

# 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

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times ranked

22759  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Role of Chromatin during Transcription. <i>Cell</i> , 2007, 128, 707-719.	13.5	3,062
2	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
3	Histone acetyltransferase complexes: one size doesn't fit all. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 284-295.	16.1	959
4	New Nomenclature for Chromatin-Modifying Enzymes. <i>Cell</i> , 2007, 131, 633-636.	13.5	849
5	Histone exchange, chromatin structure and the regulation of transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 178-189.	16.1	776
6	The TAFII250 Subunit of TFIID Has Histone Acetyltransferase Activity. <i>Cell</i> , 1996, 87, 1261-1270.	13.5	677
7	ATP-Dependent Chromatin-Remodeling Complexes. <i>Molecular and Cellular Biology</i> , 2000, 20, 1899-1910.	1.1	661
8	Histone Ubiquitination: Triggering Gene Activity. <i>Molecular Cell</i> , 2008, 29, 653-663.	4.5	610
9	Acetylation by Tip60 Is Required for Selective Histone Variant Exchange at DNA Lesions. <i>Science</i> , 2004, 306, 2084-2087.	6.0	602
10	The diverse functions of histone acetyltransferase complexes. <i>Trends in Genetics</i> , 2003, 19, 321-329.	2.9	485
11	Function and Selectivity of Bromodomains in Anchoring Chromatin-Modifying Complexes to Promoter Nucleosomes. <i>Cell</i> , 2002, 111, 369-379.	13.5	483
12	Readers of histone modifications. <i>Cell Research</i> , 2011, 21, 564-578.	5.7	478
13	Transcriptional activators direct histone acetyltransferase complexes to nucleosomes. <i>Nature</i> , 1998, 394, 498-502.	13.7	471
14	Signals and Combinatorial Functions of Histone Modifications. <i>Annual Review of Biochemistry</i> , 2011, 80, 473-499.	5.0	429
15	Binding of transcription factor TFIID to the major late promoter during in vitro nucleosome assembly potentiates subsequent initiation by RNA polymerase II. <i>Cell</i> , 1987, 51, 613-622.	13.5	412
16	A Subset of TAFIIs Are Integral Components of the SAGA Complex Required for Nucleosome Acetylation and Transcriptional Stimulation. <i>Cell</i> , 1998, 94, 45-53.	13.5	411
17	Promoter targeting and chromatin remodeling by the SWI/SNF complex. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 187-192.	1.5	404
18	Histone Acetyltransferase Complexes Stabilize SWI/SNF Binding to Promoter Nucleosomes. <i>Cell</i> , 2001, 104, 817-827.	13.5	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.	6.0	334
20	Expanded Lysine Acetylation Specificity of Gcn5 in Native Complexes. <i>Journal of Biological Chemistry</i> , 1999, 274, 5895-5900.	1.6	333
21	Inducible gene expression: diverse regulatory mechanisms. <i>Nature Reviews Genetics</i> , 2010, 11, 426-437.	7.7	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.	1.1	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.	1.6	307
24	Nucleosome mobilization catalysed by the yeast SWI/SNF complex. <i>Nature</i> , 1999, 400, 784-787.	13.7	306
25	Crosstalk among Histone Modifications. <i>Cell</i> , 2008, 135, 604-607.	13.5	304
26	Combined Action of PHD and Chromo Domains Directs the Rpd3S HDAC to Transcribed Chromatin. <i>Science</i> , 2007, 316, 1050-1054.	6.0	294
27	Analyzing chromatin remodeling complexes using shotgun proteomics and normalized spectral abundance factors. <i>Methods</i> , 2006, 40, 303-311.	1.9	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.	3.3	287
29	Set2 methylation of histone H3 lysine <sup>36</sup> suppresses histone exchange on transcribed genes. <i>Nature</i> , 2012, 489, 452-455.	13.7	281
30	Activation domains of stably bound GAL4 derivatives alleviate repression of promoters by nucleosomes. <i>Cell</i> , 1991, 64, 533-544.	13.5	265
31	Nucleosome displacement in transcription. <i>Genes and Development</i> , 2006, 20, 2009-2017.	2.7	262
32	A Role for Snf2-Related Nucleosome-Spacing Enzymes in Genome-Wide Nucleosome Organization. <i>Science</i> , 2011, 333, 1758-1760.	6.0	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.	3.6	256
34	Nucleosome Remodeling and Epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a017905-a017905.	2.3	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.	4.5	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.	3.5	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.	6.0	217
38	Global Position and Recruitment of HATs and HDACs in the Yeast Genome. <i>Molecular Cell</i> , 2004, 16, 199-209.	4.5	212
39	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
40	The Novel SLIK Histone Acetyltransferase Complex Functions in the Yeast Retrograde Response Pathway. <i>Molecular and Cellular Biology</i> , 2002, 22, 8774-8786.	1.1	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.	4.5	208
42	Histone H3 specific acetyltransferases are essential for cell cycle progression. <i>Genes and Development</i> , 2001, 15, 3144-3154.	2.7	206
43	Transcriptional regulation by the immediate early protein of pseudorabies virus during in vitro nucleosome assembly. <i>Cell</i> , 1988, 55, 211-219.	13.5	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.	4.5	195
45	Multiple functions of nucleosomes and regulatory factors in transcription. <i>Trends in Biochemical Sciences</i> , 1993, 18, 90-95.	3.7	194
46	The Something About Silencing protein, Sas3, is the catalytic subunit of NuA3, a yTAF <sub>30</sub> -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.	2.7	194
47	Nucleosome displacement in transcription. <i>Cell</i> , 1993, 72, 305-308.	13.5	187
48	The ATM-Related Cofactor Tra1 Is a Component of the Purified SAGA Complex. <i>Molecular Cell</i> , 1998, 2, 863-867.	4.5	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.	1.6	185
50	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
51	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
52	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
53	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
54	The SAGA unfolds: convergence of transcription regulators in chromatin-modifying complexes. <i>Trends in Cell Biology</i> , 1998, 8, 193-197.	3.6	164

