Jeffrey C Hansen

List of Publications by Year
in descending order

72 papers	6,796 citations	57752 44 h-index	88628 70 g-index
73 all docs	73 docs citations	73 times ranked	5231 citing authors

#	Article	IF	Citations
1	Disruption of Higher-Order Folding by Core Histone Acetylation Dramatically Enhances Transcription of Nucleosomal Arrays by RNA Polymerase III. Molecular and Cellular Biology, 1998, 18, 4629-4638.	2.3	528
2	Conformational Dynamics of the Chromatin Fiber in Solution: Determinants, Mechanisms, and Functions. Annual Review of Biophysics and Biomolecular Structure, 2002, 31, 361-392.	18.3	458
3	Chromatin Compaction by Human MeCP2. Journal of Biological Chemistry, 2003, 278, 32181-32188.	3.4	259
4	Homogeneous reconstituted oligonucleosomes, evidence for salt-dependent folding in the absence of histone H1. Biochemistry, 1989, 28, 9129-9136.	2.5	228
5	Reversible Oligonucleosome Self-Association:Â Dependence on Divalent Cations and Core Histone Tail Domainsâ€. Biochemistry, 1996, 35, 4009-4015.	2.5	224
6	Linker Histones Stabilize the Intrinsic Salt-Dependent Folding of Nucleosomal Arrays:Â Mechanistic Ramifications for Higher-Order Chromatin Foldingâ€. Biochemistry, 1998, 37, 14776-14787.	2.5	224
7	Intrinsic Protein Disorder, Amino Acid Composition, and Histone Terminal Domains. Journal of Biological Chemistry, 2006, 281, 1853-1856.	3.4	217
8	The effect of H3K79 dimethylation and H4K20 trimethylation on nucleosome and chromatin structure. Nature Structural and Molecular Biology, 2008, 15, 1122-1124.	8.2	210
9	The role of the nucleosome acidic patch in modulating higher order chromatin structure. Journal of the Royal Society Interface, 2013, 10, 20121022.	3.4	200
10	Malleable machines take shape in eukaryotic transcriptional regulation. Nature Chemical Biology, 2008, 4, 728-737.	8.0	192
11	Condensed Chromatin Behaves like a Solid on the Mesoscale InÂVitro and in Living Cells. Cell, 2020, 183, 1772-1784.e13.	28.9	186
12	Nucleosomal arrays selfâ€assemble into supramolecular globular structures lacking 30â€nm fibers. EMBO Journal, 2016, 35, 1115-1132.	7.8	164
13	Core Histone Tail Domains Mediate Oligonucleosome Folding and Nucleosomal DNA Organization through Distinct Molecular Mechanisms. Journal of Biological Chemistry, 1995, 270, 25359-25362.	3.4	161
14	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. Nature Structural Biology, 2002, 9, 263-267.	9.7	160
15	Multiple Modes of Interaction between the Methylated DNA Binding Protein MeCP2 and Chromatin. Molecular and Cellular Biology, 2007, 27, 864-877.	2.3	159
16	Dissociation of Human Copper-Zinc Superoxide Dismutase Dimers Using Chaotrope and Reductant. Journal of Biological Chemistry, 2004, 279, 54558-54566.	3.4	149
17	The essential histone variant H2A.Z regulates the equilibrium between different chromatin conformational states. Nature Structural Biology, 2002, 9, 172-6.	9.7	137
18	Hybrid Trypsinized Nucleosomal Arrays:Â Identification of Multiple Functional Roles of the H2A/H2B and H3/H4 N-Termini in Chromatin Fiber Compactionâ€. Biochemistry, 1997, 36, 11381-11388.	2.5	136

