

# Jerry L Workman

## List of Publications by Year in descending order

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228  
papers

30,308  
citations

3930

88  
h-index

4880

168  
g-index

306  
all docs

306  
docs citations

306  
times ranked

22759  
citing authors

#	ARTICLE	IF	CITATIONS
1	The linker histone Hho1 modulates the activity of ATP-dependent chromatin remodeling complexes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194781.	0.9	5
2	MPTAC links alkylation damage signaling to sterol biosynthesis. <i>Redox Biology</i> , 2022, 51, 102270.	3.9	2
3	Metabolic regulation of telomere silencing by SESAME complex-catalyzed H3T11 phosphorylation. <i>Nature Communications</i> , 2021, 12, 594.	5.8	18
4	The methyltransferase SETD2 couples transcription and splicing by engaging mRNA processing factors through its SHI domain. <i>Nature Communications</i> , 2021, 12, 1443.	5.8	42
5	The SESAME complex regulates cell senescence through the generation of acetyl-CoA. <i>Nature Metabolism</i> , 2021, 3, 983-1000.	5.1	23
6	Nucleotide Metabolism Behind Epigenetics. <i>Frontiers in Endocrinology</i> , 2021, 12, 731648.	1.5	8
7	The disordered regions of the methyltransferase SETD2 govern its function by regulating its proteolysis and phase separation. <i>Journal of Biological Chemistry</i> , 2021, 297, 101075.	1.6	8
8	Macrophages, Metabolites, and Nucleosomes: Chromatin at the Intersection between Aging and Inflammation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10274.	1.8	8
9	MOCS2 links nucleotide metabolism to nucleoli function. <i>Journal of Molecular Cell Biology</i> , 2021, , .	1.5	3
10	Structural basis of the interaction between SETD2 methyltransferase and hnRNP L paralogs for governing co-transcriptional splicing. <i>Nature Communications</i> , 2021, 12, 6452.	5.8	12
11	The SAGA core module is critical during <i>Drosophila</i> oogenesis and is broadly recruited to promoters. <i>PLoS Genetics</i> , 2021, 17, e1009668.	1.5	0
12	Regulation of SETD2 stability is important for the fidelity of H3K36me3 deposition. <i>Epigenetics and Chromatin</i> , 2020, 13, 40.	1.8	20
13	Î²-Catenin and Associated Proteins Regulate Lineage Differentiation in Ground State Mouse Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2020, 15, 662-676.	2.3	11
14	Driving integrative structural modeling with serial capture affinity purification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31861-31870.	3.3	8
15	SAGA Structures Provide Mechanistic Models for Gene Activation. <i>Trends in Biochemical Sciences</i> , 2020, 45, 547-549.	3.7	5
16	When histones are under glucose starvation. <i>Journal of Biosciences</i> , 2020, 45, 1.	0.5	3
17	The SAGA chromatin-modifying complex: the sum of its parts is greater than the whole. <i>Genes and Development</i> , 2020, 34, 1287-1303.	2.7	38
18	Yeast Nuak1 phosphorylates histone H3 threonine 11 in low glucose stress by the cooperation of AMPK and CK2 signaling. <i>ELife</i> , 2020, 9, .	2.8	7

