

Jeffrey C Hansen

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.

72
papers

5,768
citations

41
h-index

73
g-index

73
ext. papers

6,295
ext. citations

7.4
avg, IF

5.79
L-index

#	Paper	IF	Citations
72	The solid and liquid states of chromatin. <i>Epigenetics and Chromatin</i> , 2021 , 14, 50	5.8	9
71	Condensed Chromatin Behaves like a Solid on the Mesoscale In Vitro and in Living Cells. <i>Cell</i> , 2020 , 183, 1772-1784.e13	56.2	75
70	Silencing the genome with linker histones. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 15388-15390	11.5	3
69	Fluid-like chromatin: Toward understanding the real chromatin organization present in the cell. <i>Current Opinion in Cell Biology</i> , 2020 , 64, 77-89	9	37
68	Post-translational modifications and chromatin dynamics. <i>Essays in Biochemistry</i> , 2019 , 63, 89-96	7.6	26
67	The 10-nm chromatin fiber and its relationship to interphase chromosome organization. <i>Biochemical Society Transactions</i> , 2018 , 46, 67-76	5.1	40
66	The elongation factor Spn1 is a multi-functional chromatin binding protein. <i>Nucleic Acids Research</i> , 2018 , 46, 2321-2334	20.1	8
65	Linker histone H1 and protein-protein interactions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016 , 1859, 455-61	6	44
64	Acetylation Mimics Within a Single Nucleosome Alter Local DNA Accessibility In Compacted Nucleosome Arrays. <i>Scientific Reports</i> , 2016 , 6, 34808	4.9	23
63	Chromatin folding and DNA replication inhibition mediated by a highly antitumor-active tetrazolato-bridged dinuclear platinum(II) complex. <i>Scientific Reports</i> , 2016 , 6, 24712	4.9	19
62	Nucleosomal arrays self-assemble into supramolecular globular structures lacking 30-nm fibers. <i>EMBO Journal</i> , 2016 , 35, 1115-32	13	124
61	Sedimentation Velocity Analysis of Large Oligomeric Chromatin Complexes Using Interference Detection. <i>Methods in Enzymology</i> , 2015 , 562, 349-62	1.7	3
60	Proteomic characterization of the nucleolar linker histone H1 interaction network. <i>Journal of Molecular Biology</i> , 2015 , 427, 2056-71	6.5	33
59	The role of the nucleosome acidic patch in modulating higher order chromatin structure. <i>Journal of the Royal Society Interface</i> , 2013 , 10, 20121022	4.1	155
58	Linker histone H1.0 interacts with an extensive network of proteins found in the nucleolus. <i>Nucleic Acids Research</i> , 2013 , 41, 4026-35	20.1	60
57	Coil-to-helix transitions in intrinsically disordered methyl CpG binding protein 2 and its isolated domains. <i>Protein Science</i> , 2012 , 21, 531-8	6.3	21
56	Human mitotic chromosome structure: what happened to the 30-nm fibre?. <i>EMBO Journal</i> , 2012 , 31, 1621-3	13	32

