Michael J Hendzel

List of Publications by Year
in descending order

141 papers	14,557 citations	15504 65 h-index	19749 117 g-index
148 all docs	148 docs citations	148 times ranked	18245 citing authors

#	Article	IF	Citations
1	Mitosis-specific phosphorylation of histone H3 initiates primarily within pericentromeric heterochromatin during G2 and spreads in an ordered fashion coincident with mitotic chromosome condensation. Chromosoma, 1997, 106, 348-360.	2.2	1,679
2	PARP inhibition: PARP1 and beyond. Nature Reviews Cancer, 2010, 10, 293-301.	28.4	1,166
3	Enzymatic Activity Associated with Class II HDACs Is Dependent on a Multiprotein Complex Containing HDAC3 and SMRT/N-CoR. Molecular Cell, 2002, 9, 45-57.	9.7	663
4	PARP1-dependent Kinetics of Recruitment of MRE11 and NBS1 Proteins to Multiple DNA Damage Sites. Journal of Biological Chemistry, 2008, 283, 1197-1208.	3.4	469
5	Rapid exchange of histone H1.1 on chromatin in living human cells. Nature, 2000, 408, 873-876.	27.8	397
6	Proteome-wide identification of poly(ADP-ribose) binding proteins and poly(ADP-ribose)-associated protein complexes. Nucleic Acids Research, 2008, 36, 6959-6976.	14.5	359
7	RNF8- and RNF168-dependent degradation of KDM4A/JMJD2A triggers 53BP1 recruitment to DNA damage sites. EMBO Journal, 2012, 31, 1865-1878.	7.8	302
8	Increased Ser-10 Phosphorylation of Histone H3 in Mitogen-stimulated and Oncogene-transformed Mouse Fibroblasts. Journal of Biological Chemistry, 1999, 274, 24914-24920.	3.4	248
9	Promyelocytic Leukemia (Pml) Nuclear Bodies Are Protein Structures That Do Not Accumulate RNA. Journal of Cell Biology, 2000, 148, 283-292.	5.2	245
10	BMI1-mediated histone ubiquitylation promotes DNA double-strand break repair. Journal of Cell Biology, 2010, 191, 45-60.	5.2	240
11	Nucleoplasmic Î²-actin exists in a dynamic equilibrium between low-mobility polymeric species and rapidly diffusing populations. Journal of Cell Biology, 2006, 172, 541-552.	5.2	238
12	Ataxia Telangiectasia Mutated (ATM) Signaling Network Is Modulated by a Novel Poly(ADP-ribose)-dependent Pathway in the Early Response to DNA-damaging Agents. Journal of Biological Chemistry, 2007, 282, 16441-16453.	3.4	225
13	A New Family of Human Histone Deacetylases Related toSaccharomyces cerevisiae HDA1p. Journal of Biological Chemistry, 1999, 274, 11713-11720.	3.4	222
14	ATM-dependent DNA Damage-independent Mitotic Phosphorylation of H2AX in Normally Growing Mammalian Cells. Molecular Biology of the Cell, 2005, 16, 5013-5025.	2.1	220
15	The C-terminal Domain Is the Primary Determinant of Histone H1 Binding to Chromatin in Vivo. Journal of Biological Chemistry, 2004, 279, 20028-20034.	3.4	198
16	Human HDAC7 Histone Deacetylase Activity Is Associated with HDAC3in Vivo. Journal of Biological Chemistry, 2001, 276, 35826-35835.	3.4	192
17	Regulation of Global Acetylation in Mitosis through Loss of Histone Acetyltransferases and Deacetylases from Chromatin. Journal of Biological Chemistry, 2001, 276, 38307-38319.	3.4	189
18	Condensed Chromatin Behaves like a Solid on the Mesoscale InÂVitro and in Living Cells. Cell, 2020, 183, 1772-1784.e13.	28.9	186

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19	H1 Family Histones in the Nucleus. Journal of Biological Chemistry, 2005, 280, 27809-27814.	3.4	178
20	Using FRAP and mathematical modeling to determine the in vivo kinetics of nuclear proteins. Methods, 2003, 29, 14-28.	3.8	173
21	Interplay between human DNA repair proteins at a unique double-strand break in vivo. EMBO Journal, 2006, 25, 222-231.	7.8	172
22	Reduced Mobility of the Alternate Splicing Factor (Asf) through the Nucleoplasm and Steady State Speckle Compartments. Journal of Cell Biology, 2000, 150, 41-52.	5.2	168
