 2024-02-01

200
papers

17,264
citations

19608

61
h-index

17546

121
g-index

221
all docs

221
docs citations

221
times ranked

21659
citing authors

#	ARTICLE	IF	CITATIONS
1	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. <i>Nature Genetics</i> , 2005, 37, 391-400.	9.4	1,710
2	Drosophila Enhancer of Zeste/ESC Complexes Have a Histone H3 Methyltransferase Activity that Marks Chromosomal Polycomb Sites. <i>Cell</i> , 2002, 111, 185-196.	13.5	1,398
3	Acetylation of general transcription factors by histone acetyltransferases. <i>Current Biology</i> , 1997, 7, 689-692.	1.8	578
4	Identification of a specific inhibitor of the histone methyltransferase SU(VAR)3-9. , 2005, 1, 143-145.		462
5	PTMs on H3 Variants before Chromatin Assembly Potentiate Their Final Epigenetic State. <i>Molecular Cell</i> , 2006, 24, 309-316.	4.5	361
6	Two distinct modes for propagation of histone PTMs across the cell cycle. <i>Genes and Development</i> , 2015, 29, 585-590.	2.7	334
7	Synergy between CD26/DPP-IV Inhibition and G-CSF Improves Cardiac Function after Acute Myocardial Infarction. <i>Cell Stem Cell</i> , 2009, 4, 313-323.	5.2	289
8	Histone methylation by the Drosophila epigenetic transcriptional regulator Ash1. <i>Nature</i> , 2002, 419, 857-862.	13.7	283
9	Connecting Threads: Epigenetics and Metabolism. <i>Cell</i> , 2012, 148, 24-28.	13.5	282
10	hMOF Histone Acetyltransferase Is Required for Histone H4 Lysine 16 Acetylation in Mammalian Cells. <i>Molecular and Cellular Biology</i> , 2005, 25, 6798-6810.	1.1	281
11	Secretome protein enrichment identifies physiological BACE1 protease substrates in neurons. <i>EMBO Journal</i> , 2012, 31, 3157-3168.	3.5	279
12	Fast signals and slow marks: the dynamics of histone modifications. <i>Trends in Biochemical Sciences</i> , 2010, 35, 618-626.	3.7	268
13	Endotoxemia Accelerates Atherosclerosis Through Electrostatic Charge-mediated Monocyte Adhesion. <i>Circulation</i> , 2021, 143, 254-266.	1.6	266
14	Phosphorylation of histone H3T6 by PKC δ 1 controls demethylation at histone H3K4. <i>Nature</i> , 2010, 464, 792-796.	13.7	259
15	Replication Stress Interferes with Histone Recycling and Predeposition Marking of New Histones. <i>Molecular Cell</i> , 2010, 37, 736-743.	4.5	242
16	PRMT6-mediated methylation of R2 in histone H3 antagonizes H3 K4 trimethylation. <i>Genes and Development</i> , 2007, 21, 3369-3380.	2.7	238
17	Toll-like Receptor Signaling Rewires Macrophage Metabolism and Promotes Histone Acetylation via ATP-Citrate Lyase. <i>Immunity</i> , 2019, 51, 997-1011.e7.	6.6	216
18	Mislocalization of the Centromeric Histone Variant CenH3/CENP-A in Human Cells Depends on the Chaperone DAXX. <i>Molecular Cell</i> , 2014, 53, 631-644.	4.5	214

