

Hitoshi Kurumizaka

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1154851/publications.pdf>

Version: 2024-02-01

262
papers

11,769
citations

28736

57
h-index

53065

89
g-index

277
all docs

277
docs citations

277
times ranked

12548
citing authors

#	ARTICLE	IF	CITATIONS
1	Unusual nucleosome formation and transcriptome influence by the histone H3m18 variant. <i>Nucleic Acids Research</i> , 2022, 50, 72-91.	6.5	7
2	Structural studies of functional nucleosome complexes with transacting factors. <i>Proceedings of the Japan Academy Series B: Physical and Biological Sciences</i> , 2022, 98, 1-14.	1.6	2
3	Cryo-EM Analysis of Chromatin. <i>Nihon Kessho Gakkaishi</i> , 2022, 64, 65-68.	0.0	0
4	Characteristic H3 N-tail dynamics in the nucleosome core particle, nucleosome, and chromatosome. <i>IScience</i> , 2022, 25, 103937.	1.9	5
5	Structural and biochemical analyses of the nucleosome containing <i>Komagataella pastoris</i> histones. <i>Journal of Biochemistry</i> , 2022, 172, 79-88.	0.9	11
6	Structural basis for binding diversity of acetyltransferase p300 to the nucleosome. <i>IScience</i> , 2022, 25, 104563.	1.9	9
7	Evolution of Epidermal Growth Factor (EGF)-like and Zona Pellucida Domains Containing Shell Matrix Proteins in Mollusks. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
8	Contributions of Histone Variants in Nucleosome Structure and Function. <i>Journal of Molecular Biology</i> , 2021, 433, 166678.	2.0	49
9	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, .	3.3	24
10	Inactivation Mechanism of an Innate Immune DNA Sensor cGAS by Self-chromatinized DNA. <i>Seibutsu Butsuri</i> , 2021, 61, 324-326.	0.0	0
11	Structural basis of nucleosomal histone H4 lysine 20 methylation by SET8 methyltransferase. <i>Life Science Alliance</i> , 2021, 4, e202000919.	1.3	17
12	H4K20me1 and H3K27me3 are concurrently loaded onto the inactive X chromosome but dispensable for inducing gene silencing. <i>EMBO Reports</i> , 2021, 22, e51989.	2.0	40
13	Histone variant H2A.B-H2B dimers are spontaneously exchanged with canonical H2A-H2B in the nucleosome. <i>Communications Biology</i> , 2021, 4, 191.	2.0	17
14	Chromatin structure-dependent histone incorporation revealed by a genome-wide deposition assay. <i>ELife</i> , 2021, 10, .	2.8	6
15	Sequence-dependent nucleosome formation in trinucleotide repeats evaluated by in vivo chemical mapping. <i>Biochemical and Biophysical Research Communications</i> , 2021, 556, 179-184.	1.0	1
16	The N-terminal Tails of Histones H2A and H2B Adopt Two Distinct Conformations in the Nucleosome with Contact and Reduced Contact to DNA. <i>Journal of Molecular Biology</i> , 2021, 433, 167110.	2.0	16
17	Cryo-EM structure of the nucleosome core particle containing <i>Giardia lamblia</i> histones. <i>Nucleic Acids Research</i> , 2021, 49, 8934-8946.	6.5	20
18	Structural basis for DNA sequence recognition by pioneer factors in nucleosomes. <i>Current Opinion in Structural Biology</i> , 2021, 71, 59-64.	2.6	8

#	ARTICLE	IF	CITATIONS
19	Organoruthenium-catalyzed chemical protein synthesis to elucidate the functions of epigenetic modifications on heterochromatin factors. <i>Chemical Science</i> , 2021, 12, 5926-5937.	3.7	10
20	Cryo-EM structure of the CENP-A nucleosome in complex with phosphorylated CENP-C. <i>EMBO Journal</i> , 2021, 40, e105671.	3.5	35
21	Neural stem/precursor cells dynamically change their epigenetic landscape to differentially respond to BMP signaling for fate switching during brain development. <i>Genes and Development</i> , 2021, 35, 1431-1444.	2.7	11
22	Modeling population size independent tissue epigenomes by ChIP-seq with single thin sections. <i>Molecular Systems Biology</i> , 2021, 17, e10323.	3.2	1
23	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.	1.1	53
24	Cryo-EM Structures of Centromeric Tri-nucleosomes Containing a Central CENP-A Nucleosome. <i>Structure</i> , 2020, 28, 44-53.e4.	1.6	47
25	Biochemical and structural analyses of the nucleosome containing human histone H2A.J. <i>Journal of Biochemistry</i> , 2020, 167, 419-427.	0.9	6
26	Transcription through the nucleosome. <i>Current Opinion in Structural Biology</i> , 2020, 61, 42-49.	2.6	68
27	Nucleosome binding by the pioneer transcription factor OCT4. <i>Scientific Reports</i> , 2020, 10, 11832.	1.6	30
28	Essentiality of CENP-A Depends on Its Binding Mode to HJURP. <i>Cell Reports</i> , 2020, 33, 108388.	2.9	9
29	Linker DNA and histone contributions in nucleosome binding by p53. <i>Journal of Biochemistry</i> , 2020, 168, 669-675.	0.9	14
30	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.	3.3	31
31	Acetylation-modulated communication between the H3 N-terminal tail domain and the intrinsically disordered H1 C-terminal domain. <i>Nucleic Acids Research</i> , 2020, 48, 11510-11520.	6.5	12
32	Structural basis for the inhibition of cGAS by nucleosomes. <i>Science</i> , 2020, 370, 455-458.	6.0	149
33	Chromatin integration labeling for mapping DNA-binding proteins and modifications with low input. <i>Nature Protocols</i> , 2020, 15, 3334-3360.	5.5	12
34	Interaction of the pioneer transcription factor GATA3 with nucleosomes. <i>Nature Communications</i> , 2020, 11, 4136.	5.8	60
35	The N-terminal and C-terminal halves of histone H2A.Z independently function in nucleosome positioning and stability. <i>Genes To Cells</i> , 2020, 25, 538-546.	0.5	10
36	Integral approach to biomacromolecular structure by analytical-ultracentrifugation and small-angle scattering. <i>Communications Biology</i> , 2020, 3, 294.	2.0	9