23	Germline Mutations in BAP1 Impair Its Function in DNA Double-Strand Break Repair. Cancer Research, 2014, 74, 4282-4294.	0.9	168
24	RHAMM Is a Centrosomal Protein That Interacts with Dynein and Maintains Spindle Pole Stability. Molecular Biology of the Cell, 2003, 14, 2262-2276.	2.1	167
25	Overexpression of transcripts originating from the MMSET locus characterizes all t(4;14)(p16;q32)-positive multiple myeloma patients. Blood, 2005, 105, 4060-4069.	1.4	159
26	Sequential fractionation and isolation of subcellular proteins from tissue or cultured cells. MethodsX, 2015, 2, 440-445.	1.6	145
27	The Transcription Coactivator Cbp Is a Dynamic Component of the Promyelocytic Leukemia Nuclear Body. Journal of Cell Biology, 2001, 152, 1099-1106.	5.2	141
28	Catalytic Function of the PR-Set7 Histone H4 Lysine 20 Monomethyltransferase Is Essential for Mitotic Entry and Genomic Stability. Journal of Biological Chemistry, 2008, 283, 19478-19488.	3.4	137
29	PARP activation regulates the RNA-binding protein NONO in the DNA damage response to DNA double-strand breaks. Nucleic Acids Research, 2012, 40, 10287-10301.	14.5	136
30	Topoisomerase II alpha is associated with the mammalian centromere in a cell cycle- and species-specific manner and is required for proper centromere/kinetochore structure.. Journal of Cell Biology, 1996, 134, 1097-1107.	5.2	133
31	Investigation of PARP-1, PARP-2, and PARG interactomes by affinity-purification mass spectrometry. Proteome Science, 2010, 8, 22.	1.7	133
32	Kdm4b Histone Demethylase Is a DNA Damage Response Protein and Confers a Survival Advantage following Î³-Irradiation. Journal of Biological Chemistry, 2013, 288, 21376-21388.	3.4	130
33	Depletion of nuclear actin is a key mediator of quiescence in epithelial cells. Journal of Cell Science, 2011, 124, 123-132.	2.0	128
34	Mechanotransduction from the ECM to the genome: Are the pieces now in place?. Journal of Cellular Biochemistry, 2008, 104, 1964-1987.	2.6	123
35	DEAD Box 1 Facilitates Removal of RNA and Homologous Recombination at DNA Double-Strand Breaks. Molecular and Cellular Biology, 2016, 36, 2794-2810.	2.3	122
36	Poly(ADP-ribose) polymerase-1 antagonizes DNA resection at double-strand breaks. Nature Communications, 2019, 10, 2954.	12.8	122

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37	The expanding role of poly(ADP-ribose) metabolism: current challenges and new perspectives. Current Opinion in Cell Biology, 2006, 18, 145-151.	5.4	120
38	Actin dynamics and functions in the interphase nucleus: moving toward an understanding of nuclear polymeric actinThis 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, 283-306.	2.0	120
39	Chromatin Condensation Is Not Associated with Apoptosis. Journal of Biological Chemistry, 1998, 273, 24470-24478.	3.4	118
40	CBX4-mediated SUMO modification regulates BMI1 recruitment at sites of DNA damage. Nucleic Acids Research, 2012, 40, 5497-5510.	14.5	117
41	The RNF138 E3 ligase displaces Ku to promote DNA end resection and regulate DNA repair pathway choice. Nature Cell Biology, 2015, 17, 1446-1457.	10.3	113
42	Emerging roles of eraser enzymes in the dynamic control of protein ADP-ribosylation. Nature Communications, 2019, 10, 1182.	12.8	113
43	Polycomb repressive complex 2 contributes to DNA double-strand break repair. Cell Cycle, 2013, 12, 2675-2683.	2.6	112
44	Direct visualization of the elt-2 gut-specific GATA factor binding to a target promoter inside the living Caenorhabditis elegans embryo. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 11883-11888.	7.1	105
45	CBP, a transcriptional coactivator and acetyltransferase. Biochemistry and Cell Biology, 2001, 79, 253-266.	2.0	103