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55	The ADA Complex Is a Distinct Histone Acetyltransferase Complex in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 6621-6631.	1.1	162
56	Transcription Activator Interactions with Multiple SWI/SNF Subunits. <i>Molecular and Cellular Biology</i> , 2002, 22, 1615-1625.	1.1	160
57	Transcription-associated histone modifications and cryptic transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 84-97.	0.9	160
58	Psh1 Is an E3 Ubiquitin Ligase that Targets the Centromeric Histone Variant Cse4. <i>Molecular Cell</i> , 2010, 40, 444-454.	4.5	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. <i>Journal of Biological Chemistry</i> , 2004, 279, 1562-1569.	1.6	156
60	Cse4 Is Part of an Octameric Nucleosome in Budding Yeast. <i>Molecular Cell</i> , 2009, 35, 794-805.	4.5	156
61	Activation Domain-Specific and General Transcription Stimulation by Native Histone Acetyltransferase Complexes. <i>Molecular and Cellular Biology</i> , 1999, 19, 855-863.	1.1	148
62	The SWI/SNF Complex Creates Loop Domains in DNA and Polynucleosome Arrays and Can Disrupt DNA-Histone Contacts within These Domains. <i>Molecular and Cellular Biology</i> , 1999, 19, 1470-1478.	1.1	143
63	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
64	Combinatorial depletion analysis to assemble the network architecture of the SAGA and ADA chromatin remodeling complexes. <i>Molecular Systems Biology</i> , 2011, 7, 503.	3.2	140
65	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
66	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
67	In and out: histone variant exchange in chromatin. <i>Trends in Biochemical Sciences</i> , 2005, 30, 680-687.	3.7	134
68	Persistent Interactions of Core Histone Tails with Nucleosomal DNA following Acetylation and Transcription Factor Binding. <i>Molecular and Cellular Biology</i> , 1998, 18, 6293-6304.	1.1	129
69	The changing faces of HP1: From heterochromatin formation and gene silencing to euchromatic gene expression. <i>BioEssays</i> , 2011, 33, 280-289.	1.2	129
70	A Conserved Motif Present in a Class of Helix-Loop-Helix Proteins Activates Transcription by Direct Recruitment of the SAGA Complex. <i>Molecular Cell</i> , 1999, 4, 63-73.	4.5	128
71	The yeast SAS (something about silencing) protein complex contains a MYST-type putative acetyltransferase and functions with chromatin assembly factor ASF1. <i>Genes and Development</i> , 2001, 15, 3155-3168.	2.7	127
72	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

