

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	ImShot: An Open-Source Software for Probabilistic Identification of Proteins In Situ and Visualization of Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100242.	2.5	3
2	Dietary intervention improves health metrics and life expectancy of the genetically obese Titan mouse. <i>Communications Biology</i> , 2022, 5, 408.	2.0	4
3	Endotoxemia Accelerates Atherosclerosis Through Electrostatic Charge-Mediated Monocyte Adhesion. <i>Circulation</i> , 2021, 143, 254-266.	1.6	266
4	Reduced peroxisomal import triggers peroxisomal retrograde signaling. <i>Cell Reports</i> , 2021, 34, 108653.	2.9	9
5	<i>Helicobacter hepaticus</i> is required for immune targeting of bacterial heat shock protein 60 and fatal colitis in mice. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	8
6	Metabolic Analysis of Vitreous/Lens and Retina in Wild Type and Retinal Degeneration Mice. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2345.	1.8	6
7	A novel proteomics approach to epigenetic profiling of circulating nucleosomes. <i>Scientific Reports</i> , 2021, 11, 7256.	1.6	21
8	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
9	Exploring the Ion Channel TRPV2 and Testicular Macrophages in Mouse Testis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4727.	1.8	5
10	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
11	Investigation and Highly Accurate Prediction of Missed Tryptic Cleavages by Deep Learning. <i>Journal of Proteome Research</i> , 2021, 20, 3749-3757.	1.8	9
12	Pumilio2 and Staufien2 selectively balance the synaptic proteome. <i>Cell Reports</i> , 2021, 35, 109279.	2.9	14
13	Phosphorylation of the HP1 hinge region sequesters KAP1 in heterochromatin and promotes the exit from naïve pluripotency. <i>Nucleic Acids Research</i> , 2021, 49, 7406-7423.	6.5	9
14	GSNOR Contributes to Demethylation and Expression of Transposable Elements and Stress-Responsive Genes. <i>Antioxidants</i> , 2021, 10, 1128.	2.2	10
15	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
16	A systemic cell cycle block impacts stage-specific histone modification profiles during <i>Xenopus</i> embryogenesis. <i>PLoS Biology</i> , 2021, 19, e3001377.	2.6	2
17	MALDI-IMS combined with shotgun proteomics identify and localize new factors in male infertility. <i>Life Science Alliance</i> , 2021, 4, e202000672.	1.3	7
18	Discovery of Native Protein Complexes by Liquid Chromatography Followed by Quantitative Mass Spectrometry. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1336, 105-128.	0.8	0

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19	Morc3 silences endogenous retroviruses by enabling Daxx-mediated histone H3.3 incorporation. <i>Nature Communications</i> , 2021, 12, 5996.	5.8	34
20	Determining histone H4 acetylation patterns in human peripheral blood mononuclear cells using mass spectrometry. <i>Clinical Mass Spectrometry</i> , 2020, 15, 54-60.	1.9	3
21	Molecular Wiring of a Mitochondrial Translational Feedback Loop. <i>Molecular Cell</i> , 2020, 77, 887-900.e5.	4.5	22
22	BMAL1 Associates with NOP58 in the Nucleolus and Contributes to Pre-rRNA Processing. <i>IScience</i> , 2020, 23, 101151.	1.9	13
23	S-adenosyl- <scp>l</scp> -homocysteine hydrolase links methionine metabolism to the circadian clock and chromatin remodeling. <i>Science Advances</i> , 2020, 6, .	4.7	49
24	H4K20 Methylation Is Differently Regulated by Dilution and Demethylation in Proliferating and Cell-Cycle-Arrested <i>Xenopus</i> Embryos. <i>Cell Systems</i> , 2020, 11, 653-662.e8.	2.9	6
25	Histone Modifications in Stem Cell Development and Their Clinical Implications. <i>Stem Cell Reports</i> , 2020, 15, 1196-1205.	2.3	17
26	Physical Activity Dynamically Regulates the Hippocampal Proteome along the Dorso-Ventral Axis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3501.	1.8	4
27	Spt6 is a maintenance factor for centromeric CENP-A. <i>Nature Communications</i> , 2020, 11, 2919.	5.8	30
28	Harmonization of quality metrics and power calculation in multi-omic studies. <i>Nature Communications</i> , 2020, 11, 3092.	5.8	43