46	PARP-3 associates with polycomb group bodies and with components of the DNA damage repair machinery. Journal of Cellular Biochemistry, 2007, 100, 385-401.	2.6	100
47	The Î³â€H2A.X: Is it just a surrogate marker of doubleâ€strand breaks or much more?. Environmental and Molecular Mutagenesis, 2008, 49, 73-82.	2.2	94
48	Targeting poly(ADP-ribosyl)ation: a promising approach in cancer therapy. Trends in Molecular Medicine, 2005, 11, 456-463.	6.7	92
49	Organization of Highly Acetylated Chromatin around Sites of Heterogeneous Nuclear RNA Accumulation. Molecular Biology of the Cell, 1998, 9, 2491-2507.	2.1	90
50	Characterization of the histone H2A.Z-1 and H2A.Z-2 isoforms in vertebrates. BMC Biology, 2009, 7, 86.	3.8	89
51	Poly(ADP-ribosyl)ation-dependent Transient Chromatin Decondensation and Histone Displacement following Laser Microirradiation. Journal of Biological Chemistry, 2016, 291, 1789-1802.	3.4	80
52	Distinct dynamics and distribution of histone methyl-lysine derivatives in mouse development. Developmental Biology, 2004, 276, 337-351.	2.0	79
53	A Small Molecule Inhibitor of Polycomb Repressive Complex 1 Inhibits Ubiquitin Signaling at DNA Double-strand Breaks. Journal of Biological Chemistry, 2013, 288, 26944-26954.	3.4	76
54	Multiple functions of dynamic histone acetylation. Journal of Cellular Biochemistry, 1994, 55, 98-105.	2.6	75

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55	A requirement for polymerized actin in DNA double-strand break repair. Nucleus, 2012, 3, 384-395.	2.2	75
56	The relationship between histone H3 phosphorylation and acetylation throughout the mammalian cell cycleThis 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, 640-657.	2.0	73
57	Association of Human DEAD Box Protein DDX1 with a Cleavage Stimulation Factor Involved in 3â€²-End Processing of Pre-mRNA. Molecular Biology of the Cell, 2001, 12, 3046-3059.	2.1	72
58	Dynamic Changes in Histone H3 Lysine 9 Methylations. Journal of Biological Chemistry, 2006, 281, 8888-8897.	3.4	72
59	Polycomb group proteins in the DNA damage response: A link between radiation resistance and â€œstemnessâ€. Cell Cycle, 2011, 10, 883-894.	2.6	72
60	Polycomb group-mediated histone H2A monoubiquitination in epigenome regulation and nuclear processes. Nature Communications, 2020, 11, 5947.	12.8	72
61	H2A.Bbd: an X-chromosome-encoded histone involved in mammalian spermiogenesis. Nucleic Acids Research, 2010, 38, 1780-1789.	14.5	71
62	Quantitative Analysis of CBP- and P300-Induced Histone Acetylations In Vivo Using Native Chromatin. Molecular and Cellular Biology, 2003, 23, 7611-7627.	2.3	70
63	Methylation of MRE11 Regulates its Nuclear Compartmentalization. Cell Cycle, 2005, 4, 981-989.	2.6	70
64	Polycomb group protein gene silencing, non-coding RNA, stem cells, and cancerThis paper is one of a selection of papers published in this Special Issue, entitled The 30th Annual International Asilomar Chromatin and Chromosomes Conference, and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2009, 87, 711-746.	2.0	70
65	The oncogenic potential of Jumonji D2 (JMJD2/KDM4) histone demethylase overexpression. Biochemistry and Cell Biology, 2013, 91, 369-377.	2.0	68
66	MUC1 Initiates Src-CrkL-Rac1/Cdc42â€“Mediated Actin Cytoskeletal Protrusive Motility after Ligating Intercellular Adhesion Molecule-1. Molecular Cancer Research, 2008, 6, 555-567.	3.4	65
67	The Interchromatin Compartment Participates in the Structural and Functional Organization of the Cell Nucleus. BioEssays, 2020, 42, e1900132.	2.5	65
68	Direct Visualization of a Protein Nuclear Architecture. Molecular Biology of the Cell, 1999, 10, 2051-2062.	2.1	62
69	Phosphorylation of polynucleotide kinase/ phosphatase by DNA-dependent protein kinase and ataxia-telangiectasia mutated regulates its association with sites of DNA damage. Nucleic Acids Research, 2011, 39, 9224-9237.	14.5	61
