

Brian D Strahl

List of Publications by Year in descending order

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Version: 2024-02-01

169
papers

28,202
citations

21215

62
h-index

6512

162
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181
all docs

181
docs citations

181
times ranked

27241
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct developmental phenotypes result from mutation of Set8/KMT5A and histone H4 lysine 20 in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2022, , .	1.2	2
2	Combined noncanonical NF- κ B agonism and targeted BET bromodomain inhibition reverse HIV latency ex vivo. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	17
3	Taf2 mediates DNA binding of Taf14. <i>Nature Communications</i> , 2022, 13, .	5.8	4
4	The SAGA continues: The rise of cis- and trans-histone crosstalk pathways. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194600.	0.9	13
5	HDAC inhibition results in widespread alteration of the histone acetylation landscape and BRD4 targeting to gene bodies. <i>Cell Reports</i> , 2021, 34, 108638.	2.9	60
6	Catalysis-dependent and redundant roles of Dma1 and Dma2 in maintenance of genome stability in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2021, 296, 100721.	1.6	0
7	Oncohistones: corruption at the core. <i>Nature Chemical Biology</i> , 2021, 17, 370-371.	3.9	2
8	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. <i>Nature Communications</i> , 2021, 12, 2490.	5.8	63
9	Binding specificity and function of the SWI/SNF subunit SMARCA4 bromodomain interaction with acetylated histone H3K14. <i>Journal of Biological Chemistry</i> , 2021, 297, 101145.	1.6	3
10	Mechanically transduced immunosorbent assay to measure protein-protein interactions. <i>ELife</i> , 2021, 10, .	2.8	3
11	Recognition of acetylated histone by Yaf9 regulates metabolic cycling of transcription initiation and chromatin regulatory factors. <i>Genes and Development</i> , 2021, 35, 1678-1692.	2.7	3
12	Engineered Reader Proteins for Enhanced Detection of Methylated Lysine on Histones. <i>ACS Chemical Biology</i> , 2020, 15, 103-111.	1.6	15
13	An optogenetic switch for the Set2 methyltransferase provides evidence for transcription-dependent and -independent dynamics of H3K36 methylation. <i>Genome Research</i> , 2020, 30, 1605-1617.	2.4	10
14	Direct readout of heterochromatic H3K9me3 regulates DNMT1-mediated maintenance DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18439-18447.	3.3	62
15	BAHCC1 binds H3K27me3 via a conserved BAH module to mediate gene silencing and oncogenesis. <i>Nature Genetics</i> , 2020, 52, 1384-1396.	9.4	57
16	Molecular mechanism of the MORC4 ATPase activation. <i>Nature Communications</i> , 2020, 11, 5466.	5.8	14
17	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020, 370, .	6.0	24
18	The histone and non-histone methyllysine reader activities of the UHRF1 tandem Tudor domain are dispensable for the propagation of aberrant DNA methylation patterning in cancer cells. <i>Epigenetics and Chromatin</i> , 2020, 13, 44.	1.8	10

