

Jerry L Workman

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

220
papers

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h-index

160
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306
ext. papers

28,555
ext. citations

15.7
avg, IF

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L-index

#	Paper	IF	Citations
220	The role of chromatin during transcription. <i>Cell</i> , 2007 , 128, 707-19	56.2	2639
219	Histone H3 methylation by Set2 directs deacetylation of coding regions by Rpd3S to suppress spurious intragenic transcription. <i>Cell</i> , 2005 , 123, 581-92	56.2	986
218	Histone acetyltransferase complexes: one size doesn't fit all. <i>Nature Reviews Molecular Cell Biology</i> , 2007 , 8, 284-95	48.7	792
217	New nomenclature for chromatin-modifying enzymes. <i>Cell</i> , 2007 , 131, 633-6	56.2	745
216	The TAF(II)250 subunit of TFIID has histone acetyltransferase activity. <i>Cell</i> , 1996 , 87, 1261-70	56.2	632
215	ATP-dependent chromatin-remodeling complexes. <i>Molecular and Cellular Biology</i> , 2000 , 20, 1899-910	4.8	610
214	Histone exchange, chromatin structure and the regulation of transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2015 , 16, 178-89	48.7	597
213	Acetylation by Tip60 is required for selective histone variant exchange at DNA lesions. <i>Science</i> , 2004 , 306, 2084-7	33.3	544
212	Histone ubiquitination: triggering gene activity. <i>Molecular Cell</i> , 2008 , 29, 653-63	17.6	532
211	Transcriptional activators direct histone acetyltransferase complexes to nucleosomes. <i>Nature</i> , 1998 , 394, 498-502	50.4	447
210	The diverse functions of histone acetyltransferase complexes. <i>Trends in Genetics</i> , 2003 , 19, 321-9	8.5	441
209	Function and selectivity of bromodomains in anchoring chromatin-modifying complexes to promoter nucleosomes. <i>Cell</i> , 2002 , 111, 369-79	56.2	433
208	Promoter targeting and chromatin remodeling by the SWI/SNF complex. <i>Current Opinion in Genetics and Development</i> , 2000 , 10, 187-92	4.9	390
207	Signals and combinatorial functions of histone modifications. <i>Annual Review of Biochemistry</i> , 2011 , 80, 473-99	29.1	382
206	Readers of histone modifications. <i>Cell Research</i> , 2011 , 21, 564-78	24.7	382
205	A subset of TAF(II)s are integral components of the SAGA complex required for nucleosome acetylation and transcriptional stimulation. <i>Cell</i> , 1998 , 94, 45-53	56.2	377
204	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, 613-22	56.2	375

203	Histone acetyltransferase complexes stabilize swi/snf binding to promoter nucleosomes. <i>Cell</i> , 2001 , 104, 817-27	56.2	303
202	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	4.8	293
201	Recruitment of HAT complexes by direct activator interactions with the ATM-related Tra1 subunit. <i>Science</i> , 2001 , 292, 2333-7	33.3	287
200	Nucleosome mobilization catalysed by the yeast SWI/SNF complex. <i>Nature</i> , 1999 , 400, 784-7	50.4	283
199	The Set2 histone methyltransferase functions through the phosphorylated carboxyl-terminal domain of RNA polymerase II. <i>Journal of Biological Chemistry</i> , 2003 , 278, 8897-903	5.4	282
198	Expanded lysine acetylation specificity of Gcn5 in native complexes. <i>Journal of Biological Chemistry</i> , 1999 , 274, 5895-900	5.4	276
197	Inducible gene expression: diverse regulatory mechanisms. <i>Nature Reviews Genetics</i> , 2010 , 11, 426-37	30.1	275
196	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, 18385-90	11.5	262
195	Crosstalk among Histone Modifications. <i>Cell</i> , 2008 , 135, 604-7	56.2	257
194	Combined action of PHD and chromo domains directs the Rpd3S HDAC to transcribed chromatin. <i>Science</i> , 2007 , 316, 1050-4	33.3	254
193	Activation domains of stably bound GAL4 derivatives alleviate repression of promoters by nucleosomes. <i>Cell</i> , 1991 , 64, 533-44	56.2	250
192	Analyzing chromatin remodeling complexes using shotgun proteomics and normalized spectral abundance factors. <i>Methods</i> , 2006 , 40, 303-11	4.6	247
191	Nucleosome displacement in transcription. <i>Genes and Development</i> , 2006 , 20, 2009-17	12.6	233
190	Set2 methylation of histone H3 lysine 36 suppresses histone exchange on transcribed genes. <i>Nature</i> , 2012 , 489, 452-5	50.4	223
189	Activation domain-mediated targeting of the SWI/SNF complex to promoters stimulates transcription from nucleosome arrays. <i>Molecular Cell</i> , 1999 , 4, 649-55	17.6	217
188	A role for Snf2-related nucleosome-spacing enzymes in genome-wide nucleosome organization. <i>Science</i> , 2011 , 333, 1758-60	33.3	211
187	Chromatin remodelers Isw1 and Chd1 maintain chromatin structure during transcription by preventing histone exchange. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 884-92	17.6	208
186	Global position and recruitment of HATs and HDACs in the yeast genome. <i>Molecular Cell</i> , 2004 , 16, 199-209	20.6	199