55	Nucleosome distribution and linker DNA: connecting nuclear function to dynamic chromatin structure. <i>Biochemistry and Cell Biology</i> , 2011 , 89, 24-34	3.6	66
54	The linker region of macroH2A promotes self-association of nucleosomal arrays. <i>Journal of Biological Chemistry</i> , 2011 , 286, 23852-64	5.4	38
53	Biophysical analysis and small-angle X-ray scattering-derived structures of MeCP2-nucleosome complexes. <i>Nucleic Acids Research</i> , 2011 , 39, 4122-35	20.1	46
52	DNA binding restricts the intrinsic conformational flexibility of methyl CpG binding protein 2 (MeCP2). <i>Journal of Biological Chemistry</i> , 2011 , 286, 18938-48	5.4	25
51	Replacement of histone H3 with CENP-A directs global nucleosome array condensation and loosening of nucleosome superhelical termini. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 16588-93	11.5	71
50	Multifunctionality of the linker histones: an emerging role for protein-protein interactions. <i>Cell Research</i> , 2010 , 20, 519-28	24.7	69
49	Activator-dependent p300 acetylation of chromatin in vitro: enhancement of transcription by disruption of repressive nucleosome-nucleosome interactions. <i>Journal of Biological Chemistry</i> , 2010 , 285, 31954-64	5.4	51
48	Binding of the Rett syndrome protein, MeCP2, to methylated and unmethylated DNA and chromatin. <i>IUBMB Life</i> , 2010 , 62, 732-8	4.7	73
47	Histone chaperones, histone acetylation, and the fluidity of the chromogenome. <i>Journal of Cellular Physiology</i> , 2010 , 224, 289-99	7	26
46	Determinants of histone H4 N-terminal domain function during nucleosomal array oligomerization: roles of amino acid sequence, domain length, and charge density. <i>Journal of Biological Chemistry</i> , 2009 , 284, 16716-16722	5.4	27
45	Recent advances in MeCP2 structure and function. <i>Biochemistry and Cell Biology</i> , 2009 , 87, 219-27	3.6	91
44	The effect of H3K79 dimethylation and H4K20 trimethylation on nucleosome and chromatin structure. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 1122-4	17.6	176
43	Malleable machines take shape in eukaryotic transcriptional regulation. <i>Nature Chemical Biology</i> , 2008 , 4, 728-37	11.7	161
42	The silent information regulator 3 protein, SIR3p, binds to chromatin fibers and assembles a hypercondensed chromatin architecture in the presence of salt. <i>Molecular and Cellular Biology</i> , 2008 , 28, 3563-72	4.8	33
41	A charged and contoured surface on the nucleosome regulates chromatin compaction. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 1105-7	17.6	90
40	Intrinsic disorder and autonomous domain function in the multifunctional nuclear protein, MeCP2. <i>Journal of Biological Chemistry</i> , 2007 , 282, 15057-64	5.4	97
39	MeCP2-chromatin interactions include the formation of chromatosome-like structures and are altered in mutations causing Rett syndrome. <i>Journal of Biological Chemistry</i> , 2007 , 282, 28237-45	5.4	93
38	Multiple modes of interaction between the methylated DNA binding protein MeCP2 and chromatin. <i>Molecular and Cellular Biology</i> , 2007 , 27, 864-77	4.8	137

37	The H3 tail domain participates in multiple interactions during folding and self-association of nucleosome arrays. <i>Molecular and Cellular Biology</i> , 2007 , 27, 2084-91	4.8	93
36	Short and long range Inter-nucleosome interactions of the core histone tail domains. <i>FASEB Journal</i> , 2007 , 21, A38	0.9	
35	Developmental biology: holding pattern for histones. <i>Current Biology</i> , 2006 , 16, R918-20	6.3	3
34	Intrinsic protein disorder, amino acid composition, and histone terminal domains. <i>Journal of Biological Chemistry</i> , 2006 , 281, 1853-6	5.4	189
33	Linking genome structure and function through specific histone acetylation. <i>ACS Chemical Biology</i> , 2006 , 1, 69-72	4.9	12
32	In vitro chromatin self-association and its relevance to genome architecture. <i>Biochemistry and Cell Biology</i> , 2006 , 84, 411-7	3.6	14
31	Chromatin architectural proteins. <i>Chromosome Research</i> , 2006 , 14, 39-51	4.4	73
30	Characterization of the chromatin binding domains of MeCP2. <i>FASEB Journal</i> , 2006 , 20, LB48	0.9	
29	The core histone N-terminal tail domains function independently and additively during salt-dependent oligomerization of nucleosomal arrays. <i>Journal of Biological Chemistry</i> , 2005 , 280, 33701-8	5.4	110
28	Salt-dependent intra- and internucleosomal interactions of the H3 tail domain in a model oligonucleosomal array. <i>Journal of Biological Chemistry</i> , 2005 , 280, 33552-7	5.4	79
27	Identification of specific functional subdomains within the linker histone H10 C-terminal domain. <i>Journal of Biological Chemistry</i> , 2004 , 279, 8701-7	5.4	107
26	Dissociation of human copper-zinc superoxide dismutase dimers using chaotrope and reductant. Insights into the molecular basis for dimer stability. <i>Journal of Biological Chemistry</i> , 2004 , 279, 54558-66	5.4	136
25	Chromatin compaction by human MeCP2. Assembly of novel secondary chromatin structures in the absence of DNA methylation. <i>Journal of Biological Chemistry</i> , 2003 , 278, 32181-8	5.4	229
24	Revisiting the structure and functions of the linker histone C-terminal tail domain. <i>Biochemistry and Cell Biology</i> , 2003 , 81, 173-6	3.6	23
23	Formation of higher-order secondary and tertiary chromatin structures by genomic mouse mammary tumor virus promoters. <i>Genes and Development</i> , 2003 , 17, 1617-29	12.6	28
22	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
21	The essential histone variant H2A.Z regulates the equilibrium between different chromatin conformational states. <i>Nature Structural Biology</i> , 2002 , 9, 172-6		117
20	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , 2002 , 9, 263-7		148