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19	The plasticity of the pyruvate dehydrogenase complex confers a labile structure that is associated with its catalytic activity. PLoS ONE, 2020, 15, e0243489.	1.1	5
20	When histones are under glucose starvation. Journal of Biosciences, 2020, 45, .	0.5	1
21	Histone lysine de- $\beta$ -hydroxybutyrylation by SIRT3. Cell Research, 2019, 29, 694-695.	5.7	10
22	Rebooting the Epigenome: Erasure of Parental Histone Marks for Establishing the Regulatory Landscape in Zygotes. Biochemistry, 2019, 58, 4387-4388.	1.2	0
23	Exogenous pyruvate represses histone gene expression and inhibits cancer cell proliferation via the NAMPT $\rightarrow$ NAD $^+$ $\rightarrow$ SIRT1 pathway. Nucleic Acids Research, 2019, 47, 11132-11150.	6.5	32
24	NSL complex acetylates Lamin A/C. Nature Cell Biology, 2019, 21, 1177-1178.	4.6	0
25	Characterization of a metazoan ADA acetyltransferase complex. Nucleic Acids Research, 2019, 47, 3383-3394.	6.5	26
26	Identification of a nuclear localization signal and importin beta members mediating NUA1 nuclear import inhibited by oxidative stress. Journal of Cellular Biochemistry, 2019, 120, 16088-16107.	1.2	12
27	Set1-catalyzed H3K4 trimethylation antagonizes the HIR/Asf1/Rtt106 repressor complex to promote histone gene expression and chronological life span. Nucleic Acids Research, 2019, 47, 3434-3449.	6.5	29
28	Glycolysis regulates gene expression by promoting the crosstalk between H3K4 trimethylation and H3K14 acetylation in Saccharomyces cerevisiae. Journal of Genetics and Genomics, 2019, 46, 561-574.	1.7	12
29	Targeting BAF-perturbed cancers. Nature Cell Biology, 2018, 20, 1332-1333.	4.6	2
30	Histone H3 threonine 11 phosphorylation by Sch9 and CK2 regulates chronological lifespan by controlling the nutritional stress response. ELife, 2018, 7, .	2.8	30
31	MPTAC Determines APP Fragmentation via Sensing Sulfur Amino Acid Catabolism. Cell Reports, 2018, 24, 1585-1596.	2.9	12
32	Chromatin and Metabolism. Annual Review of Biochemistry, 2018, 87, 27-49.	5.0	37
33	Role of Nhp6 and Hmo1 in SWI/SNF occupancy and nucleosome landscape at gene regulatory regions. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 316-326.	0.9	12
34	Chromatin remodeller Fun30/Ft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. Nature Communications, 2017, 8, 14527.	5.8	41
35	Composition and Function of Mutant Swi/Snf Complexes. Cell Reports, 2017, 18, 2124-2134.	2.9	71
36	Enzymatic modules of the SAGA chromatin-modifying complex play distinct roles in <i>Drosophila</i> gene expression and development. Genes and Development, 2017, 31, 1588-1600.	2.7	45

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37	Myeloid Leukemia Factor Acts in a Chaperone Complex to Regulate Transcription Factor Stability and Gene Expression. <i>Journal of Molecular Biology</i> , 2017, 429, 2093-2107.	2.0	12
38	In Vitro Assembly of Nucleosomes for Binding/Remodeling Assays. <i>Methods in Molecular Biology</i> , 2017, 1528, 1-17.	0.4	2
39	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016, 11, e0155492.	1.1	27
40	Selective suppression of antisense transcription by Set2-mediated H3K36 methylation. <i>Nature Communications</i> , 2016, 7, 13610.	5.8	64
41	Reading and Interpreting the Histone Acylation Code. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 329-332.	3.0	2
42	Regulation of KAT6 Acetyltransferases and Their Roles in Cell Cycle Progression, Stem Cell Maintenance, and Human Disease. <i>Molecular and Cellular Biology</i> , 2016, 36, 1900-1907.	1.1	58
43	The Enok acetyltransferase complex interacts with Elg1 and negatively regulates PCNA unloading to promote the G1/S transition. <i>Genes and Development</i> , 2016, 30, 1198-210.	2.7	11
44	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. <i>Molecular Cell</i> , 2016, 62, 558-571.	4.5	106
45	Cytoplasmic ATXN7L3B Interferes with Nuclear Functions of the SAGA Deubiquitinase Module. <i>Molecular and Cellular Biology</i> , 2016, 36, 2855-2866.	1.1	16
46	Limiting PCNA-unloading at the G1/S transition. <i>Cell Cycle</i> , 2016, 15, 3001-3002.	1.3	2
47	Egf Signaling Directs Neoblast Repopulation by Regulating Asymmetric Cell Division in Planarians. <i>Developmental Cell</i> , 2016, 38, 413-429.	3.1	67
48	Diverse Activities of Histone Acylations Connect Metabolism to Chromatin Function. <i>Molecular Cell</i> , 2016, 63, 547-552.	4.5	73
49	USP44 Is an Integral Component of N-CoR that Contributes to Gene Repression by Deubiquitinating Histone H2B. <i>Cell Reports</i> , 2016, 17, 2382-2393.	2.9	41
50	It takes teamwork to modify chromatin. <i>Science</i> , 2016, 351, 667-667.	6.0	4
51	Histone modification as a reflection of metabolism. <i>Cell Cycle</i> , 2016, 15, 481-482.	1.3	5
52	Moco biosynthesis and the ATAC acetyltransferase engage translation initiation by inhibiting latent PKR activity. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 44-50.	1.5	11
53	Histone exchange, chromatin structure and the regulation of transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 178-189.	16.1	776
54	New Face for Chromatin-Related Mesenchymal Modulator: $\alpha$ -CHD9 Localizes to Nucleoli and Interacts With Ribosomal Genes. <i>Journal of Cellular Physiology</i> , 2015, 230, 2270-2280.	2.0	14

