

Hitoshi Kurumizaka

List of Publications by Year in descending order

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262
papers

11,769
citations

25034

57
h-index

46799

89
g-index

277
all docs

277
docs citations

277
times ranked

11383
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of the human centromeric nucleosome containing CENP-A. <i>Nature</i> , 2011, 476, 232-235.	27.8	336
2	Independent and sequential recruitment of NHEJ and HR factors to DNA damage sites in mammalian cells. <i>Journal of Cell Biology</i> , 2005, 170, 341-347.	5.2	230
3	Structure and Dynamics of a 197Åbp Nucleosome in Complex with Linker Histone H1. <i>Molecular Cell</i> , 2017, 66, 384-397.e8.	9.7	225
4	Tracking epigenetic histone modifications in single cells using Fab-based live endogenous modification labeling. <i>Nucleic Acids Research</i> , 2011, 39, 6475-6488.	14.5	219
5	Mislocalization of the Centromeric Histone Variant CenH3/CENP-A in Human Cells Depends on the Chaperone DAXX. <i>Molecular Cell</i> , 2014, 53, 631-644.	9.7	214
6	Crystal Structure of the Homologous-Pairing Domain from the Human Rad52 Recombinase in the Undecameric Form. <i>Molecular Cell</i> , 2002, 10, 359-371.	9.7	210
7	Histone acetylation: influence on transcription, nucleosome mobility and positioning, and linker histone-dependent transcriptional repression. <i>EMBO Journal</i> , 1997, 16, 2096-2107.	7.8	207
8	Structural Basis of Heterochromatin Formation by Human HP1. <i>Molecular Cell</i> , 2018, 69, 385-397.e8.	9.7	196
9	Structural basis of instability of the nucleosome containing a testis-specific histone variant, human H3T. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10454-10459.	7.1	195
10	Structural basis of replication origin recognition by the DnaA protein. <i>Nucleic Acids Research</i> , 2003, 31, 2077-2086.	14.5	183
11	Involvement of SLX4 in interstrand cross-link repair is regulated by the Fanconi anemia pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6492-6496.	7.1	169
12	Structural basis of the nucleosome transition during RNA polymerase II passage. <i>Science</i> , 2018, 362, 595-598.	12.6	157
13	Expression and purification of recombinant human histones. <i>Methods</i> , 2004, 33, 3-11.	3.8	153
14	Structural basis for the inhibition of cGAS by nucleosomes. <i>Science</i> , 2020, 370, 455-458.	12.6	149
15	Homologous Pairing Promoted by the Human Rad52 Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 35201-35208.	3.4	142
16	The N-terminal domain of the human Rad51 protein binds DNA: structure and a DNA binding surface as revealed by NMR. <i>Journal of Molecular Biology</i> , 1999, 290, 495-504.	4.2	134
17	A FancD2-Monoubiquitin Fusion Reveals Hidden Functions of Fanconi Anemia Core Complex in DNA Repair. <i>Molecular Cell</i> , 2005, 19, 841-847.	9.7	134
18	The interaction of DiaA and DnaA regulates the replication cycle in <i>E. coli</i> by directly promoting ATP-dependent DnaA-specific initiation complexes. <i>Genes and Development</i> , 2007, 21, 2083-2099.	5.9	127

