

# Craig L Peterson

## List of Publications by Year in descending order

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107  
papers

13,832  
citations

28272

55  
h-index

30920

102  
g-index

127  
all docs

127  
docs citations

127  
times ranked

12788  
citing authors

#	ARTICLE	IF	CITATIONS
1	Histone H4-K16 Acetylation Controls Chromatin Structure and Protein Interactions. <i>Science</i> , 2006, 311, 844-847.	12.6	1,881
2	Histones and histone modifications. <i>Current Biology</i> , 2004, 14, R546-R551.	3.9	1,064
3	Mechanisms of action and regulation of ATP-dependent chromatin-remodelling complexes. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 407-422.	37.0	828
4	Characterization of the yeast SWI1, SWI2, and SWI3 genes, which encode a global activator of transcription. <i>Cell</i> , 1992, 68, 573-583.	28.9	610
5	$\hat{\gamma}$ -H2AX Dephosphorylation by Protein Phosphatase 2A Facilitates DNA Double-Strand Break Repair. <i>Molecular Cell</i> , 2005, 20, 801-809.	9.7	467
6	Promoter targeting and chromatin remodeling by the SWI/SNF complex. <i>Current Opinion in Genetics and Development</i> , 2000, 10, 187-192.	3.3	404
7	MOLECULAR BIOLOGY: Chromatin Higher Order Folding--Wrapping up Transcription. <i>Science</i> , 2002, 297, 1824-1827.	12.6	364
8	Global Regulation of H2A.Z Localization by the INO80 Chromatin-Remodeling Enzyme Is Essential for Genome Integrity. <i>Cell</i> , 2011, 144, 200-213.	28.9	345
9	The SANT domain: a unique histone-tail-binding module?. <i>Nature Reviews Molecular Cell Biology</i> , 2004, 5, 158-163.	37.0	338
10	Mechanisms that regulate localization of a DNA double-strand break to the nuclear periphery. <i>Genes and Development</i> , 2009, 23, 912-927.	5.9	279
11	Cellular machineries for chromosomal DNA repair. <i>Genes and Development</i> , 2004, 18, 602-616.	5.9	253
12	Chromatin remodeling enzymes: who's on first?. <i>Current Biology</i> , 2001, 11, R185-R197.	3.9	234
13	Genomic Nucleosome Organization Reconstituted with Pure Proteins. <i>Cell</i> , 2016, 167, 709-721.e12.	28.9	227
14	Essential Role for the SANT Domain in the Functioning of Multiple Chromatin Remodeling Enzymes. <i>Molecular Cell</i> , 2002, 10, 935-942.	9.7	224
15	Global Role for Chromatin Remodeling Enzymes in Mitotic Gene Expression. <i>Cell</i> , 2000, 102, 587-598.	28.9	213
16	DNA Translocation and Loop Formation Mechanism of Chromatin Remodeling by SWI/SNF and RSC. <i>Molecular Cell</i> , 2006, 24, 559-568.	9.7	198
17	Chromatin dynamics: Interplay between remodeling enzymes and histone modifications. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 728-736.	1.9	194
18	Chromatin and the genome integrity network. <i>Nature Reviews Genetics</i> , 2013, 14, 62-75.	16.3	193