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55	Serine and SAM Responsive Complex SESAME Regulates Histone Modification Crosstalk by Sensing Cellular Metabolism. <i>Molecular Cell</i> , 2015, 60, 408-421.	4.5	136
56	Phosphorylation by Casein Kinase 2 Facilitates Psh1 Protein-assisted Degradation of Cse4 Protein. <i>Journal of Biological Chemistry</i> , 2014, 289, 29297-29309.	1.6	23
57	The expanding role for chromatin and transcription in polyglutamine disease. <i>Current Opinion in Genetics and Development</i> , 2014, 26, 96-104.	1.5	23
58	RNA-dependent dynamic histone acetylation regulates MCL1 alternative splicing. <i>Nucleic Acids Research</i> , 2014, 42, 1656-1670.	6.5	46
59	Recognizing methylated histone variant H3.3 to prevent tumors. <i>Cell Research</i> , 2014, 24, 649-650.	5.7	5
60	Loss of <i>Drosophila</i> Ataxin-7, a SAGA subunit, reduces H2B ubiquitination and leads to neural and retinal degeneration. <i>Genes and Development</i> , 2014, 28, 259-272.	2.7	51
61	Histone acetyltransferase Enok regulates oocyte polarization by promoting expression of the actin nucleation factor <i>spire</i> . <i>Genes and Development</i> , 2014, 28, 2750-2763.	2.7	34
62	Suberoylanilide Hydroxamic Acid (SAHA)-Induced Dynamics of a Human Histone Deacetylase Protein Interaction Network. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3114-3125.	2.5	26
63	<i>Drosophila</i> models reveal novel insights into mechanisms underlying neurodegeneration. <i>Fly</i> , 2014, 8, 148-152.	0.9	5
64	Pulling complexes out of complex diseases. <i>Rare Diseases (Austin, Tex)</i> , 2014, 2, e28859.	1.8	8
65	Swi/Snf dynamics on stress-responsive genes is governed by competitive bromodomain interactions. <i>Genes and Development</i> , 2014, 28, 2314-2330.	2.7	41
66	Nucleosome remodeling by the SWI/SNF complex is enhanced by yeast High Mobility Group Box (HMGB) proteins. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 764-772.	0.9	19
67	UpSETting chromatin during non-coding RNA production. <i>Epigenetics and Chromatin</i> , 2013, 6, 16.	1.8	9
68	Transcription-associated histone modifications and cryptic transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 84-97.	0.9	160
69	Remodelling without a power stroke. <i>EMBO Reports</i> , 2013, 14, 1030-1031.	2.0	0
70	Chromatin and signaling. <i>Current Opinion in Cell Biology</i> , 2013, 25, 322-326.	2.6	27
71	reSETting chromatin during transcription elongation. <i>Epigenetics</i> , 2013, 8, 10-15.	1.3	44
72	Nucleosome Remodeling and Epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a017905-a017905.	2.3	255