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19	Structural insight into nucleosome transcription by RNA polymerase II with elongation factors. <i>Science</i> , 2019, 363, 744-747.	12.6	126
20	Homologous-pairing activity of the human DNA-repair proteins Xrcc3*Rad51C. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5538-5543.	7.1	123
21	A Common Mechanism for the ATP-DnaA-dependent Formation of Open Complexes at the Replication Origin. <i>Journal of Biological Chemistry</i> , 2008, 283, 8351-8362.	3.4	123
22	RFWD3-Mediated Ubiquitination Promotes Timely Removal of Both RPA and RAD51 from DNA Damage Sites to Facilitate Homologous Recombination. <i>Molecular Cell</i> , 2017, 66, 622-634.e8.	9.7	123
23	Solution structure of the DNA binding domain of a nucleoid-associated protein, H-NS, from <i>Escherichia coli</i> . <i>FEBS Letters</i> , 1995, 360, 125-131.	2.8	121
24	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. <i>Genome Biology</i> , 2016, 17, 36.	8.8	121
25	A chromatin integration labelling method enables epigenomic profiling with lower input. <i>Nature Cell Biology</i> , 2019, 21, 287-296.	10.3	121
26	Chd2 interacts with H3.3 to determine myogenic cell fate. <i>EMBO Journal</i> , 2012, 31, 2994-3007.	7.8	117
27	Histone Variant H2A.L.2 Guides Transition Protein-Dependent Protamine Assembly in Male Germ Cells. <i>Molecular Cell</i> , 2017, 66, 89-101.e8.	9.7	116
28	Contribution of histone N-terminal tails to the structure and stability of nucleosomes. <i>FEBS Open Bio</i> , 2013, 3, 363-369.	2.3	105
29	Structural Analysis of the Hexasome, Lacking One Histone H2A/H2B Dimer from the Conventional Nucleosome. <i>Biochemistry</i> , 2012, 51, 3302-3309.	2.5	101
30	Mutations in the Gene Encoding the E2 Conjugating Enzyme UBE2T Cause Fanconi Anemia. <i>American Journal of Human Genetics</i> , 2015, 96, 1001-1007.	6.2	100
31	Structural Basis for Octameric Ring Formation and DNA Interaction of the Human Homologous-Pairing Protein Dmc1. <i>Molecular Cell</i> , 2004, 14, 363-374.	9.7	99
32	Crystal structure of the CENP-B protein-DNA complex: the DNA-binding domains of CENP-B induce kinks in the CENP-B box DNA. <i>EMBO Journal</i> , 2001, 20, 6612-6618.	7.8	97
33	Structures of human nucleosomes containing major histone H3 variants. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 578-583.	2.5	96
34	Genetically encoded system to track histone modification in vivo. <i>Scientific Reports</i> , 2013, 3, 2436.	3.3	96
35	The Nucleosome: A Powerful Regulator of Transcription. <i>Progress in Molecular Biology and Translational Science</i> , 1998, 61, 379-422.	1.9	92
36	Histone Methylation by SETD1A Protects Nascent DNA through the Nucleosome Chaperone Activity of FANCD2. <i>Molecular Cell</i> , 2018, 71, 25-41.e6.	9.7	87