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19	Evaluation of EED Inhibitors as a Class of PRC2-Targeted Small Molecules for HIV Latency Reversal. ACS Infectious Diseases, 2020, 6, 1719-1733.	1.8	17
20	Unique and Shared Roles for Histone H3K36 Methylation States in Transcription Regulation Functions. Cell Reports, 2020, 31, 107751.	2.9	35
21	The histone H4 basic patch regulates SAGA-mediated H2B deubiquitination and histone acetylation. Journal of Biological Chemistry, 2020, 295, 6561-6569.	1.6	11
22	Characterization of the plant homeodomain (PHD) reader family for their histone tail interactions. Epigenetics and Chromatin, 2020, 13, 3.	1.8	73
23	Binding to medium and long chain fatty acyls is a common property of HEAT and ARM repeat modules. Scientific Reports, 2019, 9, 14226.	1.6	3
24	Histone H3K23-specific acetylation by MORF is coupled to H3K14 acylation. Nature Communications, 2019, 10, 4724.	5.8	56
25	Recognition of Histone Crotonylation by Taf14 Links Metabolic State to Gene Expression. Molecular Cell, 2019, 76, 909-921.e3.	4.5	83
26	Lysine 27 of replication-independent histone H3.3 is required for Polycomb target gene silencing but not for gene activation. PLoS Genetics, 2019, 15, e1007932.	1.5	34
27	Selective binding of the PHD6 finger of MLL4 to histone H4K16ac links MLL4 and MOF. Nature Communications, 2019, 10, 2314.	5.8	40
28	Improved methods for the detection of histone interactions with peptide microarrays. Scientific Reports, 2019, 9, 6265.	1.6	17
29	Neutrophils: back in the thrombosis spotlight. Blood, 2019, 133, 2186-2197.	0.6	107
30	H3K9 Promotes Under-Replication of Pericentromeric Heterochromatin in Drosophila Salivary Gland Polytene Chromosomes. Genes, 2019, 10, 93.	1.0	11
31	Investigation into the Role of the Set2 Autoinhibitory Domain in H3K36 Methyltransferase Activity. FASEB Journal, 2019, 33, 622.2.	0.2	0
32	Functional Redundancy of Variant and Canonical Histone H3 Lysine 9 Modification in <i>Drosophila</i> . Genetics, 2018, 208, 229-244.	1.2	21
33	Set2 methyltransferase facilitates cell cycle progression by maintaining transcriptional fidelity. Nucleic Acids Research, 2018, 46, 1331-1344.	6.5	23
34	Quantitative Characterization of Bivalent Probes for a Dual Bromodomain Protein, Transcription Initiation Factor TFIID Subunit 1. Biochemistry, 2018, 57, 2140-2149.	1.2	16
35	Engineering Improved Photoswitches for the Control of Nucleocytoplasmic Distribution. ACS Synthetic Biology, 2018, 7, 2898-2907.	1.9	17
36	Casein Kinase II Phosphorylation of Spt6 Enforces Transcriptional Fidelity by Maintaining Spn1-Spt6 Interaction. Cell Reports, 2018, 25, 3476-3489.e5.	2.9	20

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37	Chromatin conformation and transcriptional activity are permissive regulators of DNA replication initiation in <i>Drosophila</i> . <i>Genome Research</i> , 2018, 28, 1688-1700.	2.4	29
38	Structural insights into the π - π stacking mechanism and DNA-binding activity of the YEATS domain. <i>Nature Communications</i> , 2018, 9, 4574.	5.8	45
39	Yaf9 subunit of the NuA4 and SWR1 complexes targets histone H3K27ac through its YEATS domain. <i>Nucleic Acids Research</i> , 2018, 46, 421-430.	6.5	34
40	Recognition of cancer mutations in histone H3K36 by epigenetic writers and readers. <i>Epigenetics</i> , 2018, 13, 683-692.	1.3	17
41	PBRM1 bromodomains variably influence nucleosome interactions and cellular function. <i>Journal of Biological Chemistry</i> , 2018, 293, 13592-13603.	1.6	33
42	Transcription start site profiling uncovers divergent transcription and enhancer-associated RNAs in <i>Drosophila melanogaster</i> . <i>BMC Genomics</i> , 2018, 19, 157.	1.2	34
43	<i>SETD2</i> Haploinsufficiency for Microtubule Methylation Is an Early Driver of Genomic Instability in Renal Cell Carcinoma. <i>Cancer Research</i> , 2018, 78, 3135-3146.	0.4	48
44	Spt6 Association with RNA Polymerase II Directs mRNA Turnover During Transcription. <i>Molecular Cell</i> , 2018, 70, 1054-1066.e4.	4.5	38
45	H3K36 Methylation Regulates Nutrient Stress Response in <i>Saccharomyces cerevisiae</i> by Enforcing Transcriptional Fidelity. <i>Cell Reports</i> , 2017, 19, 2371-2382.	2.9	54
46	Expanding the Reader Landscape of Histone Acylation. <i>Structure</i> , 2017, 25, 571-573.	1.6	8
47	Shaping the cellular landscape with Set2/ <i>SETD2</i> methylation. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3317-3334.	2.4	103
48	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. <i>Cell Reports</i> , 2017, 21, 455-466.	2.9	36
49	A Unique pH-Dependent Recognition of Methylated Histone H3K4 by PPS and DIDO. <i>Structure</i> , 2017, 25, 1530-1539.e3.	1.6	22
50	Redundant Functions for Nap1 and Chz1 in H2A.Z Deposition. <i>Scientific Reports</i> , 2017, 7, 10791.	1.6	13
51	Histone peptide microarray screen of chromo and Tudor domains defines new histone lysine methylation interactions. <i>Epigenetics and Chromatin</i> , 2017, 10, 12.	1.8	47
52	The Arginine Methyltransferase PRMT6 Regulates DNA Methylation and Contributes to Global DNA Hypomethylation in Cancer. <i>Cell Reports</i> , 2017, 21, 3390-3397.	2.9	60
53	Histone gene replacement reveals a post-transcriptional role for H3K36 in maintaining metazoan transcriptome fidelity. <i>ELife</i> , 2017, 6, .	2.8	42
54	Multivalent Histone and DNA Engagement by a PHD/BRD/PWWP Triple Reader Cassette Recruits ZMYND8 to K14ac-Rich Chromatin. <i>Cell Reports</i> , 2016, 17, 2724-2737.	2.9	86