185	Nucleosome core displacement in vitro via a metastable transcription factor-nucleosome complex. <i>Science</i> , 1992 , 258, 1780-4	33.3	199
184	The novel SLIK histone acetyltransferase complex functions in the yeast retrograde response pathway. <i>Molecular and Cellular Biology</i> , 2002 , 22, 8774-86	4.8	187
183	Histone H3 specific acetyltransferases are essential for cell cycle progression. <i>Genes and Development</i> , 2001 , 15, 3144-54	12.6	183
182	A mammalian chromatin remodeling complex with similarities to the yeast INO80 complex. <i>Journal of Biological Chemistry</i> , 2005 , 280, 41207-12	5.4	182
181	Phosphorylated Pol II CTD recruits multiple HDACs, including Rpd3C(S), for methylation-dependent deacetylation of ORF nucleosomes. <i>Molecular Cell</i> , 2010 , 39, 234-46	17.6	180
180	Transcriptional regulation by the immediate early protein of pseudorabies virus during in vitro nucleosome assembly. <i>Cell</i> , 1988 , 55, 211-9	56.2	179
179	Nucleosome displacement in transcription. <i>Cell</i> , 1993 , 72, 305-8	56.2	175
178	MSL complex is attracted to genes marked by H3K36 trimethylation using a sequence-independent mechanism. <i>Molecular Cell</i> , 2007 , 28, 121-33	17.6	173
177	Sgf29 binds histone H3K4me2/3 and is required for SAGA complex recruitment and histone H3 acetylation. <i>EMBO Journal</i> , 2011 , 30, 2829-42	13	172
176	Nucleosome remodeling and epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5,	10.2	171
175	Multiple functions of nucleosomes and regulatory factors in transcription. <i>Trends in Biochemical Sciences</i> , 1993 , 18, 90-5	10.3	171
174	The ATM-related cofactor Tra1 is a component of the purified SAGA complex. <i>Molecular Cell</i> , 1998 , 2, 863-7	17.6	165
173	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, 13665-70	5.4	158
172	The SAGA unfolds: convergence of transcription regulators in chromatin-modifying complexes. <i>Trends in Cell Biology</i> , 1998 , 8, 193-7	18.3	153
171	The proteasome regulatory particle alters the SAGA coactivator to enhance its interactions with transcriptional activators. <i>Cell</i> , 2005 , 123, 423-36	56.2	152
170	The ADA complex is a distinct histone acetyltransferase complex in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999 , 19, 6621-31	4.8	152
169	Infrequently transcribed long genes depend on the Set2/Rpd3S pathway for accurate transcription. <i>Genes and Development</i> , 2007 , 21, 1422-30	12.6	150
168	RSC exploits histone acetylation to abrogate the nucleosomal block to RNA polymerase II elongation. <i>Molecular Cell</i> , 2006 , 24, 481-7	17.6	149

