

# Craig L Peterson

## List of Publications by Year in descending order

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107  
papers

13,832  
citations

32410

55  
h-index

35168

102  
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127  
all docs

127  
docs citations

127  
times ranked

14272  
citing authors

#	ARTICLE	IF	CITATIONS
1	SWI/SNF senses carbon starvation with a pH-sensitive low-complexity sequence. <i>ELife</i> , 2022, 11, .	2.8	23
2	Fluorescence approaches for biochemical analysis of ATP-dependent chromatin remodeling enzymes. <i>Methods in Enzymology</i> , 2022, , .	0.4	1
3	Functional interaction between the RNA exosome and the sirtuin deacetylase Hst3 maintains transcriptional homeostasis. <i>Genes and Development</i> , 2022, 36, 17-22.	2.7	6
4	Mechanism of Long-Range Chromosome Motion Triggered by Gene Activation. <i>Developmental Cell</i> , 2020, 52, 309-320.e5.	3.1	32
5	Multivalent interactions drive nucleosome binding and efficient chromatin deacetylation by SIRT6. <i>Nature Communications</i> , 2020, 11, 5244.	5.8	36
6	INO80C Remodeler Maintains Genomic Stability by Preventing Promiscuous Transcription at Replication Origins. <i>Cell Reports</i> , 2020, 32, 108106.	2.9	9
7	Distinct transcriptional roles for Histone H3-K56 acetylation during the cell cycle in Yeast. <i>Nature Communications</i> , 2019, 10, 4372.	5.8	40
8	Yeast Sirtuin Family Members Maintain Transcription Homeostasis to Ensure Genome Stability. <i>Cell Reports</i> , 2019, 27, 2978-2989.e5.	2.9	22
9	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.	2.9	26
10	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.	3.3	17
11	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.	1.6	33
12	Mechanisms of action and regulation of ATP-dependent chromatin-remodelling complexes. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 407-422.	16.1	828
13	Chromatin remodeling: a complex affair. <i>EMBO Reports</i> , 2017, 18, 1673-1674.	2.0	7
14	Mot1, Ino80C, and NC2 Function Coordinately to Regulate Pervasive Transcription in Yeast and Mammals. <i>Molecular Cell</i> , 2017, 67, 594-607.e4.	4.5	42
15	Nucleosomes influence multiple steps during replication initiation. <i>ELife</i> , 2017, 6, .	2.8	58
16	RNA polymerase II depletion promotes transcription of alternative mRNA species. <i>BMC Molecular Biology</i> , 2016, 17, 20.	3.0	5
17	Response to Comment on "H3K9 acetylation switch regulates H2A.Z deposition by the SWR-C remodeling enzyme". <i>Science</i> , 2016, 353, 358-358.	6.0	12
18	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.	4.5	42

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19	Genomic Nucleosome Organization Reconstituted with Pure Proteins. <i>Cell</i> , 2016, 167, 709-721.e12.	13.5	227
20	The Ino80 complex prevents invasion of euchromatin into silent chromatin. <i>Genes and Development</i> , 2015, 29, 350-355.	2.7	38
21	SWI/SNF recruitment to a DNA double-strand break by the NuA4 and Gcn5 histone acetyltransferases. <i>DNA Repair</i> , 2015, 30, 38-45.	1.3	40
22	Structural analyses of the chromatin remodelling enzymes INO80-C and SWR-C. <i>Nature Communications</i> , 2015, 6, 7108.	5.8	61
23	The Histone Chaperones FACT and Spt6 Restrict H2A.Z from Intragenic Locations. <i>Molecular Cell</i> , 2015, 58, 1113-1123.	4.5	108
24	Chromatin Dynamics and the RNA Exosome Function in Concert to Regulate Transcriptional Homeostasis. <i>Cell Reports</i> , 2015, 13, 1610-1622.	2.9	34
25	Deposition of histone H2A.Z by the SWR-C remodeling enzyme prevents genome instability. <i>DNA Repair</i> , 2015, 25, 9-14.	1.3	15
26	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. <i>PLoS ONE</i> , 2015, 10, e0126420.	1.1	71
27	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.	3.3	14
28	Chromatin dynamics: Interplay between remodeling enzymes and histone modifications. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 728-736.	0.9	194
29	Solution-state conformation and stoichiometry of yeast Sir3 heterochromatin fibres. <i>Nature Communications</i> , 2014, 5, 4751.	5.8	19
30	A Histone Acetylation Switch Regulates H2A.Z Deposition by the SWR-C Remodeling Enzyme. <i>Science</i> , 2013, 340, 195-199.	6.0	168
31	Chromatin and the genome integrity network. <i>Nature Reviews Genetics</i> , 2013, 14, 62-75.	7.7	193
32	Releasing the brakes on a chromatin-remodeling enzyme. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 5-7.	3.6	13
33	Nucleosome dynamics regulates DNA processing. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 836-842.	3.6	130
34	DNA repair choice defines a common pathway for recruitment of chromatin regulators. <i>Nature Communications</i> , 2013, 4, 2084.	5.8	81
35	Chromatin dynamics. <i>Cell Cycle</i> , 2013, 12, 2337-2338.	1.3	4
36	Nucleosome Dynamics as Modular Systems that Integrate DNA Damage and Repair. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012658-a012658.	2.3	46