29	A multi-layered structure of the interphase chromocenter revealed by proximity-based biotinylation. <i>Nucleic Acids Research</i> , 2020, 48, 4161-4178.	6.5	11
30	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
31	Structure and Function of an Elongation Factor P Subfamily in Actinobacteria. <i>Cell Reports</i> , 2020, 30, 4332-4342.e5.	2.9	11
32	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
33	Mechanisms governing the pioneering and redistribution capabilities of the non-classical pioneer PU.1. <i>Nature Communications</i> , 2020, 11, 402.	5.8	76
34	New Approaches for Absolute Quantification of Stableâ€isotopeâ€Labeled Peptide Standards for Targeted Proteomics Based on a UV Active Tag. <i>Proteomics</i> , 2020, 20, e2000007.	1.3	7
35	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
36	Molecular Connectivity of Mitochondrial Gene Expression and OXPHOS Biogenesis. <i>Molecular Cell</i> , 2020, 79, 1051-1065.e10.	4.5	40

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37	Trnp1 organizes diverse nuclear membrane-less compartments in neural stem cells. <i>EMBO Journal</i> , 2020, 39, e103373.	3.5	16
38	Mapping protein networks in yeast mitochondria using proximity-dependent biotin identification coupled to proteomics. <i>STAR Protocols</i> , 2020, 1, 100219.	0.5	1
39	The Impact of One Carbon Metabolism on Histone Methylation. <i>Frontiers in Genetics</i> , 2019, 10, 764.	1.1	72
40	Quantification of Proteins and Histone Marks in Drosophila Embryos Reveals Stoichiometric Relationships Impacting Chromatin Regulation. <i>Developmental Cell</i> , 2019, 51, 632-644.e6.	3.1	50
41	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	2.4	26
42	Distinct CoREST complexes act in a cell-type-specific manner. <i>Nucleic Acids Research</i> , 2019, 47, 11649-11666.	6.5	10
43	A Drosophila cell-free system that senses DNA breaks and triggers phosphorylation signalling. <i>Nucleic Acids Research</i> , 2019, 47, 7444-7459.	6.5	4
44	Altered Localization of Hybrid Incompatibility Proteins in Drosophila. <i>Molecular Biology and Evolution</i> , 2019, 36, 1783-1792.	3.5	9
45	SETDB1-dependent heterochromatin stimulates alternative lengthening of telomeres. <i>Science Advances</i> , 2019, 5, eaav3673.	4.7	70
46	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
47	Nucleoside analogue activators of cyclic AMP-independent protein kinase A of Trypanosoma. <i>Nature Communications</i> , 2019, 10, 1421.	5.8	33
48	Multi-Reference Spectral Library Yields Almost Complete Coverage of Heterogeneous LC-MS/MS Data Sets. <i>Journal of Proteome Research</i> , 2019, 18, 1553-1566.	1.8	5
49	Measuring and Interpreting Oxygen Consumption Rates in Whole Fly Head Segments. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	1
50	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
51	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
52	MIR sequences recruit zinc finger protein ZNF768 to expressed genes. <i>Nucleic Acids Research</i> , 2019, 47, 700-715.	6.5	14
53	Shelterin and subtelomeric <scp>DNA</scp> sequences control nucleosome maintenance and genome stability. <i>EMBO Reports</i> , 2019, 20, .	2.0	30
54	Analog-sensitive cell line identifies cellular substrates of CDK9. <i>Oncotarget</i> , 2019, 10, 6934-6943.	0.8	18

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55	Analysis of Histone Modifications by Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2018, 92, e54.	2.8	15
56	Structural Architecture of the Nucleosome Remodeler ISWI Determined from Cross-Linking, Mass Spectrometry, SAXS, and Modeling. <i>Structure</i> , 2018, 26, 282-294.e6.	1.6	11
57	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
58	Regulation and function of H3K36 di-methylation by the trithorax-group protein complex AMC. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	33
59	PWWP2A binds distinct chromatin moieties and interacts with an MTA1-specific core NuRD complex. <i>Nature Communications</i> , 2018, 9, 4300.	5.8	46