#	ARTICLE	IF	CITATIONS
37	Improved Methods for Preparing the Telomere Tethering Complex Bqt1&Bqt2 for Structural Studies. Protein Journal, 2020, 39, 174-181.	0.7	0
38	Native Mass Spectrometry of Protein and DNA Complexes Prepared in Nonvolatile Buffers. Journal of the American Society for Mass Spectrometry, 2020, 31, 711-718.	1.2	15
39	Structural Studies of Overlapping Dinucleosomes in Solution. Biophysical Journal, 2020, 118, 2209-2219.	0.2	15
40	Nucleosome destabilization by nuclear non-coding RNAs. Communications Biology, 2020, 3, 60.	2.0	6
41	Synthetic hyperacetylation of nucleosomal histones. RSC Chemical Biology, 2020, 1, 56-59.	2.0	12
42	Biochemical analysis of nucleosome targeting by Tn5 transposase. Open Biology, 2019, 9, 190116.	1.5	14
43	Intrabody-based FRET probe to visualize endogenous histone acetylation. Scientific Reports, 2019, 9, 10188.	1.6	10
44	Incorporation and influence of <i>Leishmania</i> histone H3 in chromatin. Nucleic Acids Research, 2019, 47, 11637-11648.	6.5	18
45	H3K14 ubiquitylation promotes H3K9 methylation for heterochromatin assembly. EMBO Reports, 2019, 20, e48111.	2.0	35
46	Structural transition of the nucleosome during chromatin remodeling and transcription. Current Opinion in Structural Biology, 2019, 59, 107-114.	2.6	42
47	A novel mode of DnaA&DnaA interaction promotes ADP dissociation for reactivation of replication initiation activity. Nucleic Acids Research, 2019, 47, 11209-11224.	6.5	12
48	Structural and biochemical analyses of the nuclear pore complex component ELYS identify residues responsible for nucleosome binding. Communications Biology, 2019, 2, 163.	2.0	17
49	DNA damage detection in nucleosomes involves DNA register shifting. Nature, 2019, 571, 79-84.	13.7	72
50	Structure-based design of an H2A.Z.1 mutant stabilizing a nucleosome in vitro and in vivo. Biochemical and Biophysical Research Communications, 2019, 515, 719-724.	1.0	8
51	Biochemical characterization of the placeholder nucleosome for DNA hypomethylation maintenance. Biochemistry and Biophysics Reports, 2019, 18, 100634.	0.7	3
52	Structural insight into nucleosome transcription by RNA polymerase II with elongation factors. Science, 2019, 363, 744-747.	6.0	126
53	The CENP-A centromere targeting domain facilitates H4K20 monomethylation in the nucleosome by structural polymorphism. Nature Communications, 2019, 10, 576.	5.8	28
54	Structure determination of the nucleosome core particle by selenium SAD phasing. Acta Crystallographica Section D: Structural Biology, 2019, 75, 930-936.	1.1	1

#	ARTICLE	IF	CITATIONS
55	Mitotic phosphorylation of HP1 \pm regulates its cell cycle-dependent chromatin binding. <i>Journal of Biochemistry</i> , 2019, 165, 433-446.	0.9	10
56	A chromatin integration labelling method enables epigenomic profiling with lower input. <i>Nature Cell Biology</i> , 2019, 21, 287-296.	4.6	121
57	Homologous pairing activities of <i>Arabidopsis thaliana</i> RAD51 and DMC1. <i>Journal of Biochemistry</i> , 2019, 165, 289-295.	0.9	11
58	Histone H3.3 sub-variant H3mm7 is required for normal skeletal muscle regeneration. <i>Nature Communications</i> , 2018, 9, 1400.	5.8	23
59	Replication stress induces accumulation of FANCD2 at central region of large fragile genes. <i>Nucleic Acids Research</i> , 2018, 46, 2932-2944.	6.5	70
60	LC ϵ -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.	1.6	36
61	Structural Basis of Heterochromatin Formation by Human HP1. <i>Molecular Cell</i> , 2018, 69, 385-397.e8.	4.5	196
62	Structural diversity of the nucleosome. <i>Journal of Biochemistry</i> , 2018, 163, 85-95.	0.9	73
63	Cryo-EM structure of the nucleosome containing the <i>ALB1</i> enhancer DNA sequence. <i>Open Biology</i> , 2018, 8, .	1.5	31
64	SUMO modification system facilitates the exchange of histone variant H2A.Z-2 at DNA damage sites. <i>Nucleus</i> , 2018, 9, 87-94.	0.6	20
65	Crystallographic analysis of the overlapping dinucleosome as a novel chromatin unit. <i>