

Jerry L Workman

List of Publications by Year in descending order

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30,308
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3933

88
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4885

168
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306
all docs

306
docs citations

306
times ranked

22759
citing authors

#	ARTICLE	IF	CITATIONS
1	The Role of Chromatin during Transcription. Cell, 2007, 128, 707-719.	28.9	3,062
2	Histone H3 Methylation by Set2 Directs Deacetylation of Coding Regions by Rpd3S to Suppress Spurious Intragenic Transcription. Cell, 2005, 123, 581-592.	28.9	1,154
3	Histone acetyltransferase complexes: one size doesn't fit all. Nature Reviews Molecular Cell Biology, 2007, 8, 284-295.	37.0	959
4	New Nomenclature for Chromatin-Modifying Enzymes. Cell, 2007, 131, 633-636.	28.9	849
5	Histone exchange, chromatin structure and the regulation of transcription. Nature Reviews Molecular Cell Biology, 2015, 16, 178-189.	37.0	776
6	The TAFII250 Subunit of TFIID Has Histone Acetyltransferase Activity. Cell, 1996, 87, 1261-1270.	28.9	677
7	ATP-Dependent Chromatin-Remodeling Complexes. Molecular and Cellular Biology, 2000, 20, 1899-1910.	2.3	661
8	Histone Ubiquitination: Triggering Gene Activity. Molecular Cell, 2008, 29, 653-663.	9.7	610
9	Acetylation by Tip60 Is Required for Selective Histone Variant Exchange at DNA Lesions. Science, 2004, 306, 2084-2087.	12.6	602
10	The diverse functions of histone acetyltransferase complexes. Trends in Genetics, 2003, 19, 321-329.	6.7	485
11	Function and Selectivity of Bromodomains in Anchoring Chromatin-Modifying Complexes to Promoter Nucleosomes. Cell, 2002, 111, 369-379.	28.9	483
12	Readers of histone modifications. Cell Research, 2011, 21, 564-578.	12.0	478
13	Transcriptional activators direct histone acetyltransferase complexes to nucleosomes. Nature, 1998, 394, 498-502.	27.8	471
14	Signals and Combinatorial Functions of Histone Modifications. Annual Review of Biochemistry, 2011, 80, 473-499.	11.1	429
15	Binding of transcription factor TFIID to the major late promoter during in vitro nucleosome assembly potentiates subsequent initiation by RNA polymerase II. Cell, 1987, 51, 613-622.	28.9	412
16	A Subset of TAFIIs Are Integral Components of the SAGA Complex Required for Nucleosome Acetylation and Transcriptional Stimulation. Cell, 1998, 94, 45-53.	28.9	411
17	Promoter targeting and chromatin remodeling by the SWI/SNF complex. Current Opinion in Genetics and Development, 2000, 10, 187-192.	3.3	404
18	Histone Acetyltransferase Complexes Stabilize SWI/SNF Binding to Promoter Nucleosomes. Cell, 2001, 104, 817-827.	28.9	334