60	Epigenetics and Metabolism in Health and Disease. <i>Frontiers in Genetics</i> , 2018, 9, 361.	1.1	81
61	Detection of Histone Modification Dynamics during the Cell Cycle by MS-Based Proteomics. <i>Methods in Molecular Biology</i> , 2018, 1832, 61-74.	0.4	2
62	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
63	Coronin 1A, a novel player in integrin biology, controls neutrophil trafficking in innate immunity. <i>Blood</i> , 2017, 130, 847-858.	0.6	56
64	MacroH2A histone variants maintain nuclear organization and heterochromatin architecture. <i>Journal of Cell Science</i> , 2017, 130, 1570-1582.	1.2	64
65	Adrenergic Signaling Strengthens Cardiac Myocyte Cohesion. <i>Circulation Research</i> , 2017, 120, 1305-1317.	2.0	55
66	NO Augments Endothelial Reactivity by Reducing Myoendothelial Calcium Signal Spreading. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 2280-2290.	1.1	18
67	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
68	PP32 and SET/TAF- I^2 proteins regulate the acetylation of newly synthesized histone H4. <i>Nucleic Acids Research</i> , 2017, 45, 11700-11710.	6.5	21
69	ATM induces MacroD2 nuclear export upon DNA damage. <i>Nucleic Acids Research</i> , 2017, 45, 244-254.	6.5	16
70	The <i>Drosophila</i> speciation factor HMR localizes to genomic insulator sites. <i>PLoS ONE</i> , 2017, 12, e0171798.	1.1	13
71	Inside front cover: In situ detection of histone variants and modifications in mouse brain using imaging mass spectrometry. <i>Proteomics</i> , 2016, 16, NA.	1.3	0
72	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

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73	Life span extension by targeting a link between metabolism and histone acetylation in <i>Drosophila</i> . EMBO Reports, 2016, 17, 455-469.	2.0	116
74	A Focus on Chromatin Proteomics. Proteomics, 2016, 16, 379-380.	1.3	1
75	Data on the kinetics of in vitro assembled chromatin. Data in Brief, 2016, 8, 353-359.	0.5	2
76	From HDAC to KDAC: we need to revisit non-epigenetic pathways affected by inhibiting lysine deacetylases in therapy. EMBO Reports, 2016, 17, 1673-1673.	2.0	4
77	Specific threonine-4 phosphorylation and function of RNA polymerase II CTD during M phase progression. Scientific Reports, 2016, 6, 27401.	1.6	17
78	The Metabolic Impact on Histone Acetylation and Transcription in Ageing. Trends in Biochemical Sciences, 2016, 41, 700-711.	3.7	143
79	H4K20me0 marks post-replicative chromatin and recruits the TONSL-MMS22L DNA repair complex. Nature, 2016, 534, 714-718.	13.7	172
80	A Quantitative Proteomic Analysis of In Vitro Assembled Chromatin. Molecular and Cellular Proteomics, 2016, 15, 945-959.	2.5	12
81	Heptad-Specific Phosphorylation of RNA Polymerase II CTD. Molecular Cell, 2016, 61, 305-314.	4.5	118
82	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. Cell Systems, 2016, 2, 49-58.	2.9	19
83	MALDI imaging mass spectrometry as a novel tool for detecting histone modifications in clinical tissue samples. Expert Review of Proteomics, 2016, 13, 275-284.	1.3	13
84	The histone acetyltransferase p300 inhibitor C646 reduces pro-inflammatory gene expression and inhibits histone deacetylases. Biochemical Pharmacology, 2016, 102, 130-140.	2.0	46
85	Assembly of methylated KDM1A and CHD1 drives androgen receptor-dependent transcription and translocation. Nature Structural and Molecular Biology, 2016, 23, 132-139.	3.6	70
86	Cdc42-dependent actin dynamics controls maturation and secretory activity of dendritic cells. Journal of Cell Biology, 2015, 211, 553-567.	2.3	40
87	Global and Specific Responses of the Histone Acetylome to Systematic Perturbation. Molecular Cell, 2015, 57, 559-571.	4.5	119
88	Identification of <i>Drosophila</i> centromere associated proteins by quantitative affinity purification-mass spectrometry. Data in Brief, 2015, 4, 544-550.	0.5	8
89	DNA methylation requires a DNMT1 ubiquitin interacting motif (UIM) and histone ubiquitination. Cell Research, 2015, 25, 911-929.	5.7	201
90	DEAD-box helicase DDX27 regulates 3' end formation of ribosomal 47S RNA and stably associates with the PeBoW-complex. Experimental Cell Research, 2015, 334, 146-159.	1.2	26