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19	The HP1±â€“CAF1â€“SetDB1â€“containing complex provides H3K9me1 for Suv39â€“mediated K9me3 in pericentric heterochromatin. <i>EMBO Reports</i> , 2009, 10, 769-775.	2.0	201
20	DNA methylation requires a DNMT1 ubiquitin interacting motif (UIM) and histone ubiquitination. <i>Cell Research</i> , 2015, 25, 911-929.	5.7	201
21	Physical and functional association of SU(VAR)3â€“ and HDAC1 in <i>Drosophila</i> . <i>EMBO Reports</i> , 2001, 2, 915-919.	2.0	186
22	Redundant Mechanisms to Form Silent Chromatin at Pericentromeric Regions Rely on BEND3 and DNA Methylation. <i>Molecular Cell</i> , 2014, 56, 580-594.	4.5	185
23	Transcriptional activation by Myc is under negative control by the transcription factor AP-2.. <i>EMBO Journal</i> , 1995, 14, 1508-1519.	3.5	177
24	Systematic functional analysis of SARS-CoV-2 proteins uncovers viral innate immune antagonists and remaining vulnerabilities. <i>Cell Reports</i> , 2021, 35, 109126.	2.9	176
25	H3 Lysine 4 Is Acetylated at Active Gene Promoters and Is Regulated by H3 Lysine 4 Methylation. <i>PLoS Genetics</i> , 2011, 7, e1001354.	1.5	175
26	H4K20me0 marks post-replicative chromatin and recruits the TONSLâ€“MMS22L DNA repair complex. <i>Nature</i> , 2016, 534, 714-718.	13.7	172
27	dMi-2 and ISWI chromatin remodelling factors have distinct nucleosome binding and mobilization properties. <i>EMBO Journal</i> , 2000, 19, 4332-4341.	3.5	167
28	OPA1 Processing Reconstituted in Yeast Depends on the Subunit Composition of the m-AAA Protease in Mitochondria. <i>Molecular Biology of the Cell</i> , 2007, 18, 3582-3590.	0.9	162
29	Dynamics of Adaptive Microevolution of Hypermutable <i>Pseudomonas aeruginosa</i> during Chronic Pulmonary Infection in Patients with Cystic Fibrosis. <i>Journal of Infectious Diseases</i> , 2009, 200, 118-130.	1.9	155
30	Localized H3K36 methylation states define histone H4K16 acetylation during transcriptional elongation in <i>Drosophila</i> . <i>EMBO Journal</i> , 2007, 26, 4974-4984.	3.5	153
31	Distinct requirements for chromatin assembly in transcriptional repression by thyroid hormone receptor and histone deacetylase. <i>EMBO Journal</i> , 1998, 17, 520-534.	3.5	152
32	Transcription: Gene control by targeted histone acetylation. <i>Current Biology</i> , 1998, 8, R422-R424.	1.8	148
33	Activation of RNA Polymerase I Transcription by Cockayne Syndrome Group B Protein and Histone Methyltransferase G9a. <i>Molecular Cell</i> , 2007, 27, 585-595.	4.5	147
34	The Metabolic Impact on Histone Acetylation and Transcription in Ageing. <i>Trends in Biochemical Sciences</i> , 2016, 41, 700-711.	3.7	143
35	An alternatively spliced mRNA from the AP-2 gene encodes a negative regulator of transcriptional activation by AP-2.. <i>Molecular and Cellular Biology</i> , 1993, 13, 4174-4185.	1.1	136
36	Circadian acetylome reveals regulation of mitochondrial metabolic pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3339-3344.	3.3	133