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19	Recruitment of HAT Complexes by Direct Activator Interactions with the ATM-Related Tra1 Subunit. <i>Science</i> , 2001, 292, 2333-2337.	12.6	334
20	Expanded Lysine Acetylation Specificity of Gcn5 in Native Complexes. <i>Journal of Biological Chemistry</i> , 1999, 274, 5895-5900.	3.4	333
21	Inducible gene expression: diverse regulatory mechanisms. <i>Nature Reviews Genetics</i> , 2010, 11, 426-437.	16.3	323
22	Functional Organization of the Yeast SAGA Complex: Distinct Components Involved in Structural Integrity, Nucleosome Acetylation, and TATA-Binding Protein Interaction. <i>Molecular and Cellular Biology</i> , 1999, 19, 86-98.	2.3	322
23	The Set2 Histone Methyltransferase Functions through the Phosphorylated Carboxyl-terminal Domain of RNA Polymerase II. <i>Journal of Biological Chemistry</i> , 2003, 278, 8897-8903.	3.4	307
24	Nucleosome mobilization catalysed by the yeast SWI/SNF complex. <i>Nature</i> , 1999, 400, 784-787.	27.8	306
25	Crosstalk among Histone Modifications. <i>Cell</i> , 2008, 135, 604-607.	28.9	304
26	Combined Action of PHD and Chromo Domains Directs the Rpd3S HDAC to Transcribed Chromatin. <i>Science</i> , 2007, 316, 1050-1054.	12.6	294
27	Analyzing chromatin remodeling complexes using shotgun proteomics and normalized spectral abundance factors. <i>Methods</i> , 2006, 40, 303-311.	3.8	293
28	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.	7.1	287
29	Set2 methylation of histone H3 lysine 36 suppresses histone exchange on transcribed genes. <i>Nature</i> , 2012, 489, 452-455.	27.8	281
30	Activation domains of stably bound GAL4 derivatives alleviate repression of promoters by nucleosomes. <i>Cell</i> , 1991, 64, 533-544.	28.9	265
31	Nucleosome displacement in transcription: Figure 1.. <i>Genes and Development</i> , 2006, 20, 2009-2017.	5.9	262
32	A Role for Snf2-Related Nucleosome-Spacing Enzymes in Genome-Wide Nucleosome Organization. <i>Science</i> , 2011, 333, 1758-1760.	12.6	260
33	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.	8.2	256
34	Nucleosome Remodeling and Epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a017905-a017905.	5.5	255
35	Activation Domain-Mediated Targeting of the SWI/SNF Complex to Promoters Stimulates Transcription from Nucleosome Arrays. <i>Molecular Cell</i> , 1999, 4, 649-655.	9.7	231
36	Sgf29 binds histone H3K4me2/3 and is required for SAGA complex recruitment and histone H3 acetylation. <i>EMBO Journal</i> , 2011, 30, 2829-2842.	7.8	218

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37	Nucleosome core displacement in vitro via a metastable transcription factor-nucleosome complex. <i>Science</i> , 1992, 258, 1780-1784.	12.6	217
38	Global Position and Recruitment of HATs and HDACs in the Yeast Genome. <i>Molecular Cell</i> , 2004, 16, 199-209.	9.7	212
39	A Mammalian Chromatin Remodeling Complex with Similarities to the Yeast INO80 Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 41207-41212.	3.4	211
40	The Novel SLIK Histone Acetyltransferase Complex Functions in the Yeast Retrograde Response Pathway. <i>Molecular and Cellular Biology</i> , 2002, 22, 8774-8786.	2.3	209
41	Phosphorylated Pol II CTD Recruits Multiple HDACs, Including Rpd3C(S), for Methylation-Dependent Deacetylation of ORF Nucleosomes. <i>Molecular Cell</i> , 2010, 39, 234-246.	9.7	208
42	Histone H3 specific acetyltransferases are essential for cell cycle progression. <i>Genes and Development</i> , 2001, 15, 3144-3154.	5.9	206
43	Transcriptional regulation by the immediate early protein of pseudorabies virus during in vitro nucleosome assembly. <i>Cell</i> , 1988, 55, 211-219.	28.9	198
44	MSL Complex Is Attracted to Genes Marked by H3K36 Trimethylation Using a Sequence-Independent Mechanism. <i>Molecular Cell</i> , 2007, 28, 121-133.	9.7	195
45	Multiple functions of nucleosomes and regulatory factors in transcription. <i>Trends in Biochemical Sciences</i> , 1993, 18, 90-95.	7.5	194
46	The Something About Silencing protein, Sas3, is the catalytic subunit of NuA3, a yTAF ₃₀ -containing HAT complex that interacts with the Spt16 subunit of the yeast CP (Cdc68/Pob3) "FACT" complex. <i>Genes and Development</i> , 2000, 14, 1196-1208.	5.9	194
47	Nucleosome displacement in transcription. <i>Cell</i> , 1993, 72, 305-308.	28.9	187
48	The ATM-Related Cofactor Tra1 Is a Component of the Purified SAGA Complex. <i>Molecular Cell</i> , 1998, 2, 863-867.	9.7	186
49	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.	3.4	185
50	Infrequently transcribed long genes depend on the Set2/Rpd3S pathway for accurate transcription. <i>Genes and Development</i> , 2007, 21, 1422-1430.	5.9	177
51	RSC Exploits Histone Acetylation to Abrogate the Nucleosomal Block to RNA Polymerase II Elongation. <i>Molecular Cell</i> , 2006, 24, 481-487.	9.7	171
52	ATAC is a double histone acetyltransferase complex that stimulates nucleosome sliding. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 364-372.	8.2	171
53	The Proteasome Regulatory Particle Alters the SAGA Coactivator to Enhance Its Interactions with Transcriptional Activators. <i>Cell</i> , 2005, 123, 423-436.	28.9	165
54	The SAGA unfolds: convergence of transcription regulators in chromatin-modifying complexes. <i>Trends in Cell Biology</i> , 1998, 8, 193-197.	7.9	164