#	ARTICLE	IF	CITATIONS
19	DNA-binding properties of the yeast SWI/SNF complex. <i>Nature</i> , 1996, 379, 844-847.	27.8	184
20	Recruitment of the Recombinational Repair Machinery to a DNA Double-Strand Break in Yeast. <i>Molecular Cell</i> , 2003, 12, 221-232.	9.7	181
21	A Histone Acetylation Switch Regulates H2A.Z Deposition by the SWR-C Remodeling Enzyme. <i>Science</i> , 2013, 340, 195-199.	12.6	168
22	ATP-Dependent Chromatin Remodeling. <i>Current Topics in Developmental Biology</i> , 2004, 65, 115-148.	2.2	165
23	Rad54p Is a Chromatin Remodeling Enzyme Required for Heteroduplex DNA Joint Formation with Chromatin. <i>Journal of Biological Chemistry</i> , 2003, 278, 9212-9218.	3.4	164
24	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, 2437-2449.	5.9	162
25	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , 2002, 9, 263-267.	9.7	160
26	A Rik1-associated, cullin-dependent E3 ubiquitin ligase is essential for heterochromatin formation. <i>Genes and Development</i> , 2005, 19, 1705-1714.	5.9	156
27	Structural analysis of the yeast SWI/SNF chromatin remodeling complex. <i>Nature Structural Biology</i> , 2003, 10, 141-145.	9.7	145
28	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.	2.3	143
29	The Ino80 chromatin-remodeling enzyme regulates replisome function and stability. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 338-345.	8.2	143
30	SWI/SNF is required for transcriptional memory at the yeast GAL gene cluster. <i>Genes and Development</i> , 2007, 21, 997-1004.	5.9	137
31	Multiple SWItches to turn on chromatin?. <i>Current Opinion in Genetics and Development</i> , 1996, 6, 171-175.	3.3	132
32	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, 7268-7276.	3.4	132
33	Nucleosome dynamics regulates DNA processing. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 836-842.	8.2	130
34	Subunits of the Yeast SWI/SNF Complex Are Members of the Actin-related Protein (ARP) Family. <i>Journal of Biological Chemistry</i> , 1998, 273, 23641-23644.	3.4	127
35	Architecture of the SWI/SNF-Nucleosome Complex. <i>Molecular and Cellular Biology</i> , 2008, 28, 6010-6021.	2.3	125
36	SWI/SNF Chromatin Remodeling Requires Changes in DNA Topology. <i>Molecular Cell</i> , 2001, 7, 97-104.	9.7	109

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37	The Histone Chaperones FACT and Spt6 Restrict H2A.Z from Intragenic Locations. <i>Molecular Cell</i> , 2015, 58, 1113-1123.	9.7	108
38	A Native Peptide Ligation Strategy for Deciphering Nucleosomal Histone Modifications. <i>Journal of Biological Chemistry</i> , 2003, 278, 15744-15748.	3.4	107
39	Chromatin remodeling: a marriage between two families?. <i>BioEssays</i> , 1998, 20, 771-780.	2.5	105
40	Functional Delineation of Three Groups of the ATP-dependent Family of Chromatin Remodeling Enzymes. <i>Journal of Biological Chemistry</i> , 2000, 275, 18864-18870.	3.4	95
41	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, 3058-3068.	2.3	94
42	TRANSCRIPTION: Unlocking the Gates to Gene Expression. <i>Science</i> , 2002, 295, 1847-1848.	12.6	84
43	Switching on Chromatin: Mechanistic Role of Histone H4-K16 Acetylation. <i>Cell Cycle</i> , 2006, 5, 1361-1365.	2.6	81
44	DNA repair choice defines a common pathway for recruitment of chromatin regulators. <i>Nature Communications</i> , 2013, 4, 2084.	12.8	81
45	A Conserved Swi2/Snf2 ATPase Motif Couples ATP Hydrolysis to Chromatin Remodeling. <i>Molecular and Cellular Biology</i> , 2005, 25, 5880-5892.	2.3	79
46	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, 10855-10860.	3.4	77
47	Swi3p controls SWI/SNF assembly and ATP-dependent H2A-H2B displacement. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 540-547.	8.2	76
48	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, 2514-2522.	2.5	73
49	Chromatin remodeling enzymes: taming the machines. <i>EMBO Reports</i> , 2002, 3, 319-322.	4.5	73
50	Recombinational Repair within Heterochromatin Requires ATP-Dependent Chromatin Remodeling. <i>Cell</i> , 2009, 138, 1109-1121.	28.9	73
51	Recruitment of chromatin remodeling machines. , 2000, 78, 179-185.		72
52	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.	2.5	71
53	Chromatin Remodeling: Nucleosomes Bulging at the Seams. <i>Current Biology</i> , 2002, 12, R245-R247.	3.9	66
54	Chromatin Remodeling Activities Act on UV-damaged Nucleosomes and Modulate DNA Damage Accessibility to Photolyase. <i>Journal of Biological Chemistry</i> , 2003, 278, 17655-17663.	3.4	66

