

Jerry L Workman

List of Publications by Year in Descending Order

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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

26,106
citations

83
h-index

160
g-index

306
ext. papers

28,555
ext. citations

15.7
avg, IF

7.14
L-index

#	Paper	IF	Citations
220	MPTAC links alkylation damage signaling to sterol biosynthesis.. <i>Redox Biology</i> , 2022 , 51, 102270	11.3	0
219	Structural basis of the interaction between SETD2 methyltransferase and hnRNP L paralogs for governing co-transcriptional splicing. <i>Nature Communications</i> , 2021 , 12, 6452	17.4	0
218	The SAGA core module is critical during Drosophila oogenesis and is broadly recruited to promoters. <i>PLoS Genetics</i> , 2021 , 17, e1009668	6	
217	The linker histone Hho1 modulates the activity of ATP-dependent chromatin remodeling complexes.. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021 , 194781	6	0
216	MOCS2 links nucleotide metabolism to nucleoli function. <i>Journal of Molecular Cell Biology</i> , 2021 ,	6.3	1
215	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
214	The SESAME complex regulates cell senescence through the generation of acetyl-CoA. <i>Nature Metabolism</i> , 2021 , 3, 983-1000	14.6	4
213	Metabolic regulation of telomere silencing by SESAME complex-catalyzed H3T11 phosphorylation. <i>Nature Communications</i> , 2021 , 12, 594	17.4	10
212	Nucleotide Metabolism Behind Epigenetics. <i>Frontiers in Endocrinology</i> , 2021 , 12, 731648	5.7	0
211	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	5.4	1
210	Macrophages, Metabolites, and Nucleosomes: Chromatin at the Intersection between Aging and Inflammation. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
209	SAGA Structures Provide Mechanistic Models for Gene Activation. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 547-549	10.3	5
208	When histones are under glucose starvation. <i>Journal of Biosciences</i> , 2020 , 45, 1	2.3	1
207	Yeast Nuak1 phosphorylates histone H3 threonine 11 in low glucose stress by the cooperation of AMPK and CK2 signaling. <i>ELife</i> , 2020 , 9,	8.9	1
206	The plasticity of the pyruvate dehydrogenase complex confers a labile structure that is associated with its catalytic activity. <i>PLoS ONE</i> , 2020 , 15, e0243489	3.7	1
205	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
204	Regulation of SETD2 stability is important for the fidelity of H3K36me3 deposition. <i>Epigenetics and Chromatin</i> , 2020 , 13, 40	5.8	11

203	β-Catenin and Associated Proteins Regulate Lineage Differentiation in Ground State Mouse Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2020 , 15, 662-676	8	4
202	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	11.5	5
201	When histones are under glucose starvation. <i>Journal of Biosciences</i> , 2020 , 45,	2.3	1
200	NSL complex acetylates Lamin A/C. <i>Nature Cell Biology</i> , 2019 , 21, 1177-1178	23.4	
199	Characterization of a metazoan ADA acetyltransferase complex. <i>Nucleic Acids Research</i> , 2019 , 47, 3383-3394	19	
198	Identification of a nuclear localization signal and importin beta members mediating NUA1 nuclear import inhibited by oxidative stress. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 16088-16107	4.7	7
197	Histone lysine de-Hydroxybutyrylation by SIRT3. <i>Cell Research</i> , 2019 , 29, 694-695	24.7	5
196	Rebooting the Epigenome: Erasure of Parental Histone Marks for Establishing the Regulatory Landscape in Zygotes. <i>Biochemistry</i> , 2019 , 58, 4387-4388	3.2	
195	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
194	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
193	Glycolysis regulates gene expression by promoting the crosstalk between H3K4 trimethylation and H3K14 acetylation in <i>Saccharomyces cerevisiae</i> . <i>Journal of Genetics and Genomics</i> , 2019 , 46, 561-574	4	7
192	MPTAC Determines APP Fragmentation via Sensing Sulfur Amino Acid Catabolism. <i>Cell Reports</i> , 2018 , 24, 1585-1596	10.6	8
191	Chromatin and Metabolism. <i>Annual Review of Biochemistry</i> , 2018 , 87, 27-49	29.1	23
190	Targeting BAF-perturbed cancers. <i>Nature Cell Biology</i> , 2018 , 20, 1332-1333	23.4	1
189	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
188	Role of Nhp6 and Hmo1 in SWI/SNF occupancy and nucleosome landscape at gene regulatory regions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2017 , 1860, 316-326	6	6
187	Chromatin remodeller Fun30 induces nucleosome disassembly to facilitate RNA polymerase II elongation. <i>Nature Communications</i> , 2017 , 8, 14527	17.4	28
186	Composition and Function of Mutant Swi/Snf Complexes. <i>Cell Reports</i> , 2017 , 18, 2124-2134	10.6	56