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73	Molecular secrets of a parasite. <i>Nature</i> , 2013, 499, 156-157.	13.7	1
74	Set2 mediated H3 lysine 36 methylation: regulation of transcription elongation and implications in organismal development. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2013, 2, 685-700.	5.9	59
75	Directing transcription to the right way. <i>Cell Research</i> , 2013, 23, 1153-1154.	5.7	3
76	Non-coding transcription SETs up regulation. <i>Cell Research</i> , 2013, 23, 311-313.	5.7	3
77	Quantitative Proteomics Demonstrates That the RNA Polymerase II Subunits Rpb4 and Rpb7 Dissociate during Transcriptional Elongation. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1530-1538.	2.5	45
78	Chromatin Proteins: Key Responders to Stress. <i>PLoS Biology</i> , 2012, 10, e1001371.	2.6	26
79	Human Family with Sequence Similarity 60 Member A (FAM60A) Protein: a New Subunit of the Sin3 Deacetylase Complex. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1815-1828.	2.5	47
80	MAP kinases and histone modification. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 348-350.	1.5	28
81	Holding on through DNA Replication: Histone Modification or Modifier?. <i>Cell</i> , 2012, 150, 875-877.	13.5	19
82	Nucleosome Positioning: Multiple Mechanisms toward a Unifying Goal. <i>Molecular Cell</i> , 2012, 48, 1-2.	4.5	31
83	Chromatin remodelers Isw1 and Chd1 maintain chromatin structure during transcription by preventing histone exchange. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 884-892.	3.6	256
84	Set2 methylation of histone H3 lysine 36 suppresses histone exchange on transcribed genes. <i>Nature</i> , 2012, 489, 452-455.	13.7	281
85	A Metazoan ATAC Acetyltransferase Subunit That Regulates Mitogen-activated Protein Kinase Signaling Is Related to an Ancient Molybdopterin Synthase Component. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 90-99.	2.5	6
86	Histone density is maintained during transcription mediated by the chromatin remodeler RSC and histone chaperone NAP1 in vitro. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1931-1936.	3.3	79
87	SAGA function in tissue-specific gene expression. <i>Trends in Cell Biology</i> , 2012, 22, 177-184.	3.6	56
88	HP1a Targets the Drosophila KDM4A Demethylase to a Subset of Heterochromatic Genes to Regulate H3K36me3 Levels. <i>PLoS ONE</i> , 2012, 7, e39758.	1.1	23
89	A Role for Snf2-Related Nucleosome-Spacing Enzymes in Genome-Wide Nucleosome Organization. <i>Science</i> , 2011, 333, 1758-1760.	6.0	260
90	Readers of histone modifications. <i>Cell Research</i> , 2011, 21, 564-578.	5.7	478