19	New insights into unwrapping DNA from the nucleosome from a single-molecule optical tweezers method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 1752-4	11.5	12
18	Conformational dynamics of the chromatin fiber in solution: determinants, mechanisms, and functions. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2002 , 31, 361-92		412
17	Nucleosomes and the chromatin fiber. <i>Current Opinion in Genetics and Development</i> , 2001 , 11, 124-9	4.9	108
16	Sedimentation velocity analysis of macromolecular assemblies. <i>Methods in Enzymology</i> , 2000 , 321, 66-80	1.7	23
15	Analytical sedimentation of the IIAChb and IIBChb proteins of the Escherichia coli N,N'-diacetylchitobiose phosphotransferase system. Demonstration of a model phosphotransfer transition state complex. <i>Journal of Biological Chemistry</i> , 2000 , 275, 33110-5	5.4	11
14	The core histone N termini function independently of linker histones during chromatin condensation. <i>Journal of Biological Chemistry</i> , 2000 , 275, 37285-90	5.4	87
13	The yeast histone acetyltransferase A2 complex, but not free Gcn5p, binds stably to nucleosomal arrays. <i>Journal of Biological Chemistry</i> , 2000 , 275, 24928-34	5.4	38
12	Assembly of defined nucleosomal and chromatin arrays from pure components. <i>Methods in Enzymology</i> , 1999 , 304, 19-35	1.7	73
11	Linker histones stabilize the intrinsic salt-dependent folding of nucleosomal arrays: mechanistic ramifications for higher-order chromatin folding. <i>Biochemistry</i> , 1998 , 37, 14776-87	3.2	205
10	Gcn5p, a transcription-related histone acetyltransferase, acetylates nucleosomes and folded nucleosomal arrays in the absence of other protein subunits. <i>Journal of Biological Chemistry</i> , 1998 , 273, 32388-92	5.4	43
9	Disruption of higher-order folding by core histone acetylation dramatically enhances transcription of nucleosomal arrays by RNA polymerase III. <i>Molecular and Cellular Biology</i> , 1998 , 18, 4629-38	4.8	479
8	Hybrid trypsinized nucleosomal arrays: identification of multiple functional roles of the H2A/H2B and H3/H4 N-termini in chromatin fiber compaction. <i>Biochemistry</i> , 1997 , 36, 11381-8	3.2	125
7	Reversible oligonucleosome self-association: dependence on divalent cations and core histone tail domains. <i>Biochemistry</i> , 1996 , 35, 4009-15	3.2	202
6	Core histone tail domains mediate oligonucleosome folding and nucleosomal DNA organization through distinct molecular mechanisms. <i>Journal of Biological Chemistry</i> , 1995 , 270, 25359-62	5.4	147
5	Analysis of structural changes in steroid receptor proteins by partitioning. <i>Methods in Enzymology</i> , 1994 , 228, 276-86	1.7	1
4	Chromatin dynamics and the modulation of genetic activity. <i>Trends in Biochemical Sciences</i> , 1992 , 17, 187-91	10.3	62
3	Large-scale purification of plasmid insert DNA sequences using low-percentage agarose exclusion chromatography. <i>Analytical Biochemistry</i> , 1989 , 179, 167-70	3.1	13
2	Homogeneous reconstituted oligonucleosomes, evidence for salt-dependent folding in the absence of histone H1. <i>Biochemistry</i> , 1989 , 28, 9129-36	3.2	216

1 Activation of progesterone receptor by ATP. *FEBS Journal*, **1981**, 118, 547-55

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