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55	The ADA Complex Is a Distinct Histone Acetyltransferase Complex in <i>Saccharomyces cerevisiae</i> . Molecular and Cellular Biology, 1999, 19, 6621-6631.	2.3	162
56	Transcription Activator Interactions with Multiple SWI/SNF Subunits. Molecular and Cellular Biology, 2002, 22, 1615-1625.	2.3	160
57	Transcription-associated histone modifications and cryptic transcription. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 84-97.	1.9	160
58	Psh1 Is an E3 Ubiquitin Ligase that Targets the Centromeric Histone Variant Cse4. Molecular Cell, 2010, 40, 444-454.	9.7	159
59	Breast Cancer Metastasis Suppressor 1 (BRMS1) Forms Complexes with Retinoblastoma-binding Protein 1 (RBP1) and the mSin3 Histone Deacetylase Complex and Represses Transcription. Journal of Biological Chemistry, 2004, 279, 1562-1569.	3.4	156
60	Cse4 Is Part of an Octameric Nucleosome in Budding Yeast. Molecular Cell, 2009, 35, 794-805.	9.7	156
61	Activation Domain-Specific and General Transcription Stimulation by Native Histone Acetyltransferase Complexes. Molecular and Cellular Biology, 1999, 19, 855-863.	2.3	148
62	The SWI/SNF Complex Creates Loop Domains in DNA and Polynucleosome Arrays and Can Disrupt DNA-Histone Contacts within These Domains. Molecular and Cellular Biology, 1999, 19, 1470-1478.	2.3	143
63	The Deubiquitylation Activity of Ubp8 Is Dependent upon Sgf11 and Its Association with the SAGA Complex. Molecular and Cellular Biology, 2005, 25, 1173-1182.	2.3	143
64	Combinatorial depletion analysis to assemble the network architecture of the SAGA and ADA chromatin remodeling complexes. Molecular Systems Biology, 2011, 7, 503.	7.2	140
65	Serine and SAM Responsive Complex SESAME Regulates Histone Modification Crosstalk by Sensing Cellular Metabolism. Molecular Cell, 2015, 60, 408-421.	9.7	136
66	Histone H3 Lysine 36 Dimethylation (H3K36me2) Is Sufficient to Recruit the Rpd3s Histone Deacetylase Complex and to Repress Spurious Transcription. Journal of Biological Chemistry, 2009, 284, 7970-7976.	3.4	135
67	In and out: histone variant exchange in chromatin. Trends in Biochemical Sciences, 2005, 30, 680-687.	7.5	134
68	Persistent Interactions of Core Histone Tails with Nucleosomal DNA following Acetylation and Transcription Factor Binding. Molecular and Cellular Biology, 1998, 18, 6293-6304.	2.3	129
69	The changing faces of HP1: From heterochromatin formation and gene silencing to euchromatic gene expression. BioEssays, 2011, 33, 280-289.	2.5	129
70	A Conserved Motif Present in a Class of Helix-Loop-Helix Proteins Activates Transcription by Direct Recruitment of the SAGA Complex. Molecular Cell, 1999, 4, 63-73.	9.7	128
71	The yeast SAS (something about silencing) protein complex contains a MYST-type putative acetyltransferase and functions with chromatin assembly factor ASF1. Genes and Development, 2001, 15, 3155-3168.	5.9	127
72	Rtr1 Is a CTD Phosphatase that Regulates RNA Polymerase II during the Transition from Serine 5 to Serine 2 Phosphorylation. Molecular Cell, 2009, 34, 168-178.	9.7	125