167	Activation domain-specific and general transcription stimulation by native histone acetyltransferase complexes. <i>Molecular and Cellular Biology</i> , 1999 , 19, 855-63	4.8	143
166	Transcription activator interactions with multiple SWI/SNF subunits. <i>Molecular and Cellular Biology</i> , 2002 , 22, 1615-25	4.8	142
165	Cse4 is part of an octameric nucleosome in budding yeast. <i>Molecular Cell</i> , 2009 , 35, 794-805	17.6	140
164	Psh1 is an E3 ubiquitin ligase that targets the centromeric histone variant Cse4. <i>Molecular Cell</i> , 2010 , 40, 444-54	17.6	139
163	ATAC is a double histone acetyltransferase complex that stimulates nucleosome sliding. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 364-72	17.6	139
162	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, 1470-8	4.8	135
161	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, 1562-9	5.4	134
160	The deubiquitylation activity of Ubp8 is dependent upon Sgf11 and its association with the SAGA complex. <i>Molecular and Cellular Biology</i> , 2005 , 25, 1173-82	4.8	133
159	Transcription-associated histone modifications and cryptic transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013 , 1829, 84-97	6	127
158	In and out: histone variant exchange in chromatin. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 680-7	10.3	120
157	Persistent interactions of core histone tails with nucleosomal DNA following acetylation and transcription factor binding. <i>Molecular and Cellular Biology</i> , 1998 , 18, 6293-304	4.8	120
156	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, 7970-6	5.4	117
155	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	17.6	117
154	The changing faces of HP1: From heterochromatin formation and gene silencing to euchromatic gene expression: HP1 acts as a positive regulator of transcription. <i>BioEssays</i> , 2011 , 33, 280-9	4.1	116
153	The Something About Silencing protein, Sas3, is the catalytic subunit of NuA3, a yTAFII30-containing HAT complex that interacts with the Spt16 subunit of the yeast CP (Cdc68/Pob3)EACT complex. <i>Genes and Development</i> , 2000 , 14, 1196-1208	12.6	116
152	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, 168-78	17.6	112
151	Combinatorial depletion analysis to assemble the network architecture of the SAGA and ADA chromatin remodeling complexes. <i>Molecular Systems Biology</i> , 2011 , 7, 503	12.2	109
150	Recruitment of the SWI-SNF chromatin remodeling complex as a mechanism of gene activation by the glucocorticoid receptor tau1 activation domain. <i>Molecular and Cellular Biology</i> , 2000 , 20, 2004-13	4.8	108

149	Repression of GCN5 histone acetyltransferase activity via bromodomain-mediated binding and phosphorylation by the Ku-DNA-dependent protein kinase complex. <i>Molecular and Cellular Biology</i> , 1998 , 18, 1349-58	4.8	108
148	The heterochromatin protein 1 (HP1) family: put away a bias toward HP1. <i>Molecules and Cells</i> , 2008 , 26, 217-27	3.5	107
147	Serine and SAM Responsive Complex SESAME Regulates Histone Modification Crosstalk by Sensing Cellular Metabolism. <i>Molecular Cell</i> , 2015 , 60, 408-21	17.6	103
146	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, 3155-68	12.6	103
145	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, 871-82	4.8	96
144	SAGA-mediated H2B deubiquitination controls the development of neuronal connectivity in the Drosophila visual system. <i>EMBO Journal</i> , 2008 , 27, 394-405	13	94
143	Remodeling chromatin structures for transcription: what happens to the histones?. <i>BioEssays</i> , 1996 , 18, 875-84	4.1	93
142	Stable co-occupancy of transcription factors and histones at the HIV-1 enhancer. <i>EMBO Journal</i> , 1997 , 16, 2463-72	13	91
141	Two Drosophila Ada2 homologues function in different multiprotein complexes. <i>Molecular and Cellular Biology</i> , 2003 , 23, 3305-19	4.8	90
140	Sas4 and Sas5 are required for the histone acetyltransferase activity of Sas2 in the SAS complex. <i>Journal of Biological Chemistry</i> , 2003 , 278, 16887-92	5.4	89
139	Rere controls retinoic acid signalling and somite bilateral symmetry. <i>Nature</i> , 2010 , 463, 953-7	50.4	84
138	Heterochromatin protein 1a stimulates histone H3 lysine 36 demethylation by the Drosophila KDM4A demethylase. <i>Molecular Cell</i> , 2008 , 32, 696-706	17.6	84
137	The MSL3 chromodomain directs a key targeting step for dosage compensation of the Drosophila melanogaster X chromosome. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 1318-25	17.6	83
136	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, 2507-12	12.6	83
135	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, 2133-45	12.6	78
134	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, 2534-9	12.6	78
133	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, 983-90	17.6	76
132	Activation domains drive nucleosome eviction by SWI/SNF. <i>EMBO Journal</i> , 2007 , 26, 730-40	13	75