185	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
184	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	6.5	8
183	In Vitro Assembly of Nucleosomes for Binding/Remodeling Assays. <i>Methods in Molecular Biology</i> , 2017 , 1528, 1-17	1.4	2
182	Egf Signaling Directs Neoblast Repopulation by Regulating Asymmetric Cell Division in Planarians. <i>Developmental Cell</i> , 2016 , 38, 413-29	10.2	46
181	Diverse Activities of Histone Acylations Connect Metabolism to Chromatin Function. <i>Molecular Cell</i> , 2016 , 63, 547-552	17.6	56
180	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
179	CHROMATIN. It takes teamwork to modify chromatin. <i>Science</i> , 2016 , 351, 667	33.3	4
178	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	6.3	9
177	WDR76 Co-Localizes with Heterochromatin Related Proteins and Rapidly Responds to DNA Damage. <i>PLoS ONE</i> , 2016 , 11, e0155492	3.7	17
176	Selective suppression of antisense transcription by Set2-mediated H3K36 methylation. <i>Nature Communications</i> , 2016 , 7, 13610	17.4	45
175	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
174	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	12.6	8
173	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
172	Cytoplasmic ATXN7L3B Interferes with Nuclear Functions of the SAGA Deubiquitinase Module. <i>Molecular and Cellular Biology</i> , 2016 , 36, 2855-2866	4.8	13
171	New Face for Chromatin-Related Mesenchymal Modulator: n-CHD9 Localizes to Nucleoli and Interacts With Ribosomal Genes. <i>Journal of Cellular Physiology</i> , 2015 , 230, 2270-80	7	11
170	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
169	Histone exchange, chromatin structure and the regulation of transcription. <i>Nature Reviews Molecular Cell Biology</i> , 2015 , 16, 178-89	48.7	597
168	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

167	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
166	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
165	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
164	RNA-dependent dynamic histone acetylation regulates MCL1 alternative splicing. <i>Nucleic Acids Research</i> , 2014 , 42, 1656-70	20.1	35
163	Recognizing methylated histone variant H3.3 to prevent tumors. <i>Cell Research</i> , 2014 , 24, 649-50	24.7	4
162	Loss of Drosophila 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
161	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
160	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
159	Drosophila models reveal novel insights into mechanisms underlying neurodegeneration. <i>Fly</i> , 2014 , 8, 148-52	1.3	5
158	Pulling complexes out of complex diseases: Spinocerebellar Ataxia 7. <i>Rare Diseases (Austin, Tex)</i> , 2014 , 2, e28859		7
157	UpSETting chromatin during non-coding RNA production. <i>Epigenetics and Chromatin</i> , 2013 , 6, 16	5.8	8
156	Transcription-associated histone modifications and cryptic transcription. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013 , 1829, 84-97	6	127
155	Remodelling without a power stroke. <i>EMBO Reports</i> , 2013 , 14, 1030-1	6.5	
154	Chromatin and signaling. <i>Current Opinion in Cell Biology</i> , 2013 , 25, 322-6	9	25
153	reSETting chromatin during transcription elongation. <i>Epigenetics</i> , 2013 , 8, 10-5	5.7	36
152	Nucleosome remodeling and epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5,	10.2	171
151	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
150	Directing transcription to the right way. <i>Cell Research</i> , 2013 , 23, 1153-4	24.7	3