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73	Recruitment of the SWI-SNF Chromatin Remodeling Complex as a Mechanism of Gene Activation by the Glucocorticoid Receptor $\beta$ 1 Activation Domain. <i>Molecular and Cellular Biology</i> , 2000, 20, 2004-2013.	1.1	118
74	Repression of GCN5 Histone Acetyltransferase Activity via Bromodomain-Mediated Binding and Phosphorylation by the DNA-Dependent Protein Kinase Complex. <i>Molecular and Cellular Biology</i> , 1998, 18, 1349-1358.	1.1	117
75	The heterochromatin protein 1 (HP1) family: put away a bias toward HP1. <i>Molecules and Cells</i> , 2008, 26, 217-27.	1.0	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.	3.6	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.	3.5	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.	1.1	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.	4.5	106
80	Stable co-occupancy of transcription factors and histones at the HIV-1 enhancer. <i>EMBO Journal</i> , 1997, 16, 2463-2472.	3.5	103
81	Rere controls retinoic acid signalling and somite bilateral symmetry. <i>Nature</i> , 2010, 463, 953-957.	13.7	103
82	Two <i>Drosophila</i> Ada2 Homologues Function in Different Multiprotein Complexes. <i>Molecular and Cellular Biology</i> , 2003, 23, 3305-3319.	1.1	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.	1.6	99
84	Remodeling chromatin structures for transcription: What happens to the histones?. <i>BioEssays</i> , 1996, 18, 875-884.	1.2	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.	4.5	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.	1.6	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.	2.7	90
88	Introducing the acetylome. <i>Nature Biotechnology</i> , 2009, 27, 917-919.	9.4	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.	2.7	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.	2.7	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.	1.8	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.	3.5	82
95	Histone deacetylase inhibitors: Anticancer compounds. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 21-25.	1.2	81
96	Identification and Analysis of Yeast Nucleosomal Histone Acetyltransferase Complexes. <i>Methods</i> , 1998, 15, 315-321.	1.9	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.	4.5	79
98	Deacetylase Inhibitors Dissociate the Histone-Targeting ING2 Subunit from the Sin3 Complex. <i>Chemistry and Biology</i> , 2010, 17, 65-74.	6.2	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.	3.3	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.	1.6	76
101	Bookmarking genes for activation in condensed mitotic chromosomes. <i>BioEssays</i> , 1998, 20, 275-279.	1.2	76
102	Characterization of the Yeast Trimeric-SAS Acetyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2005, 280, 11987-11994.	1.6	76
103	Diverse functions of WD40 repeat proteins in histone recognition: Figure 1.. <i>Genes and Development</i> , 2008, 22, 1265-1268.	2.7	75
104	Diverse Activities of Histone Acylations Connect Metabolism to Chromatin Function. <i>Molecular Cell</i> , 2016, 63, 547-552.	4.5	73
105	Composition and Function of Mutant Swi/Snf Complexes. <i>Cell Reports</i> , 2017, 18, 2124-2134.	2.9	71
106	Structure and nucleosome interaction of the yeast NuA4 and Piccolo NuA4 histone acetyltransferase complexes. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1196-1203.	3.6	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.	2.7	67
108	Egf Signaling Directs Neoblast Repopulation by Regulating Asymmetric Cell Division in Planarians. <i>Developmental Cell</i> , 2016, 38, 413-429.	3.1	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.	1.1	66
110	The ATAC Acetyltransferase Complex Coordinates MAP Kinases to Regulate JNK Target Genes. <i>Cell</i> , 2010, 142, 726-736.	13.5	66
111	Mechanism of Transcription Factor Recruitment by Acidic Activators. <i>Journal of Biological Chemistry</i> , 2005, 280, 21779-21784.	1.6	64
112	Selective suppression of antisense transcription by Set2-mediated H3K36 methylation. <i>Nature Communications</i> , 2016, 7, 13610.	5.8	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.	1.1	61
115	In vitro analysis of transcription factor binding to nucleosomes and nucleosome disruption/displacement. <i>Methods in Enzymology</i> , 1996, 274, 276-291.	0.4	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.	2.7	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.	0.5	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.	1.1	58
120	SAGA function in tissue-specific gene expression. <i>Trends in Cell Biology</i> , 2012, 22, 177-184.	3.6	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.	1.1	53
123	Histone acetylation and chromatin remodeling: which comes first?. <i>Molecular Genetics and Metabolism</i> , 2002, 76, 1-5.	0.5	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.	2.7	51
125	H1-mediated Repression of Transcription Factor Binding to a Stably Positioned Nucleosome. <i>Journal of Biological Chemistry</i> , 1997, 272, 3635-3640.	1.6	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.	2.5	47



