

Craig L Peterson

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105
papers

11,757
citations

55
h-index

108
g-index

127
ext. papers

12,925
ext. citations

13.1
avg. IF

6.55
L-index

#	Paper	IF	Citations
105	Histone H4-K16 acetylation controls chromatin structure and protein interactions. <i>Science</i> , 2006 , 311, 844-7	33.3	1616
104	Histones and histone modifications. <i>Current Biology</i> , 2004 , 14, R546-51	6.3	934
103	Characterization of the yeast SWI1, SWI2, and SWI3 genes, which encode a global activator of transcription. <i>Cell</i> , 1992 , 68, 573-83	56.2	542
102	Mechanisms of action and regulation of ATP-dependent chromatin-remodelling complexes. <i>Nature Reviews Molecular Cell Biology</i> , 2017 , 18, 407-422	48.7	457
101	gamma-H2AX dephosphorylation by protein phosphatase 2A facilitates DNA double-strand break repair. <i>Molecular Cell</i> , 2005 , 20, 801-9	17.6	417
100	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
99	Molecular biology. Chromatin higher order folding--wrapping up transcription. <i>Science</i> , 2002 , 297, 1824-33	33.3	334
98	Global regulation of H2A.Z localization by the INO80 chromatin-remodeling enzyme is essential for genome integrity. <i>Cell</i> , 2011 , 144, 200-13	56.2	295
97	The SANT domain: a unique histone-tail-binding module?. <i>Nature Reviews Molecular Cell Biology</i> , 2004 , 5, 158-63	48.7	273
96	Mechanisms that regulate localization of a DNA double-strand break to the nuclear periphery. <i>Genes and Development</i> , 2009 , 23, 912-27	12.6	240
95	Cellular machineries for chromosomal DNA repair. <i>Genes and Development</i> , 2004 , 18, 602-16	12.6	223
94	Chromatin remodeling enzymes: who's on first?. <i>Current Biology</i> , 2001 , 11, R185-97	6.3	211
93	Global role for chromatin remodeling enzymes in mitotic gene expression. <i>Cell</i> , 2000 , 102, 587-98	56.2	197
92	Essential role for the SANT domain in the functioning of multiple chromatin remodeling enzymes. <i>Molecular Cell</i> , 2002 , 10, 935-42	17.6	191
91	DNA translocation and loop formation mechanism of chromatin remodeling by SWI/SNF and RSC. <i>Molecular Cell</i> , 2006 , 24, 559-68	17.6	174
90	DNA-binding properties of the yeast SWI/SNF complex. <i>Nature</i> , 1996 , 379, 844-7	50.4	174
89	Chromatin and the genome integrity network. <i>Nature Reviews Genetics</i> , 2013 , 14, 62-75	30.1	169

88	Recruitment of the recombinational repair machinery to a DNA double-strand break in yeast. <i>Molecular Cell</i> , 2003 , 12, 221-32	17.6	167
87	Chromatin dynamics: interplay between remodeling enzymes and histone modifications. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014 , 1839, 728-36	6	159
86	Interplay between Ino80 and Swr1 chromatin remodeling enzymes regulates cell cycle checkpoint adaptation in response to DNA damage. <i>Genes and Development</i> , 2006 , 20, 2437-49	12.6	150
85	Rad54p is a chromatin remodeling enzyme required for heteroduplex DNA joint formation with chromatin. <i>Journal of Biological Chemistry</i> , 2003 , 278, 9212-8	5.4	149
84	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , 2002 , 9, 263-7		148
83	A histone acetylation switch regulates H2A.Z deposition by the SWR-C remodeling enzyme. <i>Science</i> , 2013 , 340, 195-9	33.3	144
82	ATP-dependent chromatin remodeling. <i>Current Topics in Developmental Biology</i> , 2005 , 65, 115-48	5.3	143
81	Genomic Nucleosome Organization Reconstituted with Pure Proteins. <i>Cell</i> , 2016 , 167, 709-721.e12	56.2	138
80	A Rik1-associated, cullin-dependent E3 ubiquitin ligase is essential for heterochromatin formation. <i>Genes and Development</i> , 2005 , 19, 1705-14	12.6	136
79	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
78	Structural analysis of the yeast SWI/SNF chromatin remodeling complex. <i>Nature Structural Biology</i> , 2003 , 10, 141-5		133
77	The Ino80 chromatin-remodeling enzyme regulates replisome function and stability. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 338-45	17.6	130
76	Multiple SWItches to turn on chromatin?. <i>Current Opinion in Genetics and Development</i> , 1996 , 6, 171-5	4.9	122
75	The biochemical and phenotypic characterization of Hho1p, the putative linker histone H1 of <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 1998 , 273, 7268-76	5.4	116
74	Architecture of the SWI/SNF-nucleosome complex. <i>Molecular and Cellular Biology</i> , 2008 , 28, 6010-21	4.8	113
73	SWI/SNF is required for transcriptional memory at the yeast GAL gene cluster. <i>Genes and Development</i> , 2007 , 21, 997-1004	12.6	111
72	Subunits of the yeast SWI/SNF complex are members of the actin-related protein (ARP) family. <i>Journal of Biological Chemistry</i> , 1998 , 273, 23641-4	5.4	110
71	Nucleosome dynamics regulates DNA processing. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 836-426	4.26	104