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19	The Core Histone N-terminal Tail Domains Function Independently and Additively during Salt-dependent Oligomerization of Nucleosomal Arrays. Journal of Biological Chemistry, 2005, 280, 33701-33706.	3.4	123
20	Identification of Specific Functional Subdomains within the Linker Histone H10 C-terminal Domain. Journal of Biological Chemistry, 2004, 279, 8701-8707.	3.4	121
21	Nucleosomes and the chromatin fiber. Current Opinion in Genetics and Development, 2001, 11, 124-129.	3.3	120
22	Intrinsic Disorder and Autonomous Domain Function in the Multifunctional Nuclear Protein, MeCP2. Journal of Biological Chemistry, 2007, 282, 15057-15064.	3.4	115
23	Recent advances in MeCP2 structure and functionThis paper is one of a selection of papers published in this Special Issue, entitled 29th Annual International Asilomar Chromatin and Chromosomes Conference, and has undergone the Journalâ€™s usual peer review process.. Biochemistry and Cell Biology, 2009, 87, 219-227.	2.0	113
24	MeCP2-Chromatin Interactions Include the Formation of Chromatosome-like Structures and Are Altered in Mutations Causing Rett Syndrome. Journal of Biological Chemistry, 2007, 282, 28237-28245.	3.4	102
25	The Core Histone N Termini Function Independently of Linker Histones during Chromatin Condensation. Journal of Biological Chemistry, 2000, 275, 37285-37290.	3.4	101
26	The H3 Tail Domain Participates in Multiple Interactions during Folding and Self-Association of Nucleosome Arrays. Molecular and Cellular Biology, 2007, 27, 2084-2091.	2.3	100
27	A charged and contoured surface on the nucleosome regulates chromatin compaction. Nature Structural and Molecular Biology, 2007, 14, 1105-1107.	8.2	99
28	Nucleosome distribution and linker DNA: connecting nuclear function to dynamic chromatin structureThis paper is one of a selection of papers published in a Special Issue entitled 31st Annual International Asilomar Chromatin and Chromosomes Conference, and has undergone the Journalâ€™s usual peer review process.. Biochemistry and Cell Biology, 2011, 89, 24-34.	2.0	96
29	Salt-dependent Intra- and Internucleosomal Interactions of the H3 Tail Domain in a Model Oligonucleosomal Array. Journal of Biological Chemistry, 2005, 280, 33552-33557.	3.4	88
30	Binding of the Rett syndrome protein, MeCP2, to methylated and unmethylated DNA and chromatin. IUBMB Life, 2010, 62, 732-738.	3.4	84
31	Replacement of histone H3 with CENP-A directs global nucleosome array condensation and loosening of nucleosome superhelical termini. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16588-16593.	7.1	84
32	Assembly of defined nucleosomal and chromatin arrays from pure components. Methods in Enzymology, 1999, 304, 19-35.	1.0	81
33	Chromatin architectural proteins. Chromosome Research, 2006, 14, 39-51.	2.2	79
34	Multifunctionality of the linker histones: an emerging role for protein-protein interactions. Cell Research, 2010, 20, 519-528.	12.0	76
35	Fluid-like chromatin: Toward understanding the real chromatin organization present in the cell. Current Opinion in Cell Biology, 2020, 64, 77-89.	5.4	76
36	Linker histone H1.0 interacts with an extensive network of proteins found in the nucleolus. Nucleic Acids Research, 2013, 41, 4026-4035.	14.5	73

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37	Chromatin dynamics and the modulation of genetic activity. Trends in Biochemical Sciences, 1992, 17, 187-191.	7.5	71
38	Post-translational modifications and chromatin dynamics. Essays in Biochemistry, 2019, 63, 89-96.	4.7	64
39	Linker histone H1 and proteinâ€“protein interactions. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 455-461.	1.9	58
40	Activator-dependent p300 Acetylation of Chromatin in Vitro. Journal of Biological Chemistry, 2010, 285, 31954-31964.	3.4	55
41	The 10-nm chromatin fiber and its relationship to interphase chromosome organization. Biochemical Society Transactions, 2018, 46, 67-76.	3.4	55
42	The solid and liquid states of chromatin. Epigenetics and Chromatin, 2021, 14, 50.	3.9	55
43	Biophysical analysis and small-angle X-ray scattering-derived structures of MeCP2â€“nucleosome complexes. Nucleic Acids Research, 2011, 39, 4122-4135.	14.5	49
44	Activation of Progesterone Receptor by ATP. FEBS Journal, 1981, 118, 547-555.	0.2	47
45	The Linker Region of MacroH2A Promotes Self-association of Nucleosomal Arrays. Journal of Biological Chemistry, 2011, 286, 23852-23864.	3.4	47
46	Gcn5p, a Transcription-related Histone Acetyltransferase, Acetylates Nucleosomes and Folded Nucleosomal Arrays in the Absence of Other Protein Subunits. Journal of Biological Chemistry, 1998, 273, 32388-32392.	3.4	45
47	The Yeast Histone Acetyltransferase A2 Complex, but Not Free Gcn5p, Binds Stably to Nucleosomal Arrays. Journal of Biological Chemistry, 2000, 275, 24928-24934.	3.4	42
48	Proteomic Characterization of the Nucleolar Linker Histone H1 Interaction Network. Journal of Molecular Biology, 2015, 427, 2056-2071.	4.2	42
49	Human mitotic chromosome structure: what happened to the 30-nm fibre?. EMBO Journal, 2012, 31, 1621-1623.	7.8	36
50	The Silent Information Regulator 3 Protein, SIR3p, Binds to Chromatin Fibers and Assembles a Hypercondensed Chromatin Architecture in the Presence of Salt. Molecular and Cellular Biology, 2008, 28, 3563-3572.	2.3	34
51	Determinants of Histone H4 N-terminal Domain Function during Nucleosomal Array Oligomerization. Journal of Biological Chemistry, 2009, 284, 16716-16722.	3.4	32
52	The SIN domain of the histone octamer is essential for intramolecular folding of nucleosomal arrays. Nature Structural Biology, 2002, 9, 167-71.	9.7	31
53	Formation of higher-order secondary and tertiary chromatin structures by genomic mouse mammary tumor virus promoters. Genes and Development, 2003, 17, 1617-1629.	5.9	31
54	DNA Binding Restricts the Intrinsic Conformational Flexibility of Methyl CpG Binding Protein 2 (MeCP2). Journal of Biological Chemistry, 2011, 286, 18938-18948.	3.4	29