131	Sds3 (suppressor of defective silencing 3) is an integral component of the yeast Sin3[middle dot]Rpd3 histone deacetylase complex and is required for histone deacetylase activity. <i>Journal of Biological Chemistry</i> , 2000 , 275, 40961-6	5.4	75
130	Identification and analysis of yeast nucleosomal histone acetyltransferase complexes. <i>Methods</i> , 1998 , 15, 315-21	4.6	75
129	[6] Basic analysis of transcription factor binding to nucleosomes. <i>Methods in Molecular Genetics</i> , 1995 , 6, 108-128		74
128	Histone deacetylase inhibitors: anticancer compounds. <i>International Journal of Biochemistry and Cell Biology</i> , 2009 , 41, 21-5	5.6	72
127	SWI/SNF displaces SAGA-acetylated nucleosomes. <i>Eukaryotic Cell</i> , 2006 , 5, 1738-47		72
126	ATXN7L3 and ENY2 Coordinate Activity of Multiple H2B Deubiquitinases Important for Cellular Proliferation and Tumor Growth. <i>Molecular Cell</i> , 2016 , 62, 558-71	17.6	69
125	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	5.8	68
124	Deacetylase inhibitors dissociate the histone-targeting ING2 subunit from the Sin3 complex. <i>Chemistry and Biology</i> , 2010 , 17, 65-74		68
123	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, 12642-9	5.4	67
122	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, 1931-6	11.5	66
121	Bookmarking genes for activation in condensed mitotic chromosomes. <i>BioEssays</i> , 1998 , 20, 275-9	4.1	65
120	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, 7043-58	4.8	63
119	Gcn5 regulates the dissociation of SWI/SNF from chromatin by acetylation of Swi2/Snf2. <i>Genes and Development</i> , 2010 , 24, 2766-71	12.6	59
118	Structure and nucleosome interaction of the yeast NuA4 and Piccolo-NuA4 histone acetyltransferase complexes. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1196-203	17.6	58
117	Diverse functions of WD40 repeat proteins in histone recognition. <i>Genes and Development</i> , 2008 , 22, 1265-8	12.6	58
116	Characterization of the yeast trimeric-SAS acetyltransferase complex. <i>Journal of Biological Chemistry</i> , 2005 , 280, 11987-94	5.4	58
115	Histone acetyltransferase complexes can mediate transcriptional activation by the major glucocorticoid receptor activation domain. <i>Molecular and Cellular Biology</i> , 1999 , 19, 5952-9	4.8	58
114	Composition and Function of Mutant Swi/Snf Complexes. <i>Cell Reports</i> , 2017 , 18, 2124-2134	10.6	56