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73	Recruitment of the SWI-SNF Chromatin Remodeling Complex as a Mechanism of Gene Activation by the Glucocorticoid Receptor β 1 Activation Domain. <i>Molecular and Cellular Biology</i> , 2000, 20, 2004-2013.	2.3	118
74	Repression of GCN5 Histone Acetyltransferase Activity via Bromodomain-Mediated Binding and Phosphorylation by the α -DNA-Dependent Protein Kinase Complex. <i>Molecular and Cellular Biology</i> , 1998, 18, 1349-1358.	2.3	117
75	The heterochromatin protein 1 (HP1) family: put away a bias toward HP1. <i>Molecules and Cells</i> , 2008, 26, 217-27.	2.6	113
76	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.	8.2	110
77	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.	7.8	110
78	Host Cell Factor and an Uncharacterized SANT Domain Protein Are Stable Components of ATAC, a Novel dAda2A/dGcn5-Containing Histone Acetyltransferase Complex in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2006, 26, 871-882.	2.3	107
79	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. <i>Molecular Cell</i> , 2016, 62, 558-571.	9.7	106
80	Stable co-occupancy of transcription factors and histones at the HIV-1 enhancer. <i>EMBO Journal</i> , 1997, 16, 2463-2472.	7.8	103
81	Rere controls retinoic acid signalling and somite bilateral symmetry. <i>Nature</i> , 2010, 463, 953-957.	27.8	103
82	Two <i>Drosophila</i> Ada2 Homologues Function in Different Multiprotein Complexes. <i>Molecular and Cellular Biology</i> , 2003, 23, 3305-3319.	2.3	102
83	Sds3 (Suppressor of Defective Silencing 3) Is an Integral Component of the Yeast Sin3-Rpd3 Histone Deacetylase Complex and Is Required for Histone Deacetylase Activity. <i>Journal of Biological Chemistry</i> , 2000, 275, 40961-40966.	3.4	99
84	Remodeling chromatin structures for transcription: What happens to the histones?. <i>BioEssays</i> , 1996, 18, 875-884.	2.5	98
85	Heterochromatin Protein 1a Stimulates Histone H3 Lysine 36 Demethylation by the <i>Drosophila</i> KDM4A Demethylase. <i>Molecular Cell</i> , 2008, 32, 696-706.	9.7	97
86	Sas4 and Sas5 Are Required for the Histone Acetyltransferase Activity of Sas2 in the SAS Complex. <i>Journal of Biological Chemistry</i> , 2003, 278, 16887-16892.	3.4	96
87	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.	5.9	90
88	Introducing the acetylome. <i>Nature Biotechnology</i> , 2009, 27, 917-919.	17.5	90
89	Heterochromatin protein 1 (HP1) connects the FACT histone chaperone complex to the phosphorylated CTD of RNA polymerase II. <i>Genes and Development</i> , 2010, 24, 2133-2145.	5.9	90
90	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.	5.9	89