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55	Histone chaperones, histone acetylation, and the fluidity of the chromogenome. Journal of Cellular Physiology, 2010, 224, 289-299.	4.1	28
56	Acetylation Mimics Within a Single Nucleosome Alter Local DNA Accessibility In Compacted Nucleosome Arrays. Scientific Reports, 2016, 6, 34808.	3.3	26
57	Coilâ€toâ€helix transitions in intrinsically disordered methyl CpG binding protein 2 and its isolated domains. Protein Science, 2012, 21, 531-538.	7.6	25
58	Sedimentation velocity analysis of macromolecular assemblies. Methods in Enzymology, 2000, 321, 66-80.	1.0	24
59	Revisiting the structure and functions of the linker histone C-terminal tail domain. Biochemistry and Cell Biology, 2003, 81, 173-176.	2.0	24
60	Chromatin folding and DNA replication inhibition mediated by a highly antitumor-active tetrazolato-bridged dinuclear platinum(II) complex. Scientific Reports, 2016, 6, 24712.	3.3	20
61	The elongation factor Spn1 is a multi-functional chromatin binding protein. Nucleic Acids Research, 2018, 46, 2321-2334.	14.5	19
62	New insights into unwrapping DNA from the nucleosome from a single-molecule optical tweezers method. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1752-1754.	7.1	16
63	Large-scale purification of plasmid insert DNA sequences using low-percentage agarose exclusion chromatography. Analytical Biochemistry, 1989, 179, 167-170.	2.4	15
64	In vitro chromatin self-association and its relevance to genome architectureThis paper is one of a selection of papers published in this Special Issue, entitled 27th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2006, 84, 411-417.	2.0	15
65	Analytical Sedimentation of the IIAChb and IIBChb Proteins of the Escherichia coli N,Nâ€²-Diacetylchitobiose Phosphotransferase System. Journal of Biological Chemistry, 2000, 275, 33110-33115.	3.4	13
66	Linking Genome Structure and Function through Specific Histone Acetylation. ACS Chemical Biology, 2006, 1, 69-72.	3.4	13
67	Sedimentation Velocity Analysis of Large Oligomeric Chromatin Complexes Using Interference Detection. Methods in Enzymology, 2015, 562, 349-362.	1.0	4
68	Silencing the genome with linker histones. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15388-15390.	7.1	4
69	Developmental Biology: Holding Pattern for Histones. Current Biology, 2006, 16, R918-R920.	3.9	3
70	[25] Analysis of structural changes in steroid receptor proteins by partitioning. Methods in Enzymology, 1994, 228, 276-286.	1.0	1
71	Characterization of the chromatin binding domains of MeCP2. FASEB Journal, 2006, 20, LB48.	0.5	0
72	Short and long range Interâ€nucleosome interactions of the core histone tail domains. FASEB Journal, 2007, 21, A38.	0.5	0