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37	Preferential binding to branched DNA strands and strand-annealing activity of the human Rad51B, Rad51C, Rad51D and Xrcc2 protein complex. <i>Nucleic Acids Research</i> , 2004, 32, 2556-2565.	14.5	84
38	Testis-Specific Histone Variant H3t Gene Is Essential for Entry into Spermatogenesis. <i>Cell Reports</i> , 2017, 18, 593-600.	6.4	82
39	An interaction between a specified surface of the C-terminal domain of RecA protein and double-stranded DNA for homologous pairing. <i>Journal of Molecular Biology</i> , 1997, 274, 213-221.	4.2	80
40	DNA robustly stimulates FANCD2 monoubiquitylation in the complex with FANCI. <i>Nucleic Acids Research</i> , 2012, 40, 4553-4561.	14.5	79
41	Nucleosome formation with the testis-specific histone H3 variant, H3t, by human nucleosome assembly proteins in vitro. <i>Nucleic Acids Research</i> , 2008, 36, 2208-2218.	14.5	78
42	Crystal structure of the overlapping dinucleosome composed of hexasome and octasome. <i>Science</i> , 2017, 356, 205-208.	12.6	77
43	FANCD2 Binds CtIP and Regulates DNA-End Resection during DNA Interstrand Crosslink Repair. <i>Cell Reports</i> , 2014, 7, 1039-1047.	6.4	73
44	Structural diversity of the nucleosome. <i>Journal of Biochemistry</i> , 2018, 163, 85-95.	1.7	73
45	A Possible Role of the C-terminal Domain of the RecA Protein. <i>Journal of Biological Chemistry</i> , 1996, 271, 33515-33524.	3.4	72
46	Homologous Pairing and Ring and Filament Structure Formation Activities of the Human Xrcc2-Rad51D Complex. <i>Journal of Biological Chemistry</i> , 2002, 277, 14315-14320.	3.4	72
47	KIAA1018/FAN1 nuclease protects cells against genomic instability induced by interstrand cross-linking agents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21553-21557.	7.1	72
48	The centromeric nucleosome-like CENP-A-Wâ€“X complex induces positive supercoils into DNA. <i>Nucleic Acids Research</i> , 2014, 42, 1644-1655.	14.5	72
49	The Flexible Ends of CENP-A Nucleosome Are Required for Mitotic Fidelity. <i>Molecular Cell</i> , 2016, 63, 674-685.	9.7	72
50	DNA damage detection in nucleosomes involves DNA register shifting. <i>Nature</i> , 2019, 571, 79-84.	27.8	72
51	Human rad51 amino acid residues required for rad52 binding 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1999, 291, 537-548.	4.2	71
52	Replication stress induces accumulation of FANCD2 at central region of large fragile genes. <i>Nucleic Acids Research</i> , 2018, 46, 2932-2944.	14.5	70
53	CHD3 helicase domain mutations cause a neurodevelopmental syndrome with macrocephaly and impaired speech and language. <i>Nature Communications</i> , 2018, 9, 4619.	12.8	70
54	HIV-1 Vpr Induces DNA Double-Strand Breaks. <i>Cancer Research</i> , 2006, 66, 627-631.	0.9	69

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55	Identification of a Second DNA Binding Site in the Human Rad52 Protein. <i>Journal of Biological Chemistry</i> , 2008, 283, 24264-24273.	3.4	69
56	Transcription through the nucleosome. <i>Current Opinion in Structural Biology</i> , 2020, 61, 42-49.	5.7	68
57	Histone H2A variants confer specific properties to nucleosomes and impact on chromatin accessibility. <i>Nucleic Acids Research</i> , 2018, 46, 7675-7685.	14.5	65
58	Homologous genetic recombination as an intrinsic dynamic property of a DNA structure induced by RecA/Rad51-family proteins: A possible advantage of DNA over RNA as genomic material. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8425-8432.	7.1	64
59	Crystal structure and stable property of the cancer-associated heterotypic nucleosome containing CENP-A and H3.3. <i>Scientific Reports</i> , 2014, 4, 7115.	3.3	64
60	N-terminal phosphorylation of HP1 \pm increases its nucleosome-binding specificity. <i>Nucleic Acids Research</i> , 2014, 42, 12498-12511.	14.5	63
61	ATR $\hat{=}$ ATRIP Kinase Complex Triggers Activation of the Fanconi Anemia DNA Repair Pathway. <i>Cancer Research</i> , 2012, 72, 1149-1156.	0.9	62
62	Dynamic changes in CCAN organization through CENP-C during cell-cycle progression. <i>Molecular Biology of the Cell</i> , 2015, 26, 3768-3776.	2.1	62
63	Histone chaperone activity of Fanconi anemia proteins, FANCD2 and FANCI, is required for DNA crosslink repair. <i>EMBO Journal</i> , 2012, 31, 3524-3536.	7.8	61
64	Structural basis of a nucleosome containing histone H2A.B/H2A.Bbd that transiently associates with reorganized chromatin. <i>Scientific Reports</i> , 2013, 3, 3510.	3.3	61
65	A method for evaluating nucleosome stability with a protein-binding fluorescent dye. <i>Methods</i> , 2014, 70, 119-126.	3.8	60
66	Synthetic Posttranslational Modifications: Chemical Catalyst-Driven Regioselective Histone Acylation of Native Chromatin. <i>Journal of the American Chemical Society</i> , 2017, 139, 7568-7576.	13.7	60
67	Interaction of the pioneer transcription factor GATA3 with nucleosomes. <i>Nature Communications</i> , 2020, 11, 4136.	12.8	60
68	DIDS, a chemical compound that inhibits RAD51-mediated homologous pairing and strand exchange. <i>Nucleic Acids Research</i> , 2009, 37, 3367-3376.	14.5	59
69	Cdt1-binding protein GRWD1 is a novel histone-binding protein that facilitates MCM loading through its influence on chromatin architecture. <i>Nucleic Acids Research</i> , 2015, 43, 5898-5911.	14.5	59
70	Stable complex formation of CENP-B with the CENP-A nucleosome. <i>Nucleic Acids Research</i> , 2015, 43, 4909-4922.	14.5	59
71	Cancer-associated mutations of histones H2B, H3.1 and H2A.Z.1 affect the structure and stability of the nucleosome. <i>Nucleic Acids Research</i> , 2018, 46, 10007-10018.	14.5	58
72	Activation of the SUMO modification system is required for the accumulation of RAD51 at sites containing DNA damage. <i>Journal of Cell Science</i> , 2013, 126, 5284-92.	2.0	56