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91	Two distinct modes for propagation of histone PTMs across the cell cycle. <i>Genes and Development</i> , 2015, 29, 585-590.	2.7	334
92	Methylation of histone H3 lysine 9 occurs during translation. <i>Nucleic Acids Research</i> , 2015, 43, 9097-9106.	6.5	52
93	The Epoxyeicosatrienoic Acid Pathway Enhances Hepatic Insulin Signaling and is Repressed in Insulin-Resistant Mouse Liver*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2764-2774.	2.5	13
94	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
95	Cdc42-dependent actin dynamics controls maturation and secretory activity of dendritic cells. <i>Journal of Experimental Medicine</i> , 2015, 212, 212120IA102.	4.2	0
96	PRK1/PKN1 controls migration and metastasis of androgen-independent prostate cancer cells. <i>Oncotarget</i> , 2014, 5, 12646-12664.	0.8	36
97	LSD1 controls metastasis of androgen-independent prostate cancer cells through PXN and LPAR6. <i>Oncogenesis</i> , 2014, 3, e120-e120.	2.1	53
98	The histone variant H2A.Bbd is enriched at sites of DNA synthesis. <i>Nucleic Acids Research</i> , 2014, 42, 6405-6420.	6.5	61
99	Heterogeneous Antibody-Based Activity Assay for Lysine Specific Demethylase 1 (LSD1) on a Histone Peptide Substrate. <i>Journal of Biomolecular Screening</i> , 2014, 19, 973-978.	2.6	10
100	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
101	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
102	Identification of novel <i>Drosophila</i> centromere-associated proteins. <i>Proteomics</i> , 2014, 14, 2167-2178.	1.3	28
103	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
104	Ablation of D2 autoreceptors causes epigenetic reprogramming of cortical neurons. <i>Molecular Psychiatry</i> , 2014, 19, 1153-1153.	4.1	3
105	Epigenetic reprogramming of cortical neurons through alteration of dopaminergic circuits. <i>Molecular Psychiatry</i> , 2014, 19, 1193-1200.	4.1	14
106	Bioinformatic analysis of proteomics data. <i>BMC Systems Biology</i> , 2014, 8, S3.	3.0	131
107	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
108	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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109	A Pair of Centromeric Proteins Mediates Reproductive Isolation in <i>Drosophila</i> Species. <i>Developmental Cell</i> , 2013, 27, 412-424.	3.1	71
110	Stepwise Evolution of Essential Centromere Function in a <i>Drosophila</i> Neogene. <i>Science</i> , 2013, 340, 1211-1214.	6.0	94
111	Mouse cytomegalovirus egress protein pM50 interacts with cellular endophilin-A2. <i>Cellular Microbiology</i> , 2013, 15, 335-351.	1.1	23
112	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
113	Reply to "Chaetocin is a nonspecific inhibitor of histone lysine methyltransferases". <i>Nature Chemical Biology</i> , 2013, 9, 137-137.	3.9	17
114	RNA-Interference Components Are Dispensable for Transcriptional Silencing of the <i>Drosophila</i> Bithorax-Complex. <i>PLoS ONE</i> , 2013, 8, e65740.	1.1	7
115	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
116	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
117	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
118	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
119	Developmental regulation of N-terminal H2B methylation in <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 2012, 40, 1536-1549.	6.5	28
120	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
121	Connecting Threads: Epigenetics and Metabolism. <i>Cell</i> , 2012, 148, 24-28.	13.5	282
122	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
123	Df31 Protein and snoRNAs Maintain Accessible Higher-Order Structures of Chromatin. <i>Molecular Cell</i> , 2012, 48, 434-444.	4.5	108
124	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
125	Secretome protein enrichment identifies physiological BACE1 protease substrates in neurons. <i>EMBO Journal</i> , 2012, 31, 3157-3168.	3.5	279
126	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