70	SWI/SNF chromatin remodeling requires changes in DNA topology. <i>Molecular Cell</i> , 2001 , 7, 97-104	17.6	101
69	A native peptide ligation strategy for deciphering nucleosomal histone modifications. <i>Journal of Biological Chemistry</i> , 2003 , 278, 15744-8	5.4	97
68	Chromatin remodeling: a marriage between two families?. <i>BioEssays</i> , 1998 , 20, 771-80	4.1	95
67	SWI-SNF-mediated nucleosome remodeling: role of histone octamer mobility in the persistence of the remodeled state. <i>Molecular and Cellular Biology</i> , 2000 , 20, 3058-68	4.8	93
66	Functional delineation of three groups of the ATP-dependent family of chromatin remodeling enzymes. <i>Journal of Biological Chemistry</i> , 2000 , 275, 18864-70	5.4	87
65	The Histone Chaperones FACT and Spt6 Restrict H2A.Z from Intragenic Locations. <i>Molecular Cell</i> , 2015 , 58, 1113-23	17.6	82
64	Transcription. Unlocking the gates to gene expression. <i>Science</i> , 2002 , 295, 1847-8	33.3	81
63	Switching on chromatin: mechanistic role of histone H4-K16 acetylation. <i>Cell Cycle</i> , 2006 , 5, 1361-5	4.7	73
62	A conserved Swi2/Snf2 ATPase motif couples ATP hydrolysis to chromatin remodeling. <i>Molecular and Cellular Biology</i> , 2005 , 25, 5880-92	4.8	73
61	Swi3p controls SWI/SNF assembly and ATP-dependent H2A-H2B displacement. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 540-7	17.6	71
60	The core histone N-terminal domains are required for multiple rounds of catalytic chromatin remodeling by the SWI/SNF and RSC complexes. <i>Biochemistry</i> , 1999 , 38, 2514-22	3.2	71
59	ATP-dependent and ATP-independent roles for the Rad54 chromatin remodeling enzyme during recombinational repair of a DNA double strand break. <i>Journal of Biological Chemistry</i> , 2005 , 280, 10855-60	5.4	69
58	Recombinational repair within heterochromatin requires ATP-dependent chromatin remodeling. <i>Cell</i> , 2009 , 138, 1109-21	56.2	68
57	Chromatin remodeling enzymes: taming the machines. Third in review series on chromatin dynamics. <i>EMBO Reports</i> , 2002 , 3, 319-22	6.5	68
56	DNA repair choice defines a common pathway for recruitment of chromatin regulators. <i>Nature Communications</i> , 2013 , 4, 2084	17.4	67
55	Recruitment of chromatin remodeling machines. <i>Journal of Cellular Biochemistry</i> , 2000 , 78, 179-85	4.7	65
54	Chromatin remodeling: nucleosomes bulging at the seams. <i>Current Biology</i> , 2002 , 12, R245-7	6.3	61
53	Chromatin remodeling activities act on UV-damaged nucleosomes and modulate DNA damage accessibility to photolyase. <i>Journal of Biological Chemistry</i> , 2003 , 278, 17655-63	5.4	60