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73	Association of M18BP1/KNL2 with CENP-A Nucleosome Is Essential for Centromere Formation in Non-mammalian Vertebrates. <i>Developmental Cell</i> , 2017, 42, 181-189.e3.	7.0	56
74	Genetic variance modifies apoptosis susceptibility in mature oocytes via alterations in DNA repair capacity and mitochondrial ultrastructure. <i>Cell Death and Differentiation</i> , 2007, 14, 524-533.	11.2	55
75	Structural polymorphism in the L1 loop regions of human H2A.Z.1 and H2A.Z.2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2431-2439.	2.5	55
76	Holliday Junction Binding Activity of the Human Rad51B Protein. <i>Journal of Biological Chemistry</i> , 2003, 278, 2767-2772.	3.4	54
77	Nucleosome Formation Activity of Human Somatic Nuclear Autoantigenic Sperm Protein (sNASP). <i>Journal of Biological Chemistry</i> , 2010, 285, 11913-11921.	3.4	54
78	Sufficient Amounts of Functional HOP2/MND1 Complex Promote Interhomolog DNA Repair but Are Dispensable for Intersister DNA Repair during Meiosis in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 25, 4924-4940.	6.6	54
79	Human Centromere Protein B Induces Translational Positioning of Nucleosomes on α -Satellite Sequences. <i>Journal of Biological Chemistry</i> , 2005, 280, 41609-41618.	3.4	53
80	Histone H3.5 forms an unstable nucleosome and accumulates around transcription start sites in human testis. <i>Epigenetics and Chromatin</i> , 2016, 9, 2.	3.9	53
81	The CHD4-related syndrome: a comprehensive investigation of the clinical spectrum, genotype-phenotype correlations, and molecular basis. <i>Genetics in Medicine</i> , 2020, 22, 389-397.	2.4	53
82	Roles of the human Rad51 L1 and L2 loops in DNA binding. <i>FEBS Journal</i> , 2006, 273, 3148-3159.	4.7	52
83	A Genetically Encoded Probe for Live-Cell Imaging of H4K20 Monomethylation. <i>Journal of Molecular Biology</i> , 2016, 428, 3885-3902.	4.2	52
84	Human PSF binds to RAD51 and modulates its homologous-pairing and strand-exchange activities. <i>Nucleic Acids Research</i> , 2009, 37, 4296-4307.	14.5	51
85	Enhancing Survival of Mouse Oocytes Following Chemotherapy or Aging by Targeting Bax and Rad51. <i>PLoS ONE</i> , 2010, 5, e9204.	2.5	51
86	Evaluation of Chemical Fluorescent Dyes as a Protein Conjugation Partner for Live Cell Imaging. <i>PLoS ONE</i> , 2014, 9, e106271.	2.5	51
87	HIV-1 Vpr induces ATM-dependent cellular signal with enhanced homologous recombination. <i>Oncogene</i> , 2007, 26, 477-486.	5.9	50
88	Structural genomics projects in Japan. <i>Progress in Biophysics and Molecular Biology</i> , 2000, 73, 363-376.	2.9	49
89	Stimulation of DNA Strand Exchange by the Human TBPIP/Hop2-Mnd1 Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 5575-5581.	3.4	49
90	Bivalent interaction of the PZP domain of BRPF1 with the nucleosome impacts chromatin dynamics and acetylation. <i>Nucleic Acids Research</i> , 2016, 44, 472-484.	14.5	49