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55	Combinatorial Histone Readout by the Dual Plant Homeodomain (PHD) Fingers of Rco1 Mediates Rpd3S Chromatin Recruitment and the Maintenance of Transcriptional Fidelity. <i>Journal of Biological Chemistry</i> , 2016, 291, 14796-14802.	1.6	26
56	The Taf14 YEATS domain is a reader of histone crotonylation. <i>Nature Chemical Biology</i> , 2016, 12, 396-398.	3.9	195
57	Light-induced nuclear export reveals rapid dynamics of epigenetic modifications. <i>Nature Chemical Biology</i> , 2016, 12, 399-401.	3.9	89
58	Quantitative Analysis of Dynamic Protein Interactions during Transcription Reveals a Role for Casein Kinase II in Polymerase-associated Factor (PAF) Complex Phosphorylation and Regulation of Histone H2B Monoubiquitylation. <i>Journal of Biological Chemistry</i> , 2016, 291, 13410-13420.	1.6	15
59	Multivalent Chromatin Engagement and Inter-domain Crosstalk Regulate MORC3 ATPase. <i>Cell Reports</i> , 2016, 16, 3195-3207.	2.9	40
60	Direct interrogation of the role of H3K9 in metazoan heterochromatin function. <i>Genes and Development</i> , 2016, 30, 1866-1880.	2.7	67
61	Structure/Function Analysis of Recurrent Mutations in SETD2 Protein Reveals a Critical and Conserved Role for a SET Domain Residue in Maintaining Protein Stability and Histone H3 Lys-36 Trimethylation. <i>Journal of Biological Chemistry</i> , 2016, 291, 21283-21295.	1.6	64
62	Insights into newly discovered marks and readers of epigenetic information. <i>Nature Chemical Biology</i> , 2016, 12, 662-668.	3.9	132
63	Regulation of transcriptional elongation in pluripotency and cell differentiation by the PHD-finger protein Phf5a. <i>Nature Cell Biology</i> , 2016, 18, 1127-1138.	4.6	57
64	Histone H3 and TORC1 prevent organelle dysfunction and cell death by promoting nuclear retention of HMGB proteins. <i>Epigenetics and Chromatin</i> , 2016, 9, 34.	1.8	8
65	A course-based undergraduate research experience investigating p300 bromodomain mutations. <i>Biochemistry and Molecular Biology Education</i> , 2016, 44, 68-74.	0.5	14
66	Chromatin condensation and recruitment of PHD finger proteins to histone H3K4me3 are mutually exclusive. <i>Nucleic Acids Research</i> , 2016, 44, 6102-6112.	6.5	30
67	Histone H3K36 methylation regulates pre-mRNA splicing in <i>Saccharomyces cerevisiae</i> . <i>RNA Biology</i> , 2016, 13, 412-426.	1.5	46
68	Antigen clasp by two antigen-binding sites of an exceptionally specific antibody for histone methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2092-2097.	3.3	39
69	The essential role of acetyllysine binding by the YEATS domain in transcriptional regulation. <i>Transcription</i> , 2016, 7, 14-20.	1.7	28
70	Regulation of Methyllysine Readers through Phosphorylation. <i>ACS Chemical Biology</i> , 2016, 11, 547-553.	1.6	15
71	Hemi-methylated DNA regulates DNA methylation inheritance through allosteric activation of H3 ubiquitylation by UHRF1. <i>ELife</i> , 2016, 5, .	2.8	111
72	Neuronal Stress Pathway Mediating a Histone Methyl/Phospho Switch Is Required for Herpes Simplex Virus Reactivation. <i>Cell Host and Microbe</i> , 2015, 18, 649-658.	5.1	121