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37	The dMi-2 chromodomains are DNA binding modules important for ATP-dependent nucleosome mobilization. <i>EMBO Journal</i> , 2002, 21, 2430-2440.	3.5	132
38	Bioinformatic analysis of proteomics data. <i>BMC Systems Biology</i> , 2014, 8, S3.	3.0	131
39	A $\hat{1}^3$ -secretase-like intramembrane cleavage of TNF $\hat{1}$ by the GxGD aspartyl protease SPPL2b. <i>Nature Cell Biology</i> , 2006, 8, 894-896.	4.6	130
40	Regulated Intramembrane Proteolysis of the Interleukin-1 Receptor II by $\hat{1}$, $\hat{2}$, and $\hat{3}$ -Secretase. <i>Journal of Biological Chemistry</i> , 2007, 282, 11982-11995.	1.6	128
41	Acf1, the largest subunit of CHRAC, regulates ISWI-induced nucleosome remodelling. <i>EMBO Journal</i> , 2001, 20, 3781-3788.	3.5	127
42	The Prion Curing Agent Guanidinium Chloride Specifically Inhibits ATP Hydrolysis by Hsp104. <i>Journal of Biological Chemistry</i> , 2004, 279, 7378-7383.	1.6	124
43	Related B cell clones that populate the CSF and CNS of patients with multiple sclerosis produce CSF immunoglobulin. <i>Journal of Neuroimmunology</i> , 2011, 233, 245-248.	1.1	119
44	Global and Specific Responses of the Histone Acetylome to Systematic Perturbation. <i>Molecular Cell</i> , 2015, 57, 559-571.	4.5	119
45	Impairment of prostate cancer cell growth by a selective and reversible lysine-specific demethylase 1 inhibitor. <i>International Journal of Cancer</i> , 2012, 131, 2704-2709.	2.3	118
46	Heptad-Specific Phosphorylation of RNA Polymerase II CTD. <i>Molecular Cell</i> , 2016, 61, 305-314.	4.5	118
47	Life span extension by targeting a link between metabolism and histone acetylation in <i>Drosophila</i> . <i>EMBO Reports</i> , 2016, 17, 455-469.	2.0	116
48	HP1 Binding to Chromatin Methylated at H3K9 Is Enhanced by Auxiliary Factors. <i>Molecular and Cellular Biology</i> , 2007, 27, 453-465.	1.1	115
49	Df31 Protein and snoRNAs Maintain Accessible Higher-Order Structures of Chromatin. <i>Molecular Cell</i> , 2012, 48, 434-444.	4.5	108
50	A combination of different mass spectroscopic techniques for the analysis of dynamic changes of histone modifications. <i>Proteomics</i> , 2004, 4, 1382-1396.	1.3	102
51	Sequential Establishment of Marks on Soluble Histones H3 and H4. <i>Journal of Biological Chemistry</i> , 2011, 286, 17714-17721.	1.6	100
52	Establishment of Histone Modifications after Chromatin Assembly. <i>Nucleic Acids Research</i> , 2009, 37, 5032-5040.	6.5	94
53	Stepwise Evolution of Essential Centromere Function in a <i>Drosophila</i> Neogene. <i>Science</i> , 2013, 340, 1211-1214.	6.0	94
54	Cbp3-Cbp6 interacts with the yeast mitochondrial ribosomal tunnel exit and promotes cytochrome <i>b</i> synthesis and assembly. <i>Journal of Cell Biology</i> , 2011, 193, 1101-1114.	2.3	91