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91	Structural Basis of Homology-Directed DNA Repair Mediated by RAD52. <i>IScience</i> , 2018, 3, 50-62.	4.1	49
92	Contributions of Histone Variants in Nucleosome Structure and Function. <i>Journal of Molecular Biology</i> , 2021, 433, 166678.	4.2	49
93	Human Rad54B is a double-stranded DNA-dependent ATPase and has biochemical properties different from its structural homolog in yeast, Tid1/Rdh54. <i>Nucleic Acids Research</i> , 2002, 30, 1346-1353.	14.5	48
94	Methods for Preparing Nucleosomes Containing Histone Variants. <i>Methods in Molecular Biology</i> , 2018, 1832, 3-20.	0.9	47
95	Cryo-EM Structures of Centromeric Tri-nucleosomes Containing a Central CENP-A Nucleosome. <i>Structure</i> , 2020, 28, 44-53.e4.	3.3	47
96	Structure and function of human histone H3.Y nucleosome. <i>Nucleic Acids Research</i> , 2016, 44, 6127-6141.	14.5	44
97	FANCI-FANCD2 stabilizes the RAD51-DNA complex by binding RAD51 and protects the 5' end of DNA. <i>Nucleic Acids Research</i> , 2016, 44, 10758-10771.	14.5	44
98	Positive Role of the Mammalian TBPIP/HOP2 Protein in DMC1-mediated Homologous Pairing. <i>Journal of Biological Chemistry</i> , 2004, 279, 35263-35272.	3.4	43
99	Functional domains for assembly of histones H3 and H4 into the chromatin of <i>Xenopus</i> embryos. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 12780-12785.	7.1	42
100	Structural transition of the nucleosome during chromatin remodeling and transcription. <i>Current Opinion in Structural Biology</i> , 2019, 59, 107-114.	5.7	42
101	Inhibition of filament formation of human Rad51 protein by a small peptide derived from the BRCA2 protein. <i>Genes To Cells</i> , 2008, 13, 471-481.	1.2	41
102	From meiosis to postmeiotic events: Uncovering the molecular roles of the meiosis-specific recombinase Dmc1. <i>FEBS Journal</i> , 2010, 277, 590-598.	4.7	40
103	H4K20me1 and H3K27me3 are concurrently loaded onto the inactive X chromosome but dispensable for inducing gene silencing. <i>EMBO Reports</i> , 2021, 22, e51989.	4.5	40
104	Halenaquinone, a chemical compound that specifically inhibits the secondary DNA binding of RAD51. <i>Genes To Cells</i> , 2011, 16, 427-436.	1.2	39
105	Structural basis of pyrimidine-pyrimidone (6-4) photoproduct recognition by UV-DDB in the nucleosome. <i>Scientific Reports</i> , 2015, 5, 16330.	3.3	39
106	Comprehensive Structural Analysis of Mutant Nucleosomes Containing Lysine to Glutamine (KQ) Substitutions in the H3 and H4 Histone-Fold Domains. <i>Biochemistry</i> , 2011, 50, 7822-7832.	2.5	37
107	LC-MS/MS-based quantitative study of the acyl group- and site-selectivity of human sirtuins to acylated nucleosomes. <i>Scientific Reports</i> , 2018, 8, 2656.	3.3	36
108	CpG methylation of the CENP-B box reduces human CENP-B binding. <i>FEBS Journal</i> , 2004, 272, 282-289.	4.7	35