113	Diverse Activities of Histone Acylations Connect Metabolism to Chromatin Function. <i>Molecular Cell</i> , 2016 , 63, 547-552	17.6	56
112	Post-transcription initiation function of the ubiquitous SAGA complex in tissue-specific gene activation. <i>Genes and Development</i> , 2011 , 25, 1499-509	12.6	54
111	Mechanism of transcription factor recruitment by acidic activators. <i>Journal of Biological Chemistry</i> , 2005 , 280, 21779-84	5.4	54
110	In vitro analysis of transcription factor binding to nucleosomes and nucleosome disruption/displacement. <i>Methods in Enzymology</i> , 1996 , 274, 276-91	1.7	54
109	Control of class II gene transcription during in vitro nucleosome assembly. <i>Methods in Cell Biology</i> , 1991 , 35, 419-47	1.8	53
108	The ATAC acetyltransferase complex coordinates MAP kinases to regulate JNK target genes. <i>Cell</i> , 2010 , 142, 726-36	56.2	52
107	Analysis of nucleosome disruption by ATP-driven chromatin remodeling complexes. <i>Methods in Molecular Biology</i> , 1999 , 119, 319-31	1.4	51
106	SAGA function in tissue-specific gene expression. <i>Trends in Cell Biology</i> , 2012 , 22, 177-84	18.3	50
105	Histone acetylation and chromatin remodeling: which comes first?. <i>Molecular Genetics and Metabolism</i> , 2002 , 76, 1-5	3.7	50
104	Yng1p modulates the activity of Sas3p as a component of the yeast NuA3 Hhistone acetyltransferase complex. <i>Molecular and Cellular Biology</i> , 2002 , 22, 5047-53	4.8	48
103	Egf Signaling Directs Neoblast Repopulation by Regulating Asymmetric Cell Division in Planarians. <i>Developmental Cell</i> , 2016 , 38, 413-29	10.2	46
102	Selective suppression of antisense transcription by Set2-mediated H3K36 methylation. <i>Nature Communications</i> , 2016 , 7, 13610	17.4	45
101	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	44
100	H1-mediated repression of transcription factor binding to a stably positioned nucleosome. <i>Journal of Biological Chemistry</i> , 1997 , 272, 3635-40	5.4	42
99	A novel H2A/H4 nucleosomal histone acetyltransferase in <i>Tetrahymena thermophila</i> . <i>Molecular and Cellular Biology</i> , 1999 , 19, 2061-8	4.8	40
98	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, 259-72	12.6	39
97	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, 2364-72	4.8	39
96	reSETting chromatin during transcription elongation. <i>Epigenetics</i> , 2013 , 8, 10-5	5.7	36

95	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, 1900-7	4.8	36
94	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	10.6	35
93	RNA-dependent dynamic histone acetylation regulates MCL1 alternative splicing. <i>Nucleic Acids Research</i> , 2014 , 42, 1656-70	20.1	35
92	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, 1815-28	7.6	34
91	Opposite role of yeast ING family members in p53-dependent transcriptional activation. <i>Journal of Biological Chemistry</i> , 2003 , 278, 19171-5	5.4	34
90	Enzymatic modules of the SAGA chromatin-modifying complex play distinct roles in gene expression and development. <i>Genes and Development</i> , 2017 , 31, 1588-1600	12.6	33
89	Gal80 confers specificity on HAT complex interactions with activators. <i>Journal of Biological Chemistry</i> , 2002 , 277, 24648-52	5.4	33
88	Quantitative proteomics demonstrates that the RNA polymerase II subunits Rpb4 and Rpb7 dissociate during transcriptional elongation. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 1530-8	7.6	31
87	A novel histone fold domain-containing protein that replaces TAF6 in Drosophila SAGA is required for SAGA-dependent gene expression. <i>Genes and Development</i> , 2009 , 23, 2818-23	12.6	30
86	Chromatin remodeller Fun30 induces nucleosome disassembly to facilitate RNA polymerase II elongation. <i>Nature Communications</i> , 2017 , 8, 14527	17.4	28
85	Swi/Snf dynamics on stress-responsive genes is governed by competitive bromodomain interactions. <i>Genes and Development</i> , 2014 , 28, 2314-30	12.6	28
84	Determining protein complex connectivity using a probabilistic deletion network derived from quantitative proteomics. <i>PLoS ONE</i> , 2009 , 4, e7310	3.7	28
83	Histone acetyltransferase Enok regulates oocyte polarization by promoting expression of the actin nucleation factor spire. <i>Genes and Development</i> , 2014 , 28, 2750-63	12.6	27
82	Nucleosome positioning: multiple mechanisms toward a unifying goal. <i>Molecular Cell</i> , 2012 , 48, 1-2	17.6	26
81	Recruitment of Gcn5-containing complexes during c-Myc-dependent gene activation. Structure and function aspects. <i>Journal of Biological Chemistry</i> , 2002 , 277, 23399-406	5.4	26
80	Chromatin and signaling. <i>Current Opinion in Cell Biology</i> , 2013 , 25, 322-6	9	25
79	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, 7178-89	4.8	25
78	MAP kinases and histone modification. <i>Journal of Molecular Cell Biology</i> , 2012 , 4, 348-50	6.3	24