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55	Transcriptional Regulation of the AP-2 \hat{I} Promoter by BTEB-1 and AP-2rep, a Novel wt-1/egr-Related Zinc Finger Repressor. <i>Molecular and Cellular Biology</i> , 1999, 19, 194-204.	1.1	86
56	Epigenetics and Metabolism in Health and Disease. <i>Frontiers in Genetics</i> , 2018, 9, 361.	1.1	81
57	Mechanisms governing the pioneering and redistribution capabilities of the non-classical pioneer PU.1. <i>Nature Communications</i> , 2020, 11, 402.	5.8	76
58	Proteome analysis of mitochondrial outer membrane from <i>Neurospora crassa</i> . <i>Proteomics</i> , 2006, 6, 72-80.	1.3	74
59	Interaction of HP1 and Brg1/Brm with the Globular Domain of Histone H3 Is Required for HP1-Mediated Repression. <i>PLoS Genetics</i> , 2009, 5, e1000769.	1.5	74
60	The Impact of One Carbon Metabolism on Histone Methylation. <i>Frontiers in Genetics</i> , 2019, 10, 764.	1.1	72
61	A Pair of Centromeric Proteins Mediates Reproductive Isolation in <i>Drosophila</i> Species. <i>Developmental Cell</i> , 2013, 27, 412-424.	3.1	71
62	p300 stimulates transcription instigated by ligand-bound thyroid hormone receptor at a step subsequent to chromatin disruption. <i>EMBO Journal</i> , 1999, 18, 5634-5652.	3.5	70
63	Assembly of methylated KDM1A and CHD1 drives androgen receptor \hat{I} dependent transcription and translocation. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 132-139.	3.6	70
64	SETDB1-dependent heterochromatin stimulates alternative lengthening of telomeres. <i>Science Advances</i> , 2019, 5, eaav3673.	4.7	70
65	Tyrosine-1 of RNA Polymerase II CTD Controls Global Termination of Gene Transcription in Mammals. <i>Molecular Cell</i> , 2018, 69, 48-61.e6.	4.5	66
66	MacroH2A histone variants maintain nuclear organization and heterochromatin architecture. <i>Journal of Cell Science</i> , 2017, 130, 1570-1582.	1.2	64
67	Chromosome organization by a conserved condensin-ParB system in the actinobacterium <i>Corynebacterium glutamicum</i> . <i>Nature Communications</i> , 2020, 11, 1485.	5.8	64
68	The genomic structure of the human AP-2 transcription factor. <i>Nucleic Acids Research</i> , 1994, 22, 1413-1420.	6.5	62
69	Proteins at the Polypeptide Tunnel Exit of the Yeast Mitochondrial Ribosome. <i>Journal of Biological Chemistry</i> , 2010, 285, 19022-19028.	1.6	62
70	The histone variant H2A.Bbd is enriched at sites of DNA synthesis. <i>Nucleic Acids Research</i> , 2014, 42, 6405-6420.	6.5	61
71	Circadian Control of Fatty Acid Elongation by SIRT1 Protein-mediated Deacetylation of Acetyl-coenzyme A Synthetase 1. <i>Journal of Biological Chemistry</i> , 2014, 289, 6091-6097.	1.6	61
72	Histone Deacetylase Directs the Dominant Silencing of Transcription in Chromatin: Association with MeCP2 and the Mi-2 Chromodomain SWI/SNF ATPase. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1998, 63, 435-446.	2.0	61

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73	KMT9 monomethylates histone H4 lysine 12 and controls proliferation of prostate cancer cells. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 361-371.	3.6	57
74	Proteome dynamics at broken replication forks reveal a distinct ATM-directed repair response suppressing DNA double-strand break ubiquitination. <i>Molecular Cell</i> , 2021, 81, 1084-1099.e6.	4.5	57
75	Purification and Properties of the <i>Xenopus</i> Hat1 Acetyltransferase: Association with the 14-3-3 Proteins in the Oocyte Nucleus. <i>Biochemistry</i> , 1999, 38, 13085-13093.	1.2	56
76	Coronin 1A, a novel player in integrin biology, controls neutrophil trafficking in innate immunity. <i>Blood</i> , 2017, 130, 847-858.	0.6	56
77	Adrenergic Signaling Strengthens Cardiac Myocyte Cohesion. <i>Circulation Research</i> , 2017, 120, 1305-1317.	2.0	55
78	The <i>Drosophila</i> G9a gene encodes a multi-catalytic histone methyltransferase required for normal development. <i>Nucleic Acids Research</i> , 2006, 34, 4609-4621.	6.5	54
79	Domain Model Explains Propagation Dynamics and Stability of Histone H3K27 and H3K36 Methylation Landscapes. <i>Cell Reports</i> , 2020, 30, 1223-1234.e8.	2.9	54
80	LSD1 controls metastasis of androgen-independent prostate cancer cells through PXN and LPAR6. <i>Oncogenesis</i> , 2014, 3, e120-e120.	2.1	53
81	Methylation of histone H3 lysine 9 occurs during translation. <i>Nucleic Acids Research</i> , 2015, 43, 9097-9106.	6.5	52
82	<i>Yersinia</i> Protein Kinase YopO Is Activated by A Novel G-actin Binding Process. <i>Journal of Biological Chemistry</i> , 2007, 282, 2268-2277.	1.6	50
83	Role of the AAA protease Yme1 in folding of proteins in the intermembrane space of mitochondria. <i>Molecular Biology of the Cell</i> , 2012, 23, 4335-4346.	0.9	50
84	Quantification of Proteins and Histone Marks in <i>Drosophila</i> Embryos Reveals Stoichiometric Relationships Impacting Chromatin Regulation. <i>Developmental Cell</i> , 2019, 51, 632-644.e6.	3.1	50
85	S-adenosyl- <i>l</i> -homocysteine hydrolase links methionine metabolism to the circadian clock and chromatin remodeling. <i>Science Advances</i> , 2020, 6, .	4.7	49
86	Epigenetic regulators and histone modification. <i>Briefings in Functional Genomics & Proteomics</i> , 2006, 5, 222-227.	3.8	48
87	The analysis of histone modifications. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1932-1939.	1.1	46
88	Monomethylation of Lysine 20 on Histone H4 Facilitates Chromatin Maturation. <i>Molecular and Cellular Biology</i> , 2009, 29, 57-67.	1.1	46
89	The histone acetyltransferase p300 inhibitor C646 reduces pro-inflammatory gene expression and inhibits histone deacetylases. <i>Biochemical Pharmacology</i> , 2016, 102, 130-140.	2.0	46
90	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. <i>Nature Communications</i> , 2018, 9, 4300.	5.8	46

