

Jeffrey C Hansen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3999222/publications.pdf>

Version: 2024-02-01

72
papers

6,796
citations

57758

44
h-index

88630

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

#	ARTICLE	IF	CITATIONS
19	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, 33701-33706.	3.4	123
20	Identification of Specific Functional Subdomains within the Linker Histone H10 C-terminal Domain. <i>Journal of Biological Chemistry</i> , 2004, 279, 8701-8707.	3.4	121
21	Nucleosomes and the chromatin fiber. <i>Current Opinion in Genetics and Development</i> , 2001, 11, 124-129.	3.3	120
22	Intrinsic Disorder and Autonomous Domain Function in the Multifunctional Nuclear Protein, MeCP2. <i>Journal of Biological Chemistry</i> , 2007, 282, 15057-15064.	3.4	115
23	Recent advances in MeCP2 structure and function This 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 Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 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. <i>Journal of Biological Chemistry</i> , 2007, 282, 28237-28245.	3.4	102
25	The Core Histone N Termini Function Independently of Linker Histones during Chromatin Condensation. <i>Journal of Biological Chemistry</i> , 2000, 275, 37285-37290.	3.4	101
26	The H3 Tail Domain Participates in Multiple Interactions during Folding and Self-Association of Nucleosome Arrays. <i>Molecular and Cellular Biology</i> , 2007, 27, 2084-2091.	2.3	100
27	A charged and contoured surface on the nucleosome regulates chromatin compaction. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1105-1107.	8.2	99
28	Nucleosome distribution and linker DNA: connecting nuclear function to dynamic chromatin structure This 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 Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2011, 89, 24-34.	2.0	96
29	Salt-dependent Intra- and Internucleosomal Interactions of the H3 Tail Domain in a Model Oligonucleosomal Array. <i>Journal of Biological Chemistry</i> , 2005, 280, 33552-33557.	3.4	88
30	Binding of the Rett syndrome protein, MeCP2, to methylated and unmethylated DNA and chromatin. <i>IUBMB Life</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16588-16593.	7.1	84
32	Assembly of defined nucleosomal and chromatin arrays from pure components. <i>Methods in Enzymology</i> , 1999, 304, 19-35.	1.0	81
33	Chromatin architectural proteins. <i>Chromosome Research</i> , 2006, 14, 39-51.	2.2	79
34	Multifunctionality of the linker histones: an emerging role for protein-protein interactions. <i>Cell Research</i> , 2010, 20, 519-528.	12.0	76
35	Fluid-like chromatin: Toward understanding the real chromatin organization present in the cell. <i>Current Opinion in Cell Biology</i> , 2020, 64, 77-89.	5.4	76
36	Linker histone H1.0 interacts with an extensive network of proteins found in the nucleolus. <i>Nucleic Acids Research</i> , 2013, 41, 4026-4035.	14.5	73

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

#	ARTICLE	IF	CITATIONS
55	Histone chaperones, histone acetylation, and the fluidity of the chromogenome. <i>Journal of Cellular Physiology</i> , 2010, 224, 289-299.	4.1	28
56	Acetylation Mimics Within a Single Nucleosome Alter Local DNA Accessibility In Compacted Nucleosome Arrays. <i>Scientific Reports</i> , 2016, 6, 34808.	3.3	26
57	Coilâ€œhelix transitions in intrinsically disordered methyl CpG binding protein 2 and its isolated domains. <i>Protein Science</i> , 2012, 21, 531-538.	7.6	25
58	Sedimentation velocity analysis of macromolecular assemblies. <i>Methods in Enzymology</i> , 2000, 321, 66-80.	1.0	24
59	Revisiting the structure and functions of the linker histone C-terminal tail domain. <i>Biochemistry and Cell Biology</i> , 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. <i>Scientific Reports</i> , 2016, 6, 24712.	3.3	20
61	The elongation factor Spn1 is a multi-functional chromatin binding protein. <i>Nucleic Acids Research</i> , 2018, 46, 2321-2334.	14.5	19
62	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, 1752-1754.	7.1	16
63	Large-scale purification of plasmid insert DNA sequences using low-percentage agarose exclusion chromatography. <i>Analytical Biochemistry</i> , 1989, 179, 167-170.	2.4	15
64	In vitro chromatin self-association and its relevance to genome architecture This 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.. <i>Biochemistry and Cell Biology</i> , 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. <i>Journal of Biological Chemistry</i> , 2000, 275, 33110-33115.	3.4	13
66	Linking Genome Structure and Function through Specific Histone Acetylation. <i>ACS Chemical Biology</i> , 2006, 1, 69-72.	3.4	13
67	Sedimentation Velocity Analysis of Large Oligomeric Chromatin Complexes Using Interference Detection. <i>Methods in Enzymology</i> , 2015, 562, 349-362.	1.0	4
68	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.	7.1	4
69	Developmental Biology: Holding Pattern for Histones. <i>Current Biology</i> , 2006, 16, R918-R920.	3.9	3
70	[25] Analysis of structural changes in steroid receptor proteins by partitioning. <i>Methods in Enzymology</i> , 1994, 228, 276-286.	1.0	1
71	Characterization of the chromatin binding domains of MeCP2. <i>FASEB Journal</i> , 2006, 20, LB48.	0.5	0
72	Short and long range Interâ€œnucleosome interactions of the core histone tail domains. <i>FASEB Journal</i> , 2007, 21, A38.	0.5	0