149	Non-coding transcription SETs up regulation. <i>Cell Research</i> , 2013 , 23, 311-3	24.7	3
148	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
147	SAGA function in tissue-specific gene expression. <i>Trends in Cell Biology</i> , 2012 , 22, 177-84	18.3	50
146	Holding on through DNA replication: histone modification or modifier?. <i>Cell</i> , 2012 , 150, 875-7	56.2	18
145	Nucleosome positioning: multiple mechanisms toward a unifying goal. <i>Molecular Cell</i> , 2012 , 48, 1-2	17.6	26
144	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
143	Set2 methylation of histone H3 lysine 36 suppresses histone exchange on transcribed genes. <i>Nature</i> , 2012 , 489, 452-5	50.4	223
142	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, 90-9	7.6	5
141	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
140	Chromatin proteins: key responders to stress. <i>PLoS Biology</i> , 2012 , 10, e1001371	9.7	22
139	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
138	MAP kinases and histone modification. <i>Journal of Molecular Cell Biology</i> , 2012 , 4, 348-50	6.3	24
137	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
136	Signals and combinatorial functions of histone modifications. <i>Annual Review of Biochemistry</i> , 2011 , 80, 473-99	29.1	382
135	Signaling through chromatin: setting the scene at kinetochores. <i>Cell</i> , 2011 , 146, 671-2	56.2	1
134	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
133	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
132	Suppression of cryptic intragenic transcripts is required for embryonic stem cell self-renewal. <i>EMBO Journal</i> , 2011 , 30, 1420-1	13	4

131	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
130	A role for Snf2-related nucleosome-spacing enzymes in genome-wide nucleosome organization. <i>Science</i> , 2011 , 333, 1758-60	33.3	211
129	Readers of histone modifications. <i>Cell Research</i> , 2011 , 21, 564-78	24.7	382
128	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
127	HP1c casts light on dark matter. <i>Cell Cycle</i> , 2011 , 10, 625-30	4.7	21
126	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
125	Rere controls retinoic acid signalling and somite bilateral symmetry. <i>Nature</i> , 2010 , 463, 953-7	50.4	84
124	Inducible gene expression: diverse regulatory mechanisms. <i>Nature Reviews Genetics</i> , 2010 , 11, 426-37	30.1	275
123	WD40 repeats arrange histone tails for spreading of silencing. <i>Journal of Molecular Cell Biology</i> , 2010 , 2, 81-3	6.3	6
122	Histone acetylation in heterochromatin assembly. <i>Genes and Development</i> , 2010 , 24, 738-40	12.6	11
121	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
120	Features of the PHF8/KIAA1718 histone demethylase. <i>Cell Research</i> , 2010 , 20, 861-2	24.7	12
119	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
118	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
117	Psh1 is an E3 ubiquitin ligase that targets the centromeric histone variant Cse4. <i>Molecular Cell</i> , 2010 , 40, 444-54	17.6	139
116	The ATAC acetyltransferase complex coordinates MAP kinases to regulate JNK target genes. <i>Cell</i> , 2010 , 142, 726-36	56.2	52
115	Deacetylase inhibitors dissociate the histone-targeting ING2 subunit from the Sin3 complex. <i>Chemistry and Biology</i> , 2010 , 17, 65-74		68
114	Features of cryptic promoters and their varied reliance on bromodomain-containing factors. <i>PLoS ONE</i> , 2010 , 5, e12927	3.7	11

113	Determining protein complex connectivity using a probabilistic deletion network derived from quantitative proteomics. <i>PLoS ONE</i> , 2009 , 4, e7310	3.7	28
112	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
111	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
110	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
109	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
108	Histone deacetylase inhibitors: anticancer compounds. <i>International Journal of Biochemistry and Cell Biology</i> , 2009 , 41, 21-5	5.6	72
107	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
106	Cse4 is part of an octameric nucleosome in budding yeast. <i>Molecular Cell</i> , 2009 , 35, 794-805	17.6	140
105	Heterochromatin Protein 1a stimulates histone H3 lysine 36 demethylation by the Drosophila KDM4A demethylase. <i>FASEB Journal</i> , 2009 , 23, 325.3	0.9	
104	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
103	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
102	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
101	Histone ubiquitination: triggering gene activity. <i>Molecular Cell</i> , 2008 , 29, 653-63	17.6	532
100	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
99	Clearing the way for unpaused polymerases. <i>Cell</i> , 2008 , 134, 16-8	56.2	4
98	Crosstalk among Histone Modifications. <i>Cell</i> , 2008 , 135, 604-7	56.2	257
97	Diverse functions of WD40 repeat proteins in histone recognition. <i>Genes and Development</i> , 2008 , 22, 1265-8	12.6	58
96	The heterochromatin protein 1 (HP1) family: put away a bias toward HP1. <i>Molecules and Cells</i> , 2008 , 26, 217-27	3.5	107