70	The cytotoxicity of Î³-secretase inhibitor I to breast cancer cells is mediated by proteasome inhibition, not by Î³-secretase inhibition. Breast Cancer Research, 2009, 11, R57.	5.0	60
71	The CD20 Calcium Channel Is Localized to Microvilli and Constitutively Associated with Membrane Rafts. Journal of Biological Chemistry, 2004, 279, 19893-19901.	3.4	59
72	MeCP2 binds to nucleosome free (linker DNA) regions and to H3K9/H3K27 methylated nucleosomes in the brain. Nucleic Acids Research, 2012, 40, 2884-2897.	14.5	57

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73	The solid and liquid states of chromatin. Epigenetics and Chromatin, 2021, 14, 50.	3.9	55
74	Electron Spectroscopic Imaging of Chromatin. Methods, 1999, 17, 188-200.	3.8	53
75	Characterizing fluorescence recovery curves for nuclear proteins undergoing binding events. Bulletin of Mathematical Biology, 2004, 66, 1515-1545.	1.9	52
76	Molecular dynamics of histone H1This paper is one of a selection of papers published in this Special Issue, entitled CSBMCBâ€™s 51st Annual MeetingÂâ€“ Epigenetics and Chromatin Dynamics, and has undergone the Journalâ€™s usual peer review process.. Biochemistry and Cell Biology, 2009, 87, 189-206.	2.0	51
77	Covalent Inhibition of Ubc13 Affects Ubiquitin Signaling and Reveals Active Site Elements Important for Targeting. ACS Chemical Biology, 2015, 10, 1718-1728.	3.4	50
78	Proteomic Investigation of Phosphorylation Sites in Poly(ADP-ribose) Polymerase-1 and Poly(ADP-ribose) Glycohydrolase. Journal of Proteome Research, 2009, 8, 1014-1029.	3.7	49
79	Notch signaling as a therapeutic target for breast cancer treatment?. Breast Cancer Research, 2011, 13, 210.	5.0	47
80	Synthesis and biological testing of novel pyridoisothiazolones as histone acetyltransferase inhibitors. Bioorganic and Medicinal Chemistry, 2011, 19, 3678-3689.	3.0	43
81	Compartmentalization of regulatory proteins in the cell nucleus. Journal of Steroid Biochemistry and Molecular Biology, 2001, 76, 9-21.	2.5	41
82	Dynamic relocation of poly(ADP-ribose) glycohydrolase isoforms during radiation-induced DNA damage. Biochimica Et Biophysica Acta - Molecular Cell Research, 2006, 1763, 226-237.	4.1	40
83	Proteome-wide Identification of WRN-Interacting Proteins in Untreated and Nuclease-Treated Samples. Journal of Proteome Research, 2011, 10, 1216-1227.	3.7	39
84	Linker Histones Are Mobilized during Infection with Herpes Simplex Virus Type 1. Journal of Virology, 2008, 82, 8629-8646.	3.4	37
85	F-actin-dependent Insolubility of Chromatin-modifying Components. Journal of Biological Chemistry, 2004, 279, 25017-25023.	3.4	36
86	Improved transfection efficiency of an aliphatic lipid substituted 2 kDa polyethylenimine is attributed to enhanced nuclear association and uptake in rat bone marrow stromal cell. Journal of Gene Medicine, 2011, 13, 46-59.	2.8	36
87	Epigenetics regulate centromere formation and kinetochore function. Journal of Cellular Biochemistry, 2008, 104, 2027-2039.	2.6	35
88	Quantitative Analysis Reveals Asynchronous and more than DSB-Associated Histone H2AX Phosphorylation after Exposure to Ionizing Radiation. Radiation Research, 2006, 165, 283-292.	1.5	34
89	Reprogramming progeria fibroblasts reâ€establishes a normal epigenetic landscape. Aging Cell, 2017, 16, 870-887.	6.7	34
90	G2 histone methylation is required for the proper segregation of chromosomes. Journal of Cell Science, 2009, 122, 2957-2968.	2.0	33

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91	DNA ligase III acts as a DNA strand break sensor in the cellular orchestration of DNA strand break repair. Nucleic Acids Research, 2015, 43, 875-892.	14.5	32