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73	A Role for Widely Interspaced Zinc Finger (WIZ) in Retention of the G9a Methyltransferase on Chromatin. <i>Journal of Biological Chemistry</i> , 2015, 290, 26088-26102.	1.6	29
74	Structural Plasticity of Methyllysine Recognition by the Tandem Tudor Domain of 53BP1. <i>Structure</i> , 2015, 23, 312-321.	1.6	32
75	An Acetyl-Methyl Switch Drives a Conformational Change in p53. <i>Structure</i> , 2015, 23, 322-331.	1.6	21
76	Product Binding Enforces the Genomic Specificity of a Yeast Polycomb Repressive Complex. <i>Cell</i> , 2015, 160, 204-218.	13.5	124
77	Interrogating the Function of Metazoan Histones using Engineered Gene Clusters. <i>Developmental Cell</i> , 2015, 32, 373-386.	3.1	139
78	Identification of a Fragment-like Small Molecule Ligand for the Methyl-lysine Binding Protein, 53BP1. <i>ACS Chemical Biology</i> , 2015, 10, 1072-1081.	1.6	56
79	From Histones to Ribosomes: A Chromatin Regulator Tangoes with Translation. <i>Cancer Discovery</i> , 2015, 5, 228-230.	7.7	3
80	Non-canonical Bromodomain within DNA-PKcs Promotes DNA Damage Response and Radioresistance through Recognizing an IR-Induced Acetyl-Lysine on H2AX. <i>Chemistry and Biology</i> , 2015, 22, 849-861.	6.2	15
81	An Interactive Database for the Assessment of Histone Antibody Specificity. <i>Molecular Cell</i> , 2015, 59, 502-511.	4.5	139
82	Molecular Insights into Inhibition of the Methylated Histone-Plant Homeodomain Complexes by Calixarenes. <i>Journal of Biological Chemistry</i> , 2015, 290, 22919-22930.	1.6	33
83	An Allosteric Interaction Links USP7 to Deubiquitination and Chromatin Targeting of UHRF1. <i>Cell Reports</i> , 2015, 12, 1400-1406.	2.9	78
84	Association of Taf14 with acetylated histone H3 directs gene transcription and the DNA damage response. <i>Genes and Development</i> , 2015, 29, 1795-1800.	2.7	65
85	The PZP Domain of AF10 Senses Unmodified H3K27 to Regulate DOT1L-Mediated Methylation of H3K79. <i>Molecular Cell</i> , 2015, 60, 319-327.	4.5	78
86	A PWWP Domain-Containing Protein Targets the NuA3 Acetyltransferase Complex via Histone H3 Lysine 36 trimethylation to Coordinate Transcriptional Elongation at Coding Regions. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2883-2895.	2.5	48
87	A feed forward circuit comprising Spt6, Ctk1 and PAF regulates Pol II CTD phosphorylation and transcription elongation. <i>Nucleic Acids Research</i> , 2014, 42, 870-881.	6.5	38
88	Interpreting the language of histone and DNA modifications. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 627-643.	0.9	596
89	Catalysis-dependent stabilization of Bre1 fine-tunes histone H2B ubiquitylation to regulate gene transcription. <i>Genes and Development</i> , 2014, 28, 1647-1652.	2.7	18
90	Chromatin biochemistry enters the next generation of code 'seq-ing'. <i>Nature Methods</i> , 2014, 11, 799-800.	9.0	0