95	Combined action of PHD and chromo domains directs the Rpd3S HDAC to transcribed chromatin. <i>Science</i> , 2007 , 316, 1050-4	33.3	254
94	Histone acetyltransferase complexes: one size doesn't fit all. <i>Nature Reviews Molecular Cell Biology</i> , 2007 , 8, 284-95	48.7	792
93	Activation domains drive nucleosome eviction by SWI/SNF. <i>EMBO Journal</i> , 2007 , 26, 730-40	13	75
92	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
91	The role of chromatin during transcription. <i>Cell</i> , 2007 , 128, 707-19	56.2	2639
90	New nomenclature for chromatin-modifying enzymes. <i>Cell</i> , 2007 , 131, 633-6	56.2	745
89	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
88	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, 871-82	4.8	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, 2507-12	12.6	83
86	SWI/SNF displaces SAGA-acetylated nucleosomes. <i>Eukaryotic Cell</i> , 2006 , 5, 1738-47		72
85	Nucleosome displacement in transcription. <i>Genes and Development</i> , 2006 , 20, 2009-17	12.6	233
84	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, 7178-89	4.8	25
83	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
82	Analyzing chromatin remodeling complexes using shotgun proteomics and normalized spectral abundance factors. <i>Methods</i> , 2006 , 40, 303-11	4.6	247
81	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
80	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
79	In and out: histone variant exchange in chromatin. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 680-7	10.3	120
78	Yeast recombination enhancer is stimulated by transcription activation. <i>Molecular and Cellular Biology</i> , 2005 , 25, 7976-87	4.8	14

77	Mechanism of transcription factor recruitment by acidic activators. <i>Journal of Biological Chemistry</i> , 2005 , 280, 21779-84	5.4	54
76	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
75	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
74	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
73	Characterization of the yeast trimeric-SAS acetyltransferase complex. <i>Journal of Biological Chemistry</i> , 2005 , 280, 11987-94	5.4	58
72	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
71	The DNA repair protein yKu80 regulates the function of recombination enhancer during yeast mating type switching. <i>Molecular and Cellular Biology</i> , 2005 , 25, 8476-85	4.8	8
70	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
69	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
68	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
67	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
66	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
65	Acetylation by Tip60 is required for selective histone variant exchange at DNA lesions. <i>Science</i> , 2004 , 306, 2084-7	33.3	544
64	Global position and recruitment of HATs and HDACs in the yeast genome. <i>Molecular Cell</i> , 2004 , 16, 199-209	19.6	199
63	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
62	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
61	Assay of activator recruitment of chromatin-modifying complexes. <i>Methods in Enzymology</i> , 2003 , 371, 536-44	1.7	4
60	The diverse functions of histone acetyltransferase complexes. <i>Trends in Genetics</i> , 2003 , 19, 321-9	8.5	441

59	Transcription factors prominently in Lasker Award to Roeder. <i>Cell</i> , 2003 , 115, 243-6	56.2	
58	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
57	Two Drosophila Ada2 homologues function in different multiprotein complexes. <i>Molecular and Cellular Biology</i> , 2003 , 23, 3305-19	4.8	90
56	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
55	Gal80 confers specificity on HAT complex interactions with activators. <i>Journal of Biological Chemistry</i> , 2002 , 277, 24648-52	5.4	33
54	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
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1	The histone methyltransferase SETD2 couples transcription and splicing by engaging pre-mRNA processing factors through its SHI domain		1