92	Pin1 promotes histone H1 dephosphorylation and stabilizes its binding to chromatin. Journal of Cell Biology, 2013, 203, 57-71.	5.2	30
93	Molecular Basis for K63-Linked Ubiquitination Processes in Double-Strand DNA Break Repair: A Focus on Kinetics and Dynamics. Journal of Molecular Biology, 2017, 429, 3409-3429.	4.2	30
94	Quantification of Proteinâ€“Protein and Proteinâ€“DNA Interactions In Vivo, Using Fluorescence Recovery after Photobleaching. Methods in Enzymology, 2003, 375, 415-442.	1.0	29
95	Core Histones H2B and H4 Are Mobilized during Infection with Herpes Simplex Virus 1. Journal of Virology, 2011, 85, 13234-13252.	3.4	29
96	The F-act's of nuclear actin. Current Opinion in Cell Biology, 2014, 28, 84-89.	5.4	28
97	RNF8 E3 Ubiquitin Ligase Stimulates Ubc13 E2 Conjugating Activity That Is Essential for DNA Double Strand Break Signaling and BRCA1 Tumor Suppressor Recruitment. Journal of Biological Chemistry, 2016, 291, 9396-9410.	3.4	26
98	Changes in the nuclear matrix of chicken erythrocytes that accompany maturation. Biochemical Journal, 1996, 320, 257-265.	3.7	25
99	Fixation-dependent organization of core histones following DNA fluorescent in situ hybridization. Chromosoma, 1997, 106, 114-123.	2.2	25
100	Nuclear distribution of histone deacetylase: a marker enzyme for the internal nuclear matrix. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 1992, 1130, 307-313.	2.4	24
101	The Transcriptional Regulator CBP Has Defined Spatial Associations within Interphase Nuclei. PLoS Computational Biology, 2006, 2, e139.	3.2	24
102	Impaired in vivo binding of MeCP2 to chromatin in the absence of its DNA methyl-binding domain. Nucleic Acids Research, 2013, 41, 4888-4900.	14.5	24
103	RYBP Is a K63-Ubiquitin-Chain-Binding Protein that Inhibits Homologous Recombination Repair. Cell Reports, 2018, 22, 383-395.	6.4	23
104	CBP, a transcriptional coactivator and acetyltransferase. Biochemistry and Cell Biology, 2001, 79, 253-266.	2.0	23
105	The Differential Mobilization of Histones H3.1 and H3.3 by Herpes Simplex Virus 1 Relates Histone Dynamics to the Assembly of Viral Chromatin. PLoS Pathogens, 2013, 9, e1003695.	4.7	22
106	Poly(ADP-ribose) glycohydrolase is a component of the FMRP-associated messenger ribonucleoparticles. Biochemical Journal, 2005, 392, 499-509.	3.7	19
107	Core Histone Hyperacetylation Impacts Cooperative Behavior and High-Affinity Binding of Histone H1 to Chromatin. Biochemistry, 2010, 49, 4420-4431.	2.5	19
108	Association of ATM activation and DNA repair with induced radioresistance after low-dose irradiation. Radiation Protection Dosimetry, 2015, 166, 131-136.	0.8	18

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109	RNA polymerase II transcription and the functional organization of the mammalian cell nucleus. Chromosoma, 1995, 103, 509-516.	2.2	17
110	A Key Role for Poly(ADP-Ribose) Polymerase 3 in Ectodermal Specification and Neural Crest Development. PLoS ONE, 2011, 6, e15834.	2.5	17
111	Subnuclear localization and mobility are key indicators of PAX3 dysfunction in Waardenburg syndrome. Human Molecular Genetics, 2008, 17, 1825-1837.	2.9	16
112	Modelling the compartmentalization of splicing factors. Journal of Theoretical Biology, 2006, 239, 298-312.	1.7	15
113	Using quantitative imaging microscopy to define the target substrate specificities of histone post-translational-modifying enzymes. Methods, 2005, 36, 351-361.	3.8	14
114	Epigenetic regulation of centromere formation and kinetochore functionThis 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, 605-630.	2.0	14
115	The PAX3 Paired Domain and Homeodomain Function as a Single Binding Module In Vivo to Regulate Subnuclear Localization and Mobility by a Mechanism That Requires Base-Specific Recognition. Journal of Molecular Biology, 2010, 402, 178-193.	4.2	13