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55	Actin-related proteins (Arps): conformational switches for chromatin-remodeling machines?. <i>BioEssays</i> , 2000, 22, 666-672.	2.5	63
56	HDAC's at Work. <i>Molecular Cell</i> , 2002, 9, 921-922.	9.7	62
57	Structural analyses of the chromatin remodelling enzymes INO80-C and SWR-C. <i>Nature Communications</i> , 2015, 6, 7108.	12.8	61
58	Nucleosomes influence multiple steps during replication initiation. <i>ELife</i> , 2017, 6, .	6.0	58
59	Heterochromatin assembly: A new twist on an old model. <i>Chromosome Research</i> , 2006, 14, 83-94.	2.2	54
60	Chromatin dynamics during repair of chromosomal DNA double-strand breaks. <i>Epigenomics</i> , 2009, 1, 371-385.	2.1	54
61	ATP-dependent chromatin remodeling: going mobile. <i>FEBS Letters</i> , 2000, 476, 68-72.	2.8	52
62	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, 2805-2817.	2.1	50
63	The Interactions of Yeast SWI/SNF and RSC with the Nucleosome before and after Chromatin Remodeling. <i>Journal of Biological Chemistry</i> , 2001, 276, 12636-12644.	3.4	49
64	Structural characterization of H3K56Q nucleosomes and nucleosomal arrays. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 480-486.	1.9	49
65	Nucleosome Dynamics as Modular Systems that Integrate DNA Damage and Repair. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012658-a012658.	5.5	46
66	Role of chromatin states in transcriptional memory. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2009, 1790, 445-455.	2.4	43
67	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.	9.7	42
68	Mot1, Ino80C, and NC2 Function Coordinately to Regulate Pervasive Transcription in Yeast and Mammals. <i>Molecular Cell</i> , 2017, 67, 594-607.e4.	9.7	42
69	SWI/SNF recruitment to a DNA double-strand break by the NuA4 and Gcn5 histone acetyltransferases. <i>DNA Repair</i> , 2015, 30, 38-45.	2.8	40
70	Distinct transcriptional roles for Histone H3-K56 acetylation during the cell cycle in Yeast. <i>Nature Communications</i> , 2019, 10, 4372.	12.8	40
71	Roles of the Histone H2A-H2B Dimers and the (H3-H4) <sub>2</sub> Tetramer in Nucleosome Remodeling by the SWI-SNF Complex. <i>Journal of Biological Chemistry</i> , 2000, 275, 11545-11552.	3.4	38
72	The Ino80 complex prevents invasion of euchromatin into silent chromatin. <i>Genes and Development</i> , 2015, 29, 350-355.	5.9	38