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91	Signals and Combinatorial Functions of Histone Modifications. Annual Review of Biochemistry, 2011, 80, 473-499.	5.0	429
92	Signaling through Chromatin: Setting the Scene at Kinetochores. Cell, 2011, 146, 671-672.	13.5	1
93	Post-transcription initiation function of the ubiquitous SAGA complex in tissue-specific gene activation. Genes and Development, 2011, 25, 1499-1509.	2.7	60
94	Combinatorial depletion analysis to assemble the network architecture of the SAGA and ADA chromatin remodeling complexes. Molecular Systems Biology, 2011, 7, 503.	3.2	140
95	Suppression of cryptic intragenic transcripts is required for embryonic stem cell self-renewal. EMBO Journal, 2011, 30, 1420-1421.	3.5	4
96	The changing faces of HP1: From heterochromatin formation and gene silencing to euchromatic gene expression. BioEssays, 2011, 33, 280-289.	1.2	129
97	Structure and nucleosome interaction of the yeast NuA4 and Piccolo NuA4 histone acetyltransferase complexes. Nature Structural and Molecular Biology, 2011, 18, 1196-1203.	3.6	70
98	HP1c casts light on dark matter. Cell Cycle, 2011, 10, 625-630.	1.3	22
99	Sgf29 binds histone H3K4me2/3 and is required for SAGA complex recruitment and histone H3 acetylation. EMBO Journal, 2011, 30, 2829-2842.	3.5	218
100	Deacetylase Inhibitors Dissociate the Histone-Targeting ING2 Subunit from the Sin3 Complex. Chemistry and Biology, 2010, 17, 65-74.	6.2	79
101	Rere controls retinoic acid signalling and somite bilateral symmetry. Nature, 2010, 463, 953-957.	13.7	103
102	Inducible gene expression: diverse regulatory mechanisms. Nature Reviews Genetics, 2010, 11, 426-437.	7.7	323
103	WD40 Repeats Arrange Histone Tails for Spreading of Silencing. Journal of Molecular Cell Biology, 2010, 2, 81-83.	1.5	6
104	Histone acetylation in heterochromatin assembly: Figure 1.. Genes and Development, 2010, 24, 738-740.	2.7	13
105	Gcn5 regulates the dissociation of SWI/SNF from chromatin by acetylation of Swi2/Snf2. Genes and Development, 2010, 24, 2766-2771.	2.7	67
106	Features of the PHF8/KIAA1718 histone demethylase. Cell Research, 2010, 20, 861-862.	5.7	15
107	Heterochromatin protein 1 (HP1) connects the FACT histone chaperone complex to the phosphorylated CTD of RNA polymerase II. Genes and Development, 2010, 24, 2133-2145.	2.7	90
108	Phosphorylated Pol II CTD Recruits Multiple HDACs, Including Rpd3C(S), for Methylation-Dependent Deacetylation of ORF Nucleosomes. Molecular Cell, 2010, 39, 234-246.	4.5	208

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109	Psh1 Is an E3 Ubiquitin Ligase that Targets the Centromeric Histone Variant Cse4. <i>Molecular Cell</i> , 2010, 40, 444-454.	4.5	159
110	The ATAC Acetyltransferase Complex Coordinates MAP Kinases to Regulate JNK Target Genes. <i>Cell</i> , 2010, 142, 726-736.	13.5	66
111	Features of Cryptic Promoters and Their Varied Reliance on Bromodomain-Containing Factors. <i>PLoS ONE</i> , 2010, 5, e12927.	1.1	13
112	Determining Protein Complex Connectivity Using a Probabilistic Deletion Network Derived from Quantitative Proteomics. <i>PLoS ONE</i> , 2009, 4, e7310.	1.1	35
113	Histone H3 Lysine 36 Dimethylation (H3K36me2) Is Sufficient to Recruit the Rpd3s Histone Deacetylase Complex and to Repress Spurious Transcription. <i>Journal of Biological Chemistry</i> , 2009, 284, 7970-7976.	1.6	135
114	A novel histone fold domain-containing protein that replaces TAF6 in <i>Drosophila</i> SAGA is required for SAGA-dependent gene expression. <i>Genes and Development</i> , 2009, 23, 2818-2823.	2.7	34
115	Yeast Sgf73/Ataxin-7 serves to anchor the deubiquitination module into both SAGA and Slik(SALSA) HAT complexes. <i>Epigenetics and Chromatin</i> , 2009, 2, 2.	1.8	84
116	Introducing the acetylome. <i>Nature Biotechnology</i> , 2009, 27, 917-919.	9.4	90
117	Hit and run: X marks the spot!. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 801-803.	3.6	1
118	Activator-binding domains of the SWI/SNF chromatin remodeling complex characterized <i>in vitro</i> are required for its recruitment to promoters <i>in vivo</i> . <i>FEBS Journal</i> , 2009, 276, 2557-2565.	2.2	18
119	Histone deacetylase inhibitors: Anticancer compounds. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 21-25.	1.2	81
120	Rtr1 Is a CTD Phosphatase that Regulates RNA Polymerase II during the Transition from Serine 5 to Serine 2 Phosphorylation. <i>Molecular Cell</i> , 2009, 34, 168-178.	4.5	125
121	Cse4 Is Part of an Octameric Nucleosome in Budding Yeast. <i>Molecular Cell</i> , 2009, 35, 794-805.	4.5	156
122	Heterochromatin Protein 1a stimulates histone H3 lysine 36 demethylation by the <i>Drosophila</i> KDM4A demethylase. <i>FASEB Journal</i> , 2009, 23, 325.3.	0.2	0
123	ATAC is a double histone acetyltransferase complex that stimulates nucleosome sliding. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 364-372.	3.6	171
124	The MSL3 chromodomain directs a key targeting step for dosage compensation of the <i>Drosophila melanogaster</i> X chromosome. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1318-1325.	3.6	110
125	SAGA-mediated H2B deubiquitination controls the development of neuronal connectivity in the <i>Drosophila</i> visual system. <i>EMBO Journal</i> , 2008, 27, 394-405.	3.5	110
126	Histone Ubiquitination: Triggering Gene Activity. <i>Molecular Cell</i> , 2008, 29, 653-663.	4.5	610