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91	SET-ting the stage for DNA repair. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 655-657.	3.6	25
92	The Histone-H3K4-Specific Demethylase KDM5B Binds to Its Substrate and Product through Distinct PHD Fingers. <i>Cell Reports</i> , 2014, 6, 325-335.	2.9	145
93	A Histone Methylation Network Regulates Transgenerational Epigenetic Memory in <i>C.Âlegans</i> . <i>Cell Reports</i> , 2014, 7, 113-126.	2.9	146
94	Identification of a BET Family Bromodomain/Casein Kinase II/TAF-Containing Complex as a Regulator of Mitotic Condensin Function. <i>Cell Reports</i> , 2014, 6, 892-905.	2.9	11
95	Hitting the â€˜markâ€™™: Interpreting lysine methylation in the context of active transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1353-1361.	0.9	74
96	An RNA polymerase II-coupled function for histone H3K36 methylation in checkpoint activation and DSB repair. <i>Nature Communications</i> , 2014, 5, 3965.	5.8	104
97	Recombinant antibodies to histone post-translational modifications. <i>Nature Methods</i> , 2013, 10, 992-995.	9.0	58
98	Molecular basis for chromatin binding and regulation of MLL5. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11296-11301.	3.3	72
99	An H3K36 Methylation-Engaging Tudor Motif of Polycomb-like Proteins Mediates PRC2 Complex Targeting. <i>Molecular Cell</i> , 2013, 49, 571-582.	4.5	221
100	Dido3 PHD Modulates Cell Differentiation and Division. <i>Cell Reports</i> , 2013, 4, 148-158.	2.9	54
101	Polymerase IV occupancy at RNA-directed DNA methylation sites requires SHH1. <i>Nature</i> , 2013, 498, 385-389.	13.7	310
102	Structures of RNA polymerase II complexes with Bye1, a chromatin-binding PHF3/DIDO homologue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15277-15282.	3.3	38
103	Multivalent histone engagement by the linked tandem Tudor and PHD domains of UHRF1 is required for the epigenetic inheritance of DNA methylation. <i>Genes and Development</i> , 2013, 27, 1288-1298.	2.7	155
104	Stress-Free with Rpd3: a Unique Chromatin Complex Mediates the Response to Oxidative Stress. <i>Molecular and Cellular Biology</i> , 2013, 33, 3726-3727.	1.1	15
105	Targeted silencing of the oncogenic transcription factor SOX2 in breast cancer. <i>Nucleic Acids Research</i> , 2012, 40, 6725-6740.	6.5	138
106	Peptide Microarrays to Interrogate the â€œHistone Codeâ€: <i>Methods in Enzymology</i> , 2012, 512, 107-135.	0.4	64
107	Epigenetic reprogramming of cancer cells via targeted DNA methylation. <i>Epigenetics</i> , 2012, 7, 350-360.	1.3	189
108	Poly-acetylated chromatin signatures are preferred epitopes for site-specific histone H4 acetyl antibodies. <i>Scientific Reports</i> , 2012, 2, 489.	1.6	34