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127	RNA-dependent dynamic histone acetylation regulates MCL1 alternative splicing. <i>Nucleic Acids Research</i> , 2014, 42, 1656-1670.	6.5	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.	2.5	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.	2.7	45
130	reSETting chromatin during transcription elongation. <i>Epigenetics</i> , 2013, 8, 10-15.	1.3	44
131	A Novel H2A/H4 Nucleosomal Histone Acetyltransferase in <i>Tetrahymena thermophila</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 2061-2068.	1.1	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.	1.1	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.	5.8	42
134	Swi/Snf dynamics on stress-responsive genes is governed by competitive bromodomain interactions. <i>Genes and Development</i> , 2014, 28, 2314-2330.	2.7	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.	2.9	41
136	Chromatin remodeller Fun30Ft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. <i>Nature Communications</i> , 2017, 8, 14527.	5.8	41
137	Opposite Role of Yeast ING Family Members in p53-dependent Transcriptional Activation. <i>Journal of Biological Chemistry</i> , 2003, 278, 19171-19175.	1.6	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.	2.7	38
139	Chromatin and Metabolism. <i>Annual Review of Biochemistry</i> , 2018, 87, 27-49.	5.0	37
140	Determining Protein Complex Connectivity Using a Probabilistic Deletion Network Derived from Quantitative Proteomics. <i>PLoS ONE</i> , 2009, 4, e7310.	1.1	35
141	Gal80 Confers Specificity on HAT Complex Interactions with Activators. <i>Journal of Biological Chemistry</i> , 2002, 277, 24648-24652.	1.6	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.	2.7	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.	2.7	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.	6.5	32

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145	Nucleosome Positioning: Multiple Mechanisms toward a Unifying Goal. <i>Molecular Cell</i> , 2012, 48, 1-2.	4.5	31
146	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
147	Histone H3 threonine 11 phosphorylation by Sch9 and CK2 regulates chronological lifespan by controlling the nutritional stress response. <i>ELife</i> , 2018, 7, .	2.8	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.	6.5	29
149	MAP kinases and histone modification. <i>Journal of Molecular Cell Biology</i> , 2012, 4, 348-350.	1.5	28
150	Recruitment of Gcn5-containing Complexes during c-Myc-dependent Gene Activation. <i>Journal of Biological Chemistry</i> , 2002, 277, 23399-23406.	1.6	27
151	Chromatin and signaling. <i>Current Opinion in Cell Biology</i> , 2013, 25, 322-326.	2.6	27
152	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016, 11, e0155492.	1.1	27
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