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127	Heterochromatin Protein 1a Stimulates Histone H3 Lysine 36 Demethylation by the Drosophila KDM4A Demethylase. <i>Molecular Cell</i> , 2008, 32, 696-706.	4.5	97
128	Clearing the Way for Unpaused Polymerases. <i>Cell</i> , 2008, 134, 16-18.	13.5	5
129	Crosstalk among Histone Modifications. <i>Cell</i> , 2008, 135, 604-607.	13.5	304
130	Diverse functions of WD40 repeat proteins in histone recognition: Figure 1.. <i>Genes and Development</i> , 2008, 22, 1265-1268.	2.7	75
131	The heterochromatin protein 1 (HP1) family: put away a bias toward HP1. <i>Molecules and Cells</i> , 2008, 26, 217-27.	1.0	113
132	Infrequently transcribed long genes depend on the Set2/Rpd3S pathway for accurate transcription. <i>Genes and Development</i> , 2007, 21, 1422-1430.	2.7	177
133	The Role of Chromatin during Transcription. <i>Cell</i> , 2007, 128, 707-719.	13.5	3,062
134	New Nomenclature for Chromatin-Modifying Enzymes. <i>Cell</i> , 2007, 131, 633-636.	13.5	849
135	MSL Complex Is Attracted to Genes Marked by H3K36 Trimethylation Using a Sequence-Independent Mechanism. <i>Molecular Cell</i> , 2007, 28, 121-133.	4.5	195
136	Combined Action of PHD and Chromo Domains Directs the Rpd3S HDAC to Transcribed Chromatin. <i>Science</i> , 2007, 316, 1050-1054.	6.0	294
137	Histone acetyltransferase complexes: one size doesn't fit all. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 284-295.	16.1	959
138	Activation domains drive nucleosome eviction by SWI/SNF. <i>EMBO Journal</i> , 2007, 26, 730-740.	3.5	82
139	RSC Exploits Histone Acetylation to Abrogate the Nucleosomal Block to RNA Polymerase II Elongation. <i>Molecular Cell</i> , 2006, 24, 481-487.	4.5	171
140	Analyzing chromatin remodeling complexes using shotgun proteomics and normalized spectral abundance factors. <i>Methods</i> , 2006, 40, 303-311.	1.9	293
141	Host Cell Factor and an Uncharacterized SANT Domain Protein Are Stable Components of ATAC, a Novel dAda2A/dGcn5-Containing Histone Acetyltransferase Complex in Drosophila. <i>Molecular and Cellular Biology</i> , 2006, 26, 871-882.	1.1	107
142	SAS-mediated acetylation of histone H4 Lys 16 is required for H2A.Z incorporation at subtelomeric regions in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2006, 20, 2507-2512.	2.7	90
143	SWI/SNF Displaces SAGA-Acetylated Nucleosomes. <i>Eukaryotic Cell</i> , 2006, 5, 1738-1747.	3.4	83
144	Nucleosome displacement in transcription. <i>Genes and Development</i> , 2006, 20, 2009-2017.	2.7	262