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91	Biomarker discovery from body fluids using mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 849, 105-114.	1.2	45
92	Probing the Conformation of the ISWI ATPase Domain With Genetically Encoded Photoreactive Crosslinkers and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.012088.	2.5	45
93	Mass spectrometric analysis of protein histidine phosphorylation. <i>Amino Acids</i> , 2007, 32, 347-357.	1.2	44
94	DOT1A-dependent H3K76 methylation is required for replication regulation in <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2012, 40, 10302-10311.	6.5	43
95	Characterization of the insertase for β -barrel proteins of the outer mitochondrial membrane. <i>Journal of Cell Biology</i> , 2012, 199, 599-611.	2.3	43
96	The novel component Kgd4 recruits the E3 subunit to the mitochondrial α -ketoglutarate dehydrogenase. <i>Molecular Biology of the Cell</i> , 2014, 25, 3342-3349.	0.9	43
97	Ubiquitome Analysis Reveals PCNA-Associated Factor 15 (PAF15) as a Specific Ubiquitination Target of UHRF1 in Embryonic Stem Cells. <i>Journal of Molecular Biology</i> , 2017, 429, 3814-3824.	2.0	43
98	Harmonization of quality metrics and power calculation in multi-omic studies. <i>Nature Communications</i> , 2020, 11, 3092.	5.8	43
99	The Use of Mass Spectrometry for the Analysis of Histone Modifications. <i>Methods in Enzymology</i> , 2003, 377, 111-130.	0.4	42
100	The N-Terminus of <i>Drosophila</i> SU(VAR)3 α 9 Mediates Dimerization and Regulates Its Methyltransferase Activity. <i>Biochemistry</i> , 2004, 43, 3740-3749.	1.2	42
101	Site-specific acetylation of ISWI by GCN5. <i>BMC Molecular Biology</i> , 2007, 8, 73.	3.0	40
102	Cdc42-dependent actin dynamics controls maturation and secretory activity of dendritic cells. <i>Journal of Cell Biology</i> , 2015, 211, 553-567.	2.3	40
103	Molecular Connectivity of Mitochondrial Gene Expression and OXPHOS Biogenesis. <i>Molecular Cell</i> , 2020, 79, 1051-1065.e10.	4.5	40
104	Distinct metabolic adaptation of liver circadian pathways to acute and chronic patterns of alcohol intake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25250-25259.	3.3	38
105	Stage-Specific Histone Modification Profiles Reveal Global Transitions in the <i>Xenopus</i> Embryonic Epigenome. <i>PLoS ONE</i> , 2011, 6, e22548.	1.1	37
106	Myb-binding Protein 1a (Mybbp1a) Regulates Levels and Processing of Pre-ribosomal RNA. <i>Journal of Biological Chemistry</i> , 2012, 287, 24365-24377.	1.6	37
107	PRK1/PKN1 controls migration and metastasis of androgen-independent prostate cancer cells. <i>Oncotarget</i> , 2014, 5, 12646-12664.	0.8	36
108	The Integrity of the HMR complex is necessary for centromeric binding and reproductive isolation in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2021, 17, e1009744.	1.5	35