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37	DNA repair choice defines a common pathway for recruitment of chromatin regulators. <i>FASEB Journal</i> , 2013, 27, 760.2.	0.2	0
38	SWI/SNF remodels SIR3 heterochromatin during transcription. <i>FASEB Journal</i> , 2013, 27, 770.6.	0.2	0
39	A histone acetylation switch regulates H2A.Z deposition by the SWR remodeling enzyme. <i>FASEB Journal</i> , 2013, 27, 770.4.	0.2	0
40	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.	0.9	50
41	Global Regulation of H2A.Z Localization by the INO80 Chromatin-Remodeling Enzyme Is Essential for Genome Integrity. <i>Cell</i> , 2011, 144, 200-213.	13.5	345
42	The Ins and Outs of Heterochromatic DNA Repair. <i>Developmental Cell</i> , 2011, 20, 285-287.	3.1	7
43	SWI/SNF- and RSC-Catalyzed Nucleosome Mobilization Requires Internal DNA Loop Translocation within Nucleosomes. <i>Molecular and Cellular Biology</i> , 2011, 31, 4165-4175.	1.1	14
44	Transcriptional Memory: Mothers SET the Table for Daughters. <i>Current Biology</i> , 2010, 20, R240-R242.	1.8	3
45	Opening the DNA repair toolbox: Localization of DNA double strand breaks to the nuclear periphery. <i>Cell Cycle</i> , 2010, 9, 43-49.	1.3	29
46	Protein Complex Binding to Promoter DNA: Immobilized Template Assay. <i>Cold Spring Harbor Protocols</i> , 2010, 2010, pdb.prot5465.	0.2	1
47	Structural characterization of H3K56Q nucleosomes and nucleosomal arrays. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 480-486.	0.9	49
48	Chromatin dynamics during repair of chromosomal DNA double-strand breaks. <i>Epigenomics</i> , 2009, 1, 371-385.	1.0	54
49	Recombinational Repair within Heterochromatin Requires ATP-Dependent Chromatin Remodeling. <i>Cell</i> , 2009, 138, 1109-1121.	13.5	73
50	Role of chromatin states in transcriptional memory. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2009, 1790, 445-455.	1.1	43
51	Mechanisms that regulate localization of a DNA double-strand break to the nuclear periphery. <i>Genes and Development</i> , 2009, 23, 912-927.	2.7	279
52	The Ino80 chromatin-remodeling enzyme regulates replisome function and stability. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 338-345.	3.6	143
53	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.	4.5	30
54	Chicken Erythrocyte Histone Octamer Preparation. <i>Cold Spring Harbor Protocols</i> , 2008, 2008, pdb.prot5112.	0.2	9