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109	Tandem PHD Fingers of MORF/MOZ Acetyltransferases Display Selectivity for Acetylated Histone H3 and Are Required for the Association with Chromatin. <i>Journal of Molecular Biology</i> , 2012, 424, 328-338.	2.0	75
110	Broad Ranges of Affinity and Specificity of Anti-Histone Antibodies Revealed by a Quantitative Peptide Immunoprecipitation Assay. <i>Journal of Molecular Biology</i> , 2012, 424, 391-399.	2.0	67
111	Long noncoding RNAs are rarely translated in two human cell lines. <i>Genome Research</i> , 2012, 22, 1646-1657.	2.4	346
112	DNA Replication Origin Function Is Promoted by H3K4 Di-methylation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2012, 192, 371-384.	1.2	38
113	Association of UHRF1 with methylated H3K9 directs the maintenance of DNA methylation. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1155-1160.	3.6	313
114	RNA Polymerase II Carboxyl-terminal Domain Phosphorylation Regulates Protein Stability of the Set2 Methyltransferase and Histone H3 Di- and Trimethylation at Lysine 36. <i>Journal of Biological Chemistry</i> , 2012, 287, 3249-3256.	1.6	50
115	Antibody recognition of histone post-translational modifications: emerging issues and future prospects. <i>Epigenomics</i> , 2011, 3, 247-249.	1.0	41
116	OPERating ON Chromatin, a Colorful Language where Context Matters. <i>Journal of Molecular Biology</i> , 2011, 409, 36-46.	2.0	321
117	Identification of Lysine 37 of Histone H2B as a Novel Site of Methylation. <i>PLoS ONE</i> , 2011, 6, e16244.	1.1	29
118	Influence of Combinatorial Histone Modifications on Antibody and Effector Protein Recognition. <i>Current Biology</i> , 2011, 21, 53-58.	1.8	161
119	Thermodynamic Stability of Histone H3 Is a Necessary but not Sufficient Driving Force for its Evolutionary Conservation. <i>PLoS Computational Biology</i> , 2011, 7, e1001042.	1.5	20
120	The Ccr4-Not Complex Interacts with the mRNA Export Machinery. <i>PLoS ONE</i> , 2011, 6, e18302.	1.1	46
121	Histone H2BK123 monoubiquitination is the critical determinant for H3K4 and H3K79 trimethylation by COMPASS and Dot1. <i>Journal of Cell Biology</i> , 2009, 186, 371-377.	2.3	118
122	Protein modifications in transcription elongation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2009, 1789, 26-36.	0.9	59
123	The Set2/Rpd3S Pathway Suppresses Cryptic Transcription without Regard to Gene Length or Transcription Frequency. <i>PLoS ONE</i> , 2009, 4, e4886.	1.1	57
124	The histone methylase Set2p and the histone deacetylase Rpd3p repress meiotic recombination at the HIS4 meiotic recombination hotspot in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2008, 7, 1298-1308.	1.3	41
125	Roles for Ctk1 and Spt6 in Regulating the Different Methylation States of Histone H3 Lysine 36. <i>Molecular and Cellular Biology</i> , 2008, 28, 4915-4926.	1.1	140
126	Epigenomics: A Roadmap to Chromatin. <i>Science</i> , 2008, 322, 853-853.	6.0	9