116	Matrix metalloproteinaseâ€2 mediates ribosomal RNA transcription by cleaving nucleolar histones. FEBS Journal, 2021, 288, 6736-6751.	4.7	13
117	The integration of tissue structure and nuclear function. Biochemistry and Cell Biology, 2001, 79, 267-274.	2.0	12
118	BCL10 is recruited to sites of DNA damage to facilitate DNA double-strand break repair. Cell Cycle, 2016, 15, 84-94.	2.6	12
119	The relationship between histone posttranslational modification and DNA damage signaling and repair. International Journal of Radiation Biology, 2019, 95, 382-393.	1.8	12
120	Visualization of miniSOG Tagged DNA Repair Proteins in Combination with Electron Spectroscopic Imaging (ESI). Journal of Visualized Experiments, 2015, , .	0.3	11
121	Acetylation and methylation of histones H3 and H4 in chicken immature erythrocytes are not directly coupled. Biochemical and Biophysical Research Communications, 1992, 185, 414-419.	2.1	10
122	Interaction of chromatin with a histone H1 containing swapped N- and C-terminal domains. Bioscience Reports, 2015, 35, .	2.4	10
123	Trichostatin A decreases the levels of MeCP2 expression and phosphorylation and increases its chromatin binding affinity. Epigenetics, 2017, 12, 934-944.	2.7	10
124	Domain analysis of PNKPâ€“XRCC1 interactions: Influence of genetic variants of XRCC1. Journal of Biological Chemistry, 2019, 294, 520-530.	3.4	10
125	Characterization and comparison of protein complexes initiated by the intracellular domain of individual Notch paralogs. Biochemical and Biophysical Research Communications, 2011, 407, 479-485.	2.1	6
126	The integration of tissue structure and nuclear function. Biochemistry and Cell Biology, 2001, 79, 267-274.	2.0	6

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127	Nuclear matrix proteins bind very tightly to specific regions of the chicken histone H5 gene. Biochemistry and Cell Biology, 1992, 70, 822-829.	2.0	3
128	Modeling transcription factor binding events to DNA using a random walker/jumper representation on a 1D/2D lattice with different affinity sites. Physical Biology, 2007, 4, 256-267.	1.8	3
129	Conversations between chromatin modifications and DNA double strand break repair: A commentary. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2013, 750, 1-4.	1.0	3
130	Immunofluorescence of Histone Proteins. Methods in Molecular Biology, 2017, 1528, 165-171.	0.9	3
131	Shuttling towards a predictive assay for radiotherapy. Translational Cancer Research, 2016, 5, S742-S746.	1.0	3
132	A Method for Assessing Kinetic Changes of Histone H1 after Post-Translational Modifications. , 2009, , .		2
133	DNA Repair Foci Formation and Function at DNA Double-Strand Breaks. , 2016, , 219-237.		2
134	Using a model comparison approach to describe the assembly pathway for histone H1. PLoS ONE, 2018, 13, e0191562.	2.5	2
135	Heterogeneity of Organization of Subcompartments in DSB Repair Foci. Frontiers in Genetics, 0, 13, .	2.3	2
136	Reduction of histone acetylation in mitosis through loss of histone acetyltransferases and deacetylases from chromatin. Biochemistry and Cell Biology, 1999, 77, 400.	2.0	1
137	Conference Scene: Epigenetics Eh! The first formal meeting of the Canadian epigenetics community. Epigenomics, 2011, 3, 409-415.	2.1	1
138	Depletion of nuclear actin is a key mediator of quiescence in epithelial cells. Development (Cambridge), 2011, 138, e0207-e0207.	2.5	1
139	Introduction: Genome Biology. Genome, 2021, 64, v-vii.	2.0	0
140	Nucleolar Matrix Metalloproteinaseâ€2 Regulates rRNA Transcription. FASEB Journal, 2018, 32, lb416.	0.5	0
141	RNA polymerase II transcription and the functional organization of the mammalian cell nucleus. Chromosoma, 1995, 103, 509-516.	2.2	0