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55	Salt Gradient Dialysis Reconstitution of Nucleosomes. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5113.	0.2	4
56	Architecture of the SWI/SNF-Nucleosome Complex. Molecular and Cellular Biology, 2008, 28, 6010-6021.	1.1	125
57	SWI/SNF is required for transcriptional memory at the yeast GAL gene cluster. Genes and Development, 2007, 21, 997-1004.	2.7	137
58	Swi3p controls SWI/SNF assembly and ATP-dependent H2A-H2B displacement. Nature Structural and Molecular Biology, 2007, 14, 540-547.	3.6	76
59	Genome Integrity: A HAT Needs a Chaperone. Current Biology, 2007, 17, R324-R326.	1.8	11
60	Histone H4-K16 Acetylation Controls Chromatin Structure and Protein Interactions. Science, 2006, 311, 844-847.	6.0	1,881
61	Interplay between Ino80 and Swr1 chromatin remodeling enzymes regulates cell cycle checkpoint adaptation in response to DNA damage. Genes and Development, 2006, 20, 2437-2449.	2.7	162
62	DNA Translocation and Loop Formation Mechanism of Chromatin Remodeling by SWI/SNF and RSC. Molecular Cell, 2006, 24, 559-568.	4.5	198
63	Heterochromatin assembly: A new twist on an old model. Chromosome Research, 2006, 14, 83-94.	1.0	54
64	Switching on Chromatin: Mechanistic Role of Histone H4-K16 Acetylation. Cell Cycle, 2006, 5, 1361-1365.	1.3	81
65	A Conserved Swi2/Snf2 ATPase Motif Couples ATP Hydrolysis to Chromatin Remodeling. Molecular and Cellular Biology, 2005, 25, 5880-5892.	1.1	79
66	ATP-dependent and ATP-independent Roles for the Rad54 Chromatin Remodeling Enzyme during Recombinational Repair of a DNA Double Strand Break. Journal of Biological Chemistry, 2005, 280, 10855-10860.	1.6	77
67	A Rik1-associated, cullin-dependent E3 ubiquitin ligase is essential for heterochromatin formation. Genes and Development, 2005, 19, 1705-1714.	2.7	156
68	̢-H2AX Dephosphorylation by Protein Phosphatase 2A Facilitates DNA Double-Strand Break Repair. Molecular Cell, 2005, 20, 801-809.	4.5	467
69	Cellular machineries for chromosomal DNA repair. Genes and Development, 2004, 18, 602-616.	2.7	253
70	The SANT domain: a unique histone-tail-binding module?. Nature Reviews Molecular Cell Biology, 2004, 5, 158-163.	16.1	338
71	Histones and histone modifications. Current Biology, 2004, 14, R546-R551.	1.8	1,064
72	ATP-Dependent Chromatin Remodeling. Current Topics in Developmental Biology, 2004, 65, 115-148.	1.0	165

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73	Transcriptional Activation: Getting a Grip on Condensed Chromatin. <i>Current Biology</i> , 2003, 13, R195-R197.	1.8	11
74	Structural analysis of the yeast SWI/SNF chromatin remodeling complex. <i>Nature Structural Biology</i> , 2003, 10, 141-145.	9.7	145
75	Coupling tandem affinity purification and quantitative tyrosine iodination to determine subunit stoichiometry of protein complexes. <i>Methods</i> , 2003, 31, 104-109.	1.9	8
76	Recruitment of the Recombinational Repair Machinery to a DNA Double-Strand Break in Yeast. <i>Molecular Cell</i> , 2003, 12, 221-232.	4.5	181
77	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.	1.6	66
78	Rad54p Is a Chromatin Remodeling Enzyme Required for Heteroduplex DNA Joint Formation with Chromatin. <i>Journal of Biological Chemistry</i> , 2003, 278, 9212-9218.	1.6	164
79	A Native Peptide Ligation Strategy for Deciphering Nucleosomal Histone Modifications. <i>Journal of Biological Chemistry</i> , 2003, 278, 15744-15748.	1.6	107
80	MOLECULAR BIOLOGY: Chromatin Higher Order Folding--Wrapping up Transcription. <i>Science</i> , 2002, 297, 1824-1827.	6.0	364
81	HDAC's at Work. <i>Molecular Cell</i> , 2002, 9, 921-922.	4.5	62
82	Essential Role for the SANT Domain in the Functioning of Multiple Chromatin Remodeling Enzymes. <i>Molecular Cell</i> , 2002, 10, 935-942.	4.5	224
83	TRANSCRIPTION: Unlocking the Gates to Gene Expression. <i>Science</i> , 2002, 295, 1847-1848.	6.0	84
84	Chromatin Remodeling: Nucleosomes Bulging at the Seams. <i>Current Biology</i> , 2002, 12, R245-R247.	1.8	66
85	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
86	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , 2002, 9, 263-267.	9.7	160
87	Chromatin remodeling enzymes: taming the machines. <i>EMBO Reports</i> , 2002, 3, 319-322.	2.0	73
88	SWI/SNF Chromatin Remodeling Requires Changes in DNA Topology. <i>Molecular Cell</i> , 2001, 7, 97-104.	4.5	109
89	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.	1.6	49
90	Chromatin remodeling enzymes: who's on first?. <i>Current Biology</i> , 2001, 11, R185-R197.	1.8	234