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109	ESC, ESCL and their roles in Polycomb Group mechanisms. <i>Mechanisms of Development</i> , 2008, 125, 527-541.	1.7	34
110	Epstein-Barr virus-mediated transformation of B cells induces global chromatin changes independent to the acquisition of proliferation. <i>Nucleic Acids Research</i> , 2014, 42, 249-263.	6.5	34
111	Morc3 silences endogenous retroviruses by enabling Daxx-mediated histone H3.3 incorporation. <i>Nature Communications</i> , 2021, 12, 5996.	5.8	34
112	Modifications of the Histone N-Terminal Domains: Evidence for an "Epigenetic Code"?. <i>Molecular Biotechnology</i> , 2001, 17, 01-14.	1.3	33
113	Regulation and function of H3K36 di-methylation by the trithorax-group protein complex AMC. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	33
114	Nucleoside analogue activators of cyclic AMP-independent protein kinase A of <i>Trypanosoma</i> . <i>Nature Communications</i> , 2019, 10, 1421.	5.8	33
115	Analysis of Histone Modifications by Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2008, 51, Unit 14.10.	2.8	32
116	Msp1 cooperates with the proteasome for extraction of arrested mitochondrial import intermediates. <i>Molecular Biology of the Cell</i> , 2020, 31, 753-767.	0.9	32
117	Every methyl counts – Epigenetic calculus. <i>FEBS Letters</i> , 2011, 585, 2001-2007.	1.3	31
118	MSL2 Combines Sensor and Effector Functions in Homeostatic Control of the <i>Drosophila</i> Dosage Compensation Machinery. <i>Molecular Cell</i> , 2012, 48, 647-654.	4.5	31
119	Clonal analysis of <i>Inquilinus limosus</i> isolates from six cystic fibrosis patients and specific serum antibody response. <i>Journal of Medical Microbiology</i> , 2006, 55, 1425-1433.	0.7	30
120	Shelterin and subtelomeric <sc>DNA</sc> sequences control nucleosome maintenance and genome stability. <i>EMBO Reports</i> , 2019, 20, .	2.0	30
121	Spt6 is a maintenance factor for centromeric CENP-A. <i>Nature Communications</i> , 2020, 11, 2919.	5.8	30
122	Proteomic screen in the simple metazoan <i>Hydra</i> identifies 14-3-3 binding proteins implicated in cellular metabolism, cytoskeletal organisation and Ca ²⁺ signalling. <i>BMC Cell Biology</i> , 2007, 8, 31.	3.0	29
123	The ribosome receptors Mrx15 and Mba1 jointly organize cotranslational insertion and protein biogenesis in mitochondria. <i>Molecular Biology of the Cell</i> , 2018, 29, 2386-2396.	0.9	29
124	Developmental regulation of N-terminal H2B methylation in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2012, 40, 1536-1549.	6.5	28
125	Identification of novel <i>Drosophila</i> centromere-associated proteins. <i>Proteomics</i> , 2014, 14, 2167-2178.	1.3	28
126	Fine Mapping of Posttranslational Modifications of the Linker Histone H1 from <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2008, 3, e1553.	1.1	26