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127	Global histone H3 lysine 4 methylation patterns in human breast cancer. <i>FASEB Journal</i> , 2008, 22, 470.1.	0.2	0
128	Identification of Histone H3 Lysine 36 Acetylation as a Highly Conserved Histone Modification. <i>Journal of Biological Chemistry</i> , 2007, 282, 7632-7640.	1.6	126
129	CCR4/NOT complex associates with the proteasome and regulates histone methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5836-5841.	3.3	75
130	H2B ubiquitylation in transcriptional control: a FACT-finding mission. <i>Genes and Development</i> , 2007, 21, 737-743.	2.7	57
131	The RNA Polymerase II Kinase Ctk1 Regulates Positioning of a 5â€² Histone Methylation Boundary along Genes. <i>Molecular and Cellular Biology</i> , 2007, 27, 721-731.	1.1	54
132	Unlocking Cell Fate. <i>Science</i> , 2007, 318, 403-404.	6.0	20
133	H2B Ubiquitylation Acts as a Barrier to Ctk1 Nucleosomal Recruitment Prior to Removal by Ubp8 within a SAGA-Related Complex. <i>Molecular Cell</i> , 2007, 27, 275-288.	4.5	196
134	Organismal Differences in Post-translational Modifications in Histones H3 and H4. <i>Journal of Biological Chemistry</i> , 2007, 282, 7641-7655.	1.6	267
135	The Set2 methyltransferase associates with Ssn6 yet Tup1-Ssn6 repression is independent of histone methylation. <i>Biochemical and Biophysical Research Communications</i> , 2006, 339, 905-914.	1.0	5
136	Accelerated nuclei preparation and methods for analysis of histone modifications in yeast. <i>Methods</i> , 2006, 40, 296-302.	1.9	27
137	Opposing roles for Set2 and yFACT in regulating TBP binding at promoters. <i>EMBO Journal</i> , 2006, 25, 4479-4489.	3.5	64
138	Structure and Carboxyl-terminal Domain (CTD) Binding of the Set2 SRI Domain That Couples Histone H3 Lys36 Methylation to Transcription*. <i>Journal of Biological Chemistry</i> , 2006, 281, 13-15.	1.6	76
139	BUR Kinase Selectively Regulates H3 K4 Trimethylation and H2B Ubiquitylation through Recruitment of the PAF Elongation Complex. <i>Current Biology</i> , 2005, 15, 1487-1493.	1.8	147
140	Methylation of Histone H3 Lysine 36 Is Required for Normal Development in <i>Neurospora crassa</i> . <i>Eukaryotic Cell</i> , 2005, 4, 1455-1464.	3.4	88
141	Histone H3 K36 Methylation Is Associated with Transcription Elongation in <i>Schizosaccharomyces pombe</i> . <i>Eukaryotic Cell</i> , 2005, 4, 1446-1454.	3.4	106
142	Role of Protein Methylation in Regulation of Transcription. <i>Endocrine Reviews</i> , 2005, 26, 147-170.	8.9	392
143	A Novel Domain in Set2 Mediates RNA Polymerase II Interaction and Couples Histone H3 K36 Methylation with Transcript Elongation. <i>Molecular and Cellular Biology</i> , 2005, 25, 3305-3316.	1.1	440
144	Histone H2B Ubiquitylation Is Associated with Elongating RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2005, 25, 637-651.	1.1	299

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145	Dimethylation of Histone H3 at Lysine 36 Demarcates Regulatory and Nonregulatory Chromatin Genome-Wide. <i>Molecular and Cellular Biology</i> , 2005, 25, 9447-9459.	1.1	166
146	Cotranscriptional Set2 Methylation of Histone H3 Lysine 36 Recruits a Repressive Rpd3 Complex. <i>Cell</i> , 2005, 123, 593-605.	13.5	712
147	Evidence for nucleosome depletion at active regulatory regions genome-wide. <i>Nature Genetics</i> , 2004, 36, 900-905.	9.4	644
148	A nucleosomal function for I κ B kinase- α in NF- κ B-dependent gene expression. <i>Nature</i> , 2003, 423, 659-663.	13.7	510
149	Phosphorylation of RNA polymerase II CTD regulates H3 methylation in yeast. <i>Genes and Development</i> , 2003, 17, 654-663.	2.7	363
150	Involvement of Histone Methylation and Phosphorylation in Regulation of Transcription by Thyroid Hormone Receptor. <i>Molecular and Cellular Biology</i> , 2002, 22, 5688-5697.	1.1	128
151	Set2 Is a Nucleosomal Histone H3-Selective Methyltransferase That Mediates Transcriptional Repression. <i>Molecular and Cellular Biology</i> , 2002, 22, 1298-1306.	1.1	495
152	The nature of FSH induction by GnRH. <i>Trends in Endocrinology and Metabolism</i> , 2002, 13, 257-263.	3.1	35
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