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127	The RNA Helicase Rm62 Cooperates with SU(VAR)3-9 to Re-Silence Active Transcription in <i>Drosophila melanogaster</i> . PLoS ONE, 2011, 6, e20761.	1.1	9
128	Stage-Specific Histone Modification Profiles Reveal Global Transitions in the <i>Xenopus</i> Embryonic Epigenome. PLoS ONE, 2011, 6, e22548.	1.1	37
129	Related B cell clones that populate the CSF and CNS of patients with multiple sclerosis produce CSF immunoglobulin. Journal of Neuroimmunology, 2011, 233, 245-248.	1.1	119
130	Every methyl counts – Epigenetic calculus. FEBS Letters, 2011, 585, 2001-2007.	1.3	31
131	Cbp3 – Cbp6 interacts with the yeast mitochondrial ribosomal tunnel exit and promotes cytochrome <i>b</i> synthesis and assembly. Journal of Cell Biology, 2011, 193, 1101-1114.	2.3	91
132	Sequential Establishment of Marks on Soluble Histones H3 and H4. Journal of Biological Chemistry, 2011, 286, 17714-17721.	1.6	100
133	Cbp3 – Cbp6 interacts with the yeast mitochondrial ribosomal tunnel exit and promotes cytochrome <i>b</i> synthesis and assembly. Journal of Cell Biology, 2011, 194, 155-155.	2.3	0
134	Fast signals and slow marks: the dynamics of histone modifications. Trends in Biochemical Sciences, 2010, 35, 618-626.	3.7	268
135	Remodeling of nuclear architecture by the thiodioxopiperazine metabolite chaetocin. Experimental Cell Research, 2010, 316, 1662-1680.	1.2	23
136	Phosphorylation of histone H3T6 by PKC ζ controls demethylation at histone H3K4. Nature, 2010, 464, 792-796.	13.7	259
137	Proteins at the Polypeptide Tunnel Exit of the Yeast Mitochondrial Ribosome. Journal of Biological Chemistry, 2010, 285, 19022-19028.	1.6	62
138	Replication Stress Interferes with Histone Recycling and Predeposition Marking of New Histones. Molecular Cell, 2010, 37, 736-743.	4.5	242
139	Phosphorylation of SU(VAR)3 ω by the Chromosomal Kinase JIL-1. PLoS ONE, 2010, 5, e10042.	1.1	21
140	Establishment of Histone Modifications after Chromatin Assembly. Nucleic Acids Research, 2009, 37, 5032-5040.	6.5	94
141	Cross-talk between Type Three Secretion System and Metabolism in <i>Yersinia</i> . Journal of Biological Chemistry, 2009, 284, 12165-12177.	1.6	17
142	Interaction of HP1 and Brg1/Brm with the Globular Domain of Histone H3 Is Required for HP1-Mediated Repression. PLoS Genetics, 2009, 5, e1000769.	1.5	74
143	Monomethylation of Lysine 20 on Histone H4 Facilitates Chromatin Maturation. Molecular and Cellular Biology, 2009, 29, 57-67.	1.1	46
144	The HP1 – CAF1 – SetDB1-containing complex provides H3K9me1 for Suv39-mediated K9me3 in pericentric heterochromatin. EMBO Reports, 2009, 10, 769-775.	2.0	201

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145	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
146	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
147	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
148	ESC, ESCL and their roles in Polycomb Group mechanisms. <i>Mechanisms of Development</i> , 2008, 125, 527-541.	1.7	34
149	Analysis of Histone Modifications by Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2008, 51, Unit 14.10.	2.8	32
150	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
151	Yersinia 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
152	PRMT6-mediated methylation of R2 in histone H3 antagonizes H3 K4 trimethylation. <i>Genes and Development</i> , 2007, 21, 3369-3380.	2.7	238
153	Regulated Intramembrane Proteolysis of the Interleukin-1 Receptor II by $\hat{1}\pm$, $\hat{1}^2$, and $\hat{1}^3$ -Secretase. <i>Journal of Biological Chemistry</i> , 2007, 282, 11982-11995.	1.6	128
154	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
155	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
156	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
157	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
158	Proteomic screen in the simple metazoan Hydra 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
159	Site-specific acetylation of ISWI by GCN5. <i>BMC Molecular Biology</i> , 2007, 8, 73.	3.0	40
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