77	Chromatin and Metabolism. <i>Annual Review of Biochemistry</i> , 2018 , 87, 27-49	29.1	23
76	Chromatin proteins: key responders to stress. <i>PLoS Biology</i> , 2012 , 10, e1001371	9.7	22
75	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, 1429-30	11.5	22
74	HP1c casts light on dark matter. <i>Cell Cycle</i> , 2011 , 10, 625-30	4.7	21
73	HP1a targets the Drosophila KDM4A demethylase to a subset of heterochromatic genes to regulate H3K36me3 levels. <i>PLoS ONE</i> , 2012 , 7, e39758	3.7	20
72	Characterization of a metazoan ADA acetyltransferase complex. <i>Nucleic Acids Research</i> , 2019 , 47, 3383-3394	19	
71	The expanding role for chromatin and transcription in polyglutamine disease. <i>Current Opinion in Genetics and Development</i> , 2014 , 26, 96-104	4.9	19
70	Phosphorylation by casein kinase 2 facilitates Psh1 protein-assisted degradation of Cse4 protein. <i>Journal of Biological Chemistry</i> , 2014 , 289, 29297-309	5.4	18
69	Suberoylanilide hydroxamic acid (SAHA)-induced dynamics of a human histone deacetylase protein interaction network. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3114-25	7.6	18
68	Holding on through DNA replication: histone modification or modifier?. <i>Cell</i> , 2012 , 150, 875-7	56.2	18
67	Exogenous pyruvate represses histone gene expression and inhibits cancer cell proliferation via the NAMPT-NAD ⁺ -SIRT1 pathway. <i>Nucleic Acids Research</i> , 2019 , 47, 11132-11150	20.1	17
66	Activator-binding domains of the SWI/SNF chromatin remodeling complex characterized in vitro are required for its recruitment to promoters in vivo. <i>FEBS Journal</i> , 2009 , 276, 2557-65	5.7	17
65	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016 , 11, e0155492	3.7	17
64	The SAGA chromatin-modifying complex: the sum of its parts is greater than the whole. <i>Genes and Development</i> , 2020 , 34, 1287-1303	12.6	15
63	Yeast recombination enhancer is stimulated by transcription activation. <i>Molecular and Cellular Biology</i> , 2005 , 25, 7976-87	4.8	14
62	The methyltransferase SETD2 couples transcription and splicing by engaging mRNA processing factors through its SHI domain. <i>Nature Communications</i> , 2021 , 12, 1443	17.4	14
61	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	20.1	14
60	Histone H3 threonine 11 phosphorylation by Sch9 and CK2 regulates chronological lifespan by controlling the nutritional stress response. <i>ELife</i> , 2018 , 7,	8.9	14

59	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, 764-72	6	13
58	Cytoplasmic ATXN7L3B Interferes with Nuclear Functions of the SAGA Deubiquitinase Module. <i>Molecular and Cellular Biology</i> , 2016 , 36, 2855-2866	4.8	13
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