52	HDACs at work: everyone doing their part. <i>Molecular Cell</i> , 2002 , 9, 921-2	17.6	59
51	Actin-related proteins (Arps): conformational switches for chromatin-remodeling machines?. <i>BioEssays</i> , 2000 , 22, 666-72	4.1	57
50	A multilaboratory comparison of calibration accuracy and the performance of external references in analytical ultracentrifugation. <i>PLoS ONE</i> , 2015 , 10, e0126420	3.7	55
49	Structural analyses of the chromatin remodelling enzymes INO80-C and SWR-C. <i>Nature Communications</i> , 2015 , 6, 7108	17.4	50
48	ATP-dependent chromatin remodeling: going mobile. <i>FEBS Letters</i> , 2000 , 476, 68-72	3.8	50
47	Chromatin dynamics during repair of chromosomal DNA double-strand breaks. <i>Epigenomics</i> , 2009 , 1, 371-85	4.4	48
46	The interactions of yeast SWI/SNF and RSC with the nucleosome before and after chromatin remodeling. <i>Journal of Biological Chemistry</i> , 2001 , 276, 12636-44	5.4	47
45	Heterochromatin assembly: a new twist on an old model. <i>Chromosome Research</i> , 2006 , 14, 83-94	4.4	46
44	Nucleosome dynamics as modular systems that integrate DNA damage and repair. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5,	10.2	45
43	Structural characterization of H3K56Q nucleosomes and nucleosomal arrays. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010 , 1799, 480-6	6	43
42	Chromatin remodeling by the SWI/SNF complex is essential for transcription mediated by the yeast cell wall integrity MAPK pathway. <i>Molecular Biology of the Cell</i> , 2012 , 23, 2805-17	3.5	40
41	Role of chromatin states in transcriptional memory. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2009 , 1790, 445-55	4	37
40	Nucleosomes influence multiple steps during replication initiation. <i>ELife</i> , 2017 , 6,	8.9	36
39	Hsp90 and p23 Molecular Chaperones Control Chromatin Architecture by Maintaining the Functional Pool of the RSC Chromatin Remodeler. <i>Molecular Cell</i> , 2016 , 64, 888-899	17.6	35
38	Roles of the histone H2A-H2B dimers and the (H3-H4)(2) tetramer in nucleosome remodeling by the SWI-SNF complex. <i>Journal of Biological Chemistry</i> , 2000 , 275, 11545-52	5.4	35
37	SWI/SNF recruitment to a DNA double-strand break by the NuA4 and Gcn5 histone acetyltransferases. <i>DNA Repair</i> , 2015 , 30, 38-45	4.3	34
36	The Ino80 complex prevents invasion of euchromatin into silent chromatin. <i>Genes and Development</i> , 2015 , 29, 350-5	12.6	34
35	Mot1, Ino80C, and NC2 Function Coordinately to Regulate Pervasive Transcription in Yeast and Mammals. <i>Molecular Cell</i> , 2017 , 67, 594-607.e4	17.6	29