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91	Recruitment of chromatin remodeling machines. , 2000, 78, 179-185.		72
92	Actin-related proteins (Arps): conformational switches for chromatin-remodeling machines?. BioEssays, 2000, 22, 666-672.	1.2	63
93	Functional Delineation of Three Groups of the ATP-dependent Family of Chromatin Remodeling Enzymes. Journal of Biological Chemistry, 2000, 275, 18864-18870.	1.6	95
94	SWI-SNF-Mediated Nucleosome Remodeling: Role of Histone Octamer Mobility in the Persistence of the Remodeled State. Molecular and Cellular Biology, 2000, 20, 3058-3068.	1.1	94
95	Roles of the Histone H2A-H2B Dimers and the (H3-H4) <sub>2</sub> Tetramer in Nucleosome Remodeling by the SWI-SNF Complex. Journal of Biological Chemistry, 2000, 275, 11545-11552.	1.6	38
96	Promoter targeting and chromatin remodeling by the SWI/SNF complex. Current Opinion in Genetics and Development, 2000, 10, 187-192.	1.5	404
97	Global Role for Chromatin Remodeling Enzymes in Mitotic Gene Expression. Cell, 2000, 102, 587-598.	13.5	213
98	ATP-dependent chromatin remodeling: going mobile. FEBS Letters, 2000, 476, 68-72.	1.3	52
99	Actin-related proteins (Arps): conformational switches for chromatin-remodeling machines?. BioEssays, 2000, 22, 666-672.	1.2	1
100	The Core Histone N-Terminal Domains Are Required for Multiple Rounds of Catalytic Chromatin Remodeling by the SWI/SNF and RSC Complexes. Biochemistry, 1999, 38, 2514-2522.	1.2	73
101	The SWI/SNF Complex Creates Loop Domains in DNA and Polynucleosome Arrays and Can Disrupt DNA-Histone Contacts within These Domains. Molecular and Cellular Biology, 1999, 19, 1470-1478.	1.1	143
102	Chromatin remodeling: a marriage between two families?. BioEssays, 1998, 20, 771-780.	1.2	105
103	The Biochemical and Phenotypic Characterization of Hho1p, the Putative Linker Histone H1 of <i>Saccharomyces cerevisiae</i> . Journal of Biological Chemistry, 1998, 273, 7268-7276.	1.6	132
104	Subunits of the Yeast SWI/SNF Complex Are Members of the Actin-related Protein (ARP) Family. Journal of Biological Chemistry, 1998, 273, 23641-23644.	1.6	127
105	Multiple SWitches to turn on chromatin?. Current Opinion in Genetics and Development, 1996, 6, 171-175.	1.5	132
106	DNA-binding properties of the yeast SWI/SNF complex. Nature, 1996, 379, 844-847.	13.7	184
107	Characterization of the yeast SWI1, SWI2, and SWI3 genes, which encode a global activator of transcription. Cell, 1992, 68, 573-583.	13.5	610