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91	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.	3.9	84
92	SWI/SNF Displaces SAGA-Acetylated Nucleosomes. <i>Eukaryotic Cell</i> , 2006, 5, 1738-1747.	3.4	83
93	[6] Basic analysis of transcription factor binding to nucleosomes. <i>Methods in Molecular Genetics</i> , 1995, 6, 108-128.	0.6	82
94	Activation domains drive nucleosome eviction by SWI/SNF. <i>EMBO Journal</i> , 2007, 26, 730-740.	7.8	82
95	Histone deacetylase inhibitors: Anticancer compounds. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 21-25.	2.8	81
96	Identification and Analysis of Yeast Nucleosomal Histone Acetyltransferase Complexes. <i>Methods</i> , 1998, 15, 315-321.	3.8	80
97	Targeting Activity Is Required for SWI/SNF Function In Vivo and Is Accomplished through Two Partially Redundant Activator-Interaction Domains. <i>Molecular Cell</i> , 2003, 12, 983-990.	9.7	79
98	Deacetylase Inhibitors Dissociate the Histone-Targeting ING2 Subunit from the Sin3 Complex. <i>Chemistry and Biology</i> , 2010, 17, 65-74.	6.0	79
99	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.	7.1	79
100	SWI/SNF Stimulates the Formation of Disparate Activator-Nucleosome Complexes but Is Partially Redundant with Cooperative Binding. <i>Journal of Biological Chemistry</i> , 1997, 272, 12642-12649.	3.4	76
101	Bookmarking genes for activation in condensed mitotic chromosomes. <i>BioEssays</i> , 1998, 20, 275-279.	2.5	76
102	Characterization of the Yeast Trimeric-SAS Acetyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 11987-11994.	3.4	76
103	Diverse functions of WD40 repeat proteins in histone recognition: Figure 1.. <i>Genes and Development</i> , 2008, 22, 1265-1268.	5.9	75
104	Diverse Activities of Histone Acylations Connect Metabolism to Chromatin Function. <i>Molecular Cell</i> , 2016, 63, 547-552.	9.7	73
105	Composition and Function of Mutant Swi/Snf Complexes. <i>Cell Reports</i> , 2017, 18, 2124-2134.	6.4	71
106	Structure and nucleosome interaction of the yeast NuA4 and Piccoloâ€NuA4 histone acetyltransferase complexes. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1196-1203.	8.2	70
107	Gcn5 regulates the dissociation of SWI/SNF from chromatin by acetylation of Swi2/Snf2. <i>Genes and Development</i> , 2010, 24, 2766-2771.	5.9	67
108	Egf Signaling Directs Neoblast Repopulation by Regulating Asymmetric Cell Division in Planarians. <i>Developmental Cell</i> , 2016, 38, 413-429.	7.0	67

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109	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.	2.3	66
110	The ATAC Acetyltransferase Complex Coordinates MAP Kinases to Regulate JNK Target Genes. <i>Cell</i> , 2010, 142, 726-736.	28.9	66
111	Mechanism of Transcription Factor Recruitment by Acidic Activators. <i>Journal of Biological Chemistry</i> , 2005, 280, 21779-21784.	3.4	64
112	Selective suppression of antisense transcription by Set2-mediated H3K36 methylation. <i>Nature Communications</i> , 2016, 7, 13610.	12.8	64
113	Location and function of linker histones. <i>Nature Structural Biology</i> , 1998, 5, 1025-1028.	9.7	63
114	Histone Acetyltransferase Complexes Can Mediate Transcriptional Activation by the Major Glucocorticoid Receptor Activation Domain. <i>Molecular and Cellular Biology</i> , 1999, 19, 5952-5959.	2.3	61
115	In vitro analysis of transcription factor binding to nucleosomes and nucleosome disruption/displacement. <i>Methods in Enzymology</i> , 1996, 274, 276-291.	1.0	60
116	Post-transcription initiation function of the ubiquitous SAGA complex in tissue-specific gene activation. <i>Genes and Development</i> , 2011, 25, 1499-1509.	5.9	60
117	Chapter 16 Control of Class II Gene Transcription during in Vitro Nucleosome Assembly. <i>Methods in Cell Biology</i> , 1991, 35, 419-447.	1.1	59
118	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
119	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.	2.3	58
120	SAGA function in tissue-specific gene expression. <i>Trends in Cell Biology</i> , 2012, 22, 177-184.	7.9	56
121	Analysis of Nucleosome Disruption by ATP-Driven Chromatin Remodeling Complexes. , 1999, 119, 319-332.		53
122	Yng1p Modulates the Activity of Sas3p as a Component of the Yeast NuA3 Histone Acetyltransferase Complex. <i>Molecular and Cellular Biology</i> , 2002, 22, 5047-5053.	2.3	53
123	Histone acetylation and chromatin remodeling: which comes first?. <i>Molecular Genetics and Metabolism</i> , 2002, 76, 1-5.	1.1	52
124	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.	5.9	51
125	H1-mediated Repression of Transcription Factor Binding to a Stably Positioned Nucleosome. <i>Journal of Biological Chemistry</i> , 1997, 272, 3635-3640.	3.4	48
126	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.	3.8	47