34	A Rad51 presynaptic filament is sufficient to capture nucleosomal homology during recombinational repair of a DNA double-strand break. <i>Molecular Cell</i> , 2008 , 30, 803-10	17.6	29
33	Opening the DNA repair toolbox: localization of DNA double strand breaks to the nuclear periphery. <i>Cell Cycle</i> , 2010 , 9, 43-9	4.7	28
32	The SIN domain of the histone octamer is essential for intramolecular folding of nucleosomal arrays. <i>Nature Structural Biology</i> , 2002 , 9, 167-71		26
31	Nucleosome-like, Single-stranded DNA (ssDNA)-Histone Octamer Complexes and the Implication for DNA Double Strand Break Repair. <i>Journal of Biological Chemistry</i> , 2017 , 292, 5271-5281	5.4	25
30	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015 , 13, 1610-22	10.6	22
29	Mechanism of Long-Range Chromosome Motion Triggered by Gene Activation. <i>Developmental Cell</i> , 2020 , 52, 309-320.e5	10.2	22
28	Distinct transcriptional roles for Histone H3-K56 acetylation during the cell cycle in Yeast. <i>Nature Communications</i> , 2019 , 10, 4372	17.4	15
27	Deposition of histone H2A.Z by the SWR-C remodeling enzyme prevents genome instability. <i>DNA Repair</i> , 2015 , 25, 9-14	4.3	15
26	Solution-state conformation and stoichiometry of yeast Sir3 heterochromatin fibres. <i>Nature Communications</i> , 2014 , 5, 4751	17.4	15
25	Yeast Sirtuin Family Members Maintain Transcription Homeostasis to Ensure Genome Stability. <i>Cell Reports</i> , 2019 , 27, 2978-2989.e5	10.6	14
24	Transient Kinetic Analysis of SWR1C-Catalyzed H2A.Z Deposition Unravels the Impact of Nucleosome Dynamics and the Asymmetry of Histone Exchange. <i>Cell Reports</i> , 2019 , 27, 374-386.e4	10.6	13
23	Response to Comment on "A histone acetylation switch regulates H2A.Z deposition by the SWR-C remodeling enzyme". <i>Science</i> , 2016 , 353, 358	33.3	11
22	Transcriptional activation: getting a grip on condensed chromatin. <i>Current Biology</i> , 2003 , 13, R195-7	6.3	11
21	SWI/SNF- and RSC-catalyzed nucleosome mobilization requires internal DNA loop translocation within nucleosomes. <i>Molecular and Cellular Biology</i> , 2011 , 31, 4165-75	4.8	10
20	Multivalent interactions drive nucleosome binding and efficient chromatin deacetylation by SIRT6. <i>Nature Communications</i> , 2020 , 11, 5244	17.4	10
19	Direct interactions promote eviction of the Sir3 heterochromatin protein by the SWI/SNF chromatin remodeling enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17827-32	11.5	9
18	SIR proteins create compact heterochromatin fibers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 12447-12452	11.5	9
17	Chicken erythrocyte histone octamer preparation. <i>Cold Spring Harbor Protocols</i> , 2008 , 2008, pdb.prot51122		8

16	Genome integrity: a HAT needs a chaperone. <i>Current Biology</i> , 2007 , 17, R324-6	6.3	8
15	The ins and outs of heterochromatic DNA repair. <i>Developmental Cell</i> , 2011 , 20, 285-7	10.2	7
14	Coupling tandem affinity purification and quantitative tyrosine iodination to determine subunit stoichiometry of protein complexes. <i>Methods</i> , 2003 , 31, 104-9	4.6	7
13	INO80C Remodeler Maintains Genomic Stability by Preventing Promiscuous Transcription at Replication Origins. <i>Cell Reports</i> , 2020 , 32, 108106	10.6	5
12	RNA polymerase II depletion promotes transcription of alternative mRNA species. <i>BMC Molecular Biology</i> , 2016 , 17, 20	4.5	5
11	Chromatin remodeling: a complex affair. <i>EMBO Reports</i> , 2017 , 18, 1673-1674	6.5	2
10	Salt gradient dialysis reconstitution of nucleosomes. <i>Cold Spring Harbor Protocols</i> , 2008 , 2008, pdb.prot5113	1.1	2
9	SWI/SNF senses carbon starvation with a pH-sensitive low complexity sequence.. <i>ELife</i> , 2022 , 11,	8.9	2
8	Protein complex binding to promoter DNA: immobilized template assay. <i>Cold Spring Harbor Protocols</i> , 2010 , 2010, pdb.prot5465	1.2	1
7	Transcriptional memory: mothers SET the table for daughters. <i>Current Biology</i> , 2010 , 20, R240-2	6.3	1
6	Transient kinetic analysis of SWR1C-catalyzed H2A.Z deposition unravels the impact of nucleosome dynamics and the asymmetry of stepwise histone exchange		1
5	SWI/SNF senses carbon starvation with a pH-sensitive low complexity sequence		1
4	Actin-related proteins (Arps): conformational switches for chromatin-remodeling machines? 2000 , 22, 666		1
3	DNA repair choice defines a common pathway for recruitment of chromatin regulators. <i>FASEB Journal</i> , 2013 , 27, 760.2	0.9	
2	SWI/SNF remodels SIR3 heterochromatin during transcription. <i>FASEB Journal</i> , 2013 , 27, 770.6	0.9	
1	A histone acetylation switch regulates H2A.Z deposition by the SWR-C remodeling enzyme. <i>FASEB Journal</i> , 2013 , 27, 770.4	0.9	