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73	Multivalent interactions drive nucleosome binding and efficient chromatin deacetylation by SIRT6. <i>Nature Communications</i> , 2020, 11, 5244.	12.8	36
74	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015, 13, 1610-1622.	6.4	34
75	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.	3.4	33
76	Mechanism of Long-Range Chromosome Motion Triggered by Gene Activation. <i>Developmental Cell</i> , 2020, 52, 309-320.e5.	7.0	32
77	The SIN domain of the histone octamer is essential for intramolecular folding of nucleosomal arrays. <i>Nature Structural Biology</i> , 2002, 9, 167-71.	9.7	31
78	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, 803-810.	9.7	30
79	Opening the DNA repair toolbox: Localization of DNA double strand breaks to the nuclear periphery. <i>Cell Cycle</i> , 2010, 9, 43-49.	2.6	29
80	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.	6.4	26
81	SWI/SNF senses carbon starvation with a pH-sensitive low-complexity sequence. <i>ELife</i> , 2022, 11, .	6.0	23
82	Yeast Sirtuin Family Members Maintain Transcription Homeostasis to Ensure Genome Stability. <i>Cell Reports</i> , 2019, 27, 2978-2989.e5.	6.4	22
83	Solution-state conformation and stoichiometry of yeast Sir3 heterochromatin fibres. <i>Nature Communications</i> , 2014, 5, 4751.	12.8	19
84	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.	7.1	17
85	Deposition of histone H2A.Z by the SWR-C remodeling enzyme prevents genome instability. <i>DNA Repair</i> , 2015, 25, 9-14.	2.8	15
86	SWI/SNF- and RSC-Catalyzed Nucleosome Mobilization Requires Internal DNA Loop Translocation within Nucleosomes. <i>Molecular and Cellular Biology</i> , 2011, 31, 4165-4175.	2.3	14
87	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, 17827-17832.	7.1	14
88	Releasing the brakes on a chromatin-remodeling enzyme. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 5-7.	8.2	13
89	Response to Comment on "H2A histone acetylation switch regulates H2A.Z deposition by the SWR-C remodeling enzyme". <i>Science</i> , 2016, 353, 358-358.	12.6	12
90	Transcriptional Activation: Getting a Grip on Condensed Chromatin. <i>Current Biology</i> , 2003, 13, R195-R197.	3.9	11

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91	Genome Integrity: A HAT Needs a Chaperone. <i>Current Biology</i> , 2007, 17, R324-R326.	3.9	11
92	Chicken Erythrocyte Histone Octamer Preparation. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5112.	0.3	9
93	INO80C Remodeler Maintains Genomic Stability by Preventing Promiscuous Transcription at Replication Origins. <i>Cell Reports</i> , 2020, 32, 108106.	6.4	9
94	Coupling tandem affinity purification and quantitative tyrosine iodination to determine subunit stoichiometry of protein complexes. <i>Methods</i> , 2003, 31, 104-109.	3.8	8
95	The Ins and Outs of Heterochromatic DNA Repair. <i>Developmental Cell</i> , 2011, 20, 285-287.	7.0	7
96	Chromatin remodeling: a complex affair. <i>EMBO Reports</i> , 2017, 18, 1673-1674.	4.5	7
97	Functional interaction between the RNA exosome and the sirtuin deacetylase Hst3 maintains transcriptional homeostasis. <i>Genes and Development</i> , 2022, 36, 17-22.	5.9	6
98	RNA polymerase II depletion promotes transcription of alternative mRNA species. <i>BMC Molecular Biology</i> , 2016, 17, 20.	3.0	5
99	Salt Gradient Dialysis Reconstitution of Nucleosomes. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5113.	0.3	4
100	Chromatin dynamics. <i>Cell Cycle</i> , 2013, 12, 2337-2338.	2.6	4
101	Transcriptional Memory: Mothers SET the Table for Daughters. <i>Current Biology</i> , 2010, 20, R240-R242.	3.9	3
102	Protein Complex Binding to Promoter DNA: Immobilized Template Assay. <i>Cold Spring Harbor Protocols</i> , 2010, 2010, pdb.prot5465.	0.3	1
103	Actin-related proteins (Arps): conformational switches for chromatin remodeling machines?. <i>BioEssays</i> , 2000, 22, 666-672.	2.5	1
104	Fluorescence approaches for biochemical analysis of ATP-dependent chromatin remodeling enzymes. <i>Methods in Enzymology</i> , 2022, , .	1.0	1
105	DNA repair choice defines a common pathway for recruitment of chromatin regulators. <i>FASEB Journal</i> , 2013, 27, 760.2.	0.5	0
106	SWI/SNF remodels SIR3 heterochromatin during transcription. <i>FASEB Journal</i> , 2013, 27, 770.6.	0.5	0
107	A histone acetylation switch regulates H2A.Z deposition by the SWR remodeling enzyme. <i>FASEB Journal</i> , 2013, 27, 770.4.	0.5	0