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127	DEAD-box helicase DDX27 regulates 3' end formation of ribosomal 47S RNA and stably associates with the PeBoW-complex. <i>Experimental Cell Research</i> , 2015, 334, 146-159.	1.2	26
128	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	2.4	26
129	Remodeling of nuclear architecture by the thiodioxopiperazine metabolite chaetocin. <i>Experimental Cell Research</i> , 2010, 316, 1662-1680.	1.2	23
130	Mouse cytomegalovirus egress protein pM50 interacts with cellular endophilin-A2. <i>Cellular Microbiology</i> , 2013, 15, 335-351.	1.1	23
131	Site-specific methylation and acetylation of lysine residues in the C-terminal domain (CTD) of RNA polymerase II. <i>Transcription</i> , 2015, 6, 91-101.	1.7	22
132	Molecular Wiring of a Mitochondrial Translational Feedback Loop. <i>Molecular Cell</i> , 2020, 77, 887-900.e5.	4.5	22
133	Drosophila HP1c Is Regulated by an Auto-Regulatory Feedback Loop through Its Binding Partner Woc. <i>PLoS ONE</i> , 2009, 4, e5089.	1.1	21
134	PP32 and SET/TAF- β proteins regulate the acetylation of newly synthesized histone H4. <i>Nucleic Acids Research</i> , 2017, 45, 11700-11710.	6.5	21
135	A novel proteomics approach to epigenetic profiling of circulating nucleosomes. <i>Scientific Reports</i> , 2021, 11, 7256.	1.6	21
136	Phosphorylation of SU(VAR) β 9 by the Chromosomal Kinase JIL-1. <i>PLoS ONE</i> , 2010, 5, e10042.	1.1	21
137	In situ detection of histone variants and modifications in mouse brain using imaging mass spectrometry. <i>Proteomics</i> , 2016, 16, 437-447.	1.3	19
138	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. <i>Cell Systems</i> , 2016, 2, 49-58.	2.9	19
139	Histone Modifications: An Assembly Line for Active Chromatin?. <i>Current Biology</i> , 2003, 13, R22-R24.	1.8	18
140	NO Augments Endothelial Reactivity by Reducing Myoendothelial Calcium Signal Spreading. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 2280-2290.	1.1	18
141	Analog-sensitive cell line identifies cellular substrates of CDK9. <i>Oncotarget</i> , 2019, 10, 6934-6943.	0.8	18
142	The sounds of silence--histone deacetylation meets histone methylation. <i>Genetica</i> , 2003, 117, 159-164.	0.5	17
143	Cross-talk between Type Three Secretion System and Metabolism in <i>Yersinia</i> . <i>Journal of Biological Chemistry</i> , 2009, 284, 12165-12177.	1.6	17
144	Reply to "Chaetocin is a nonspecific inhibitor of histone lysine methyltransferases". <i>Nature Chemical Biology</i> , 2013, 9, 137-137.	3.9	17

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145	Specific threonine-4 phosphorylation and function of RNA polymerase II CTD during M phase progression. <i>Scientific Reports</i> , 2016, 6, 27401.	1.6	17
146	Histone Modifications in Stem Cell Development and Their Clinical Implications. <i>Stem Cell Reports</i> , 2020, 15, 1196-1205.	2.3	17
147	ATM induces MacroD2 nuclear export upon DNA damage. <i>Nucleic Acids Research</i> , 2017, 45, 244-254.	6.5	16
148	Trnp1 organizes diverse nuclear membrane-less compartments in neural stem cells. <i>EMBO Journal</i> , 2020, 39, e103373.	3.5	16
149	Analysis of Histone Modifications by Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2018, 92, e54.	2.8	15
150	The complete murine cDNA sequence of the transcription factor AP-2. <i>Nucleic Acids Research</i> , 1993, 21, 4844-4844.	6.5	14
151	Epigenetic reprogramming of cortical neurons through alteration of dopaminergic circuits. <i>Molecular Psychiatry</i> , 2014, 19, 1193-1200.	4.1	14
152	MIR sequences recruit zinc finger protein ZNF768 to expressed genes. <i>Nucleic Acids Research</i> , 2019, 47, 700-715.	6.5	14
153	Pumilio2 and Stauf2 selectively balance the synaptic proteome. <i>Cell Reports</i> , 2021, 35, 109279.	2.9	14
154	Chromatomics—the analysis of the chromatome. <i>Molecular BioSystems</i> , 2005, 1, 112-116.	2.9	13
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