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145	The Essential Gene <i>wda</i> Encodes a WD40 Repeat Subunit of <i>Drosophila</i> SAGA Required for Histone H3 Acetylation. <i>Molecular and Cellular Biology</i> , 2006, 26, 7178-7189.	1.1	30
146	In and out: histone variant exchange in chromatin. <i>Trends in Biochemical Sciences</i> , 2005, 30, 680-687.	3.7	134
147	Yeast Recombination Enhancer Is Stimulated by Transcription Activation. <i>Molecular and Cellular Biology</i> , 2005, 25, 7976-7987.	1.1	18
148	Mechanism of Transcription Factor Recruitment by Acidic Activators. <i>Journal of Biological Chemistry</i> , 2005, 280, 21779-21784.	1.6	64
149	Preferential occupancy of histone variant H2AZ at inactive promoters influences local histone modifications and chromatin remodeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18385-18390.	3.3	287
150	The Deubiquitylation Activity of Ubp8 Is Dependent upon Sgf11 and Its Association with the SAGA Complex. <i>Molecular and Cellular Biology</i> , 2005, 25, 1173-1182.	1.1	143
151	A Mammalian Chromatin Remodeling Complex with Similarities to the Yeast INO80 Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 41207-41212.	1.6	211
152	Characterization of the Yeast Trimeric-SAS Acetyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 11987-11994.	1.6	76
153	The Mammalian YL1 Protein Is a Shared Subunit of the TRRAP/TIP60 Histone Acetyltransferase and SRCAP Complexes. <i>Journal of Biological Chemistry</i> , 2005, 280, 13665-13670.	1.6	185
154	The DNA Repair Protein $\gamma$ Ku80 Regulates the Function of Recombination Enhancer during Yeast Mating Type Switching. <i>Molecular and Cellular Biology</i> , 2005, 25, 8476-8485.	1.1	9
155	The HIR corepressor complex binds to nucleosomes generating a distinct protein/DNA complex resistant to remodeling by SWI/SNF. <i>Genes and Development</i> , 2005, 19, 2534-2539.	2.7	89
156	The Proteasome Regulatory Particle Alters the SAGA Coactivator to Enhance Its Interactions with Transcriptional Activators. <i>Cell</i> , 2005, 123, 423-436.	13.5	165
157	Histone H3 Methylation by Set2 Directs Deacetylation of Coding Regions by Rpd3S to Suppress Spurious Intragenic Transcription. <i>Cell</i> , 2005, 123, 581-592.	13.5	1,154
158	Breast Cancer Metastasis Suppressor 1 (BRMS1) Forms Complexes with Retinoblastoma-binding Protein 1 (RBP1) and the mSin3 Histone Deacetylase Complex and Represses Transcription. <i>Journal of Biological Chemistry</i> , 2004, 279, 1562-1569.	1.6	156
159	In Vitro Targeting Reveals Intrinsic Histone Tail Specificity of the Sin3/Histone Deacetylase and N-CoR/SMRT Corepressor Complexes. <i>Molecular and Cellular Biology</i> , 2004, 24, 2364-2372.	1.1	43
160	RPAP1, a Novel Human RNA Polymerase II-Associated Protein Affinity Purified with Recombinant Wild-Type and Mutated Polymerase Subunits. <i>Molecular and Cellular Biology</i> , 2004, 24, 7043-7058.	1.1	66
161	Histone H3 variants and modifications on transcribed genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1429-1430.	3.3	26
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