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109	Structural and biochemical analyses of monoubiquitinated human histones H2B and H4. <i>Open Biology</i> , 2016, 6, 160090.	3.6	35
110	Histone H3 Methylated at Arginine 17 Is Essential for Reprogramming the Paternal Genome in Zygotes. <i>Cell Reports</i> , 2017, 20, 2756-2765.	6.4	35
111	H3K14 ubiquitylation promotes H3K9 methylation for heterochromatin assembly. <i>EMBO Reports</i> , 2019, 20, e48111.	4.5	35
112	Cryo-EM structure of the CENP-A nucleosome in complex with phosphorylated CENP-C. <i>EMBO Journal</i> , 2021, 40, e105671.	7.8	35
113	The DnaA homolog of the hyperthermophilic eubacterium <i>Thermotoga maritima</i> forms an open complex with a minimal 149-bp origin region in an ATP-dependent manner. <i>Genes To Cells</i> , 2006, 11, 425-438.	1.2	33
114	Structural and functional analyses of the DMC1-M200V polymorphism found in the human population. <i>Nucleic Acids Research</i> , 2008, 36, 4181-4190.	14.5	33
115	Current progress on structural studies of nucleosomes containing histone H3 variants. <i>Current Opinion in Structural Biology</i> , 2013, 23, 109-115.	5.7	32
116	Cryogenic coherent x-ray diffraction imaging for biological non-crystalline particles using the KOTŌBUKI-1 diffraction apparatus at SACLA. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2015, 48, 184003.	1.5	32
117	Phosphorylation of CBX2 controls its nucleosome-binding specificity. <i>Journal of Biochemistry</i> , 2017, 162, 343-355.	1.7	31
118	Cryo-EM structure of the nucleosome containing the <i>ALB1</i> enhancer DNA sequence. <i>Open Biology</i> , 2018, 8, .	3.6	31
119	Acetylated histone H4 tail enhances histone H3 tail acetylation by altering their mutual dynamics in the nucleosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19661-19663.	7.1	31
120	Nucleosome binding by the pioneer transcription factor OCT4. <i>Scientific Reports</i> , 2020, 10, 11832.	3.3	30
121	Two Arginine Residues Suppress the Flexibility of Nucleosomal DNA in the Canonical Nucleosome Core. <i>PLoS ONE</i> , 2015, 10, e0120635.	2.5	30
122	The Mutant RecA Proteins, RecAR243Q and RecAK245N, Exhibit Defective DNA Binding in Homologous Pairing. <i>Archives of Biochemistry and Biophysics</i> , 1999, 365, 83-91.	3.0	29
123	Synthetic Chromatin Acylation by an Artificial Catalyst System. <i>CheM</i> , 2017, 2, 840-859.	11.7	29
124	Direct Inhibition of TNF- α Promoter Activity by Fanconi Anemia Protein FANCD2. <i>PLoS ONE</i> , 2011, 6, e23324.	2.5	29
125	Structural and biochemical analyses of hemimethylated DNA binding by the SeqA protein. <i>Nucleic Acids Research</i> , 2004, 32, 82-92.	14.5	28
126	The actin-related protein hArap8 accumulates on the mitotic chromosomes and functions in chromosome alignment. <i>Experimental Cell Research</i> , 2008, 314, 859-868.	2.6	28