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127	RNA-dependent dynamic histone acetylation regulates MCL1 alternative splicing. <i>Nucleic Acids Research</i> , 2014, 42, 1656-1670.	14.5	46
128	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.	3.8	45
129	Enzymatic modules of the SAGA chromatin-modifying complex play distinct roles in <i>Drosophila</i> gene expression and development. <i>Genes and Development</i> , 2017, 31, 1588-1600.	5.9	45
130	reSETting chromatin during transcription elongation. <i>Epigenetics</i> , 2013, 8, 10-15.	2.7	44
131	A Novel H2A/H4 Nucleosomal Histone Acetyltransferase in <i>Tetrahymena thermophila</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 2061-2068.	2.3	43
132	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.	2.3	43
133	The methyltransferase SETD2 couples transcription and splicing by engaging mRNA processing factors through its SHI domain. <i>Nature Communications</i> , 2021, 12, 1443.	12.8	42
134	Swi/Snf dynamics on stress-responsive genes is governed by competitive bromodomain interactions. <i>Genes and Development</i> , 2014, 28, 2314-2330.	5.9	41
135	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.	6.4	41
136	Chromatin remodeller Fun30Ft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. <i>Nature Communications</i> , 2017, 8, 14527.	12.8	41
137	Opposite Role of Yeast ING Family Members in p53-dependent Transcriptional Activation. <i>Journal of Biological Chemistry</i> , 2003, 278, 19171-19175.	3.4	38
138	The SAGA chromatin-modifying complex: the sum of its parts is greater than the whole. <i>Genes and Development</i> , 2020, 34, 1287-1303.	5.9	38
139	Chromatin and Metabolism. <i>Annual Review of Biochemistry</i> , 2018, 87, 27-49.	11.1	37
140	Determining Protein Complex Connectivity Using a Probabilistic Deletion Network Derived from Quantitative Proteomics. <i>PLoS ONE</i> , 2009, 4, e7310.	2.5	35
141	Gal80 Confers Specificity on HAT Complex Interactions with Activators. <i>Journal of Biological Chemistry</i> , 2002, 277, 24648-24652.	3.4	34
142	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.	5.9	34
143	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.	5.9	34
144	Exogenous pyruvate represses histone gene expression and inhibits cancer cell proliferation via the NAMPTâ€NAD+â€SIRT1 pathway. <i>Nucleic Acids Research</i> , 2019, 47, 11132-11150.	14.5	32

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145	Nucleosome Positioning: Multiple Mechanisms toward a Unifying Goal. <i>Molecular Cell</i> , 2012, 48, 1-2.	9.7	31
146	The Essential Gene wda Encodes a WD40 Repeat Subunit of Drosophila SAGA Required for Histone H3 Acetylation. <i>Molecular and Cellular Biology</i> , 2006, 26, 7178-7189.	2.3	30
147	Histone H3 threonine 11 phosphorylation by Sch9 and CK2 regulates chronological lifespan by controlling the nutritional stress response. <i>ELife</i> , 2018, 7, .	6.0	30
148	Set1-catalyzed H3K4 trimethylation antagonizes the HIR/Asf1/Rtt106 repressor complex to promote histone gene expression and chronological life span. <i>Nucleic Acids Research</i> , 2019, 47, 3434-3449.	14.5	29
149	MAP kinases and histone modification. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 348-350.	3.3	28
150	Recruitment of Gcn5-containing Complexes during c-Myc-dependent Gene Activation. <i>Journal of Biological Chemistry</i> , 2002, 277, 23399-23406.	3.4	27
151	Chromatin and signaling. <i>Current Opinion in Cell Biology</i> , 2013, 25, 322-326.	5.4	27
152	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016, 11, e0155492.	2.5	27
153	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.	7.1	26
154	Chromatin Proteins: Key Responders to Stress. <i>PLoS Biology</i> , 2012, 10, e1001371.	5.6	26
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156	Characterization of a metazoan ADA acetyltransferase complex. <i>Nucleic Acids Research</i> , 2019, 47, 3383-3394.	14.5	26
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