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127	The CENP-A centromere targeting domain facilitates H4K20 monomethylation in the nucleosome by structural polymorphism. <i>Nature Communications</i> , 2019, 10, 576.	12.8	28
128	Location of Tyrosine 315, a Target for Phosphorylation by cAbl Tyrosine Kinase, at the Edge of the Subunitâ€™Subunit Interface of the Human Rad51 Filament. <i>Journal of Molecular Biology</i> , 2004, 339, 797-804.	4.2	27
129	c-ABL tyrosine kinase stabilizes RAD51 chromatin association. <i>Biochemical and Biophysical Research Communications</i> , 2009, 382, 286-291.	2.1	27
130	GEMIN2 promotes accumulation of RAD51 at double-strand breaks in homologous recombination. <i>Nucleic Acids Research</i> , 2010, 38, 5059-5074.	14.5	27
131	Comparison between the CENP-A and histone H3 structures in nucleosomes. <i>Nucleus</i> , 2012, 3, 6-11.	2.2	27
132	Nap1 stimulates homologous recombination by RAD51 and RAD54 in higher-ordered chromatin containing histone H1. <i>Scientific Reports</i> , 2014, 4, 4863.	3.3	27
133	Crystal structures of heterotypic nucleosomes containing histones H2A.Z and H2A. <i>Open Biology</i> , 2016, 6, 160127.	3.6	27
134	Crystal Structure of the Human Centromere Protein B (CENP-B) Dimerization Domain at 1.65-Å... Resolution. <i>Journal of Biological Chemistry</i> , 2003, 278, 51454-51461.	3.4	26
135	Conclusive Evidence of the Reconstituted Hexasome Proven by Native Mass Spectrometry. <i>Biochemistry</i> , 2013, 52, 5155-5157.	2.5	26
136	Distinct Features of the Histone Core Structure in Nucleosomes Containing the Histone H2A.B Variant. <i>Biophysical Journal</i> , 2014, 106, 2206-2213.	0.5	26
137	Mutational analyses of the human Rad51-Tyr315 residue, a site for phosphorylation in leukaemia cells. <i>Genes To Cells</i> , 2004, 9, 781-790.	1.2	24
138	Vertebrate Spt2 is a novel nucleolar histone chaperone that assists in ribosomal DNA transcription. <i>Journal of Cell Science</i> , 2013, 126, 1323-32.	2.0	24
139	Live-cell epigenome manipulation by synthetic histone acetylation catalyst system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	24
140	The Lys313 residue of the human Rad51 protein negatively regulates the strandâ€™exchange activity. <i>Genes To Cells</i> , 2008, 13, 91-103.	1.2	23
141	Filament formation and robust strand exchange activities of the rice DMC1A and DMC1B proteins. <i>Nucleic Acids Research</i> , 2008, 36, 4266-4276.	14.5	23
142	Histone H3.3 sub-variant H3mm7 is required for normal skeletal muscle regeneration. <i>Nature Communications</i> , 2018, 9, 1400.	12.8	23
143	Role of the N-terminal Domain of the Human DMC1 Protein in Octamer Formation and DNA Binding. <i>Journal of Biological Chemistry</i> , 2005, 280, 28382-28387.	3.4	22
144	The ATR-Chk1 pathway plays a role in the generation of centrosome aberrations induced by Rad51C dysfunction. <i>Nucleic Acids Research</i> , 2009, 37, 3959-3968.	14.5	22

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145	Gas-Phase Structure of the Histone Multimers Characterized by Ion Mobility Mass Spectrometry and Molecular Dynamics Simulation. <i>Analytical Chemistry</i> , 2013, 85, 4165-4171.	6.5	22
146	Influence of DNA methylation on positioning and DNA flexibility of nucleosomes with pericentric satellite DNA. <i>Open Biology</i> , 2015, 5, 150128.	3.6	22
147	Xeroderma pigmentosum group C protein interacts with histones: regulation by acetylated states of histone H3. <i>Genes To Cells</i> , 2017, 22, 310-327.	1.2	22
148	C-terminal acidic domain of histone chaperone human NAP1 is an efficient binding assistant for histone H2A/H2B, but not H3/H4. <i>Genes To Cells</i> , 2016, 21, 252-263.	1.2	21
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150	Deimination stabilizes histone H2A/H2B dimers as revealed by electrospray ionization mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2010, 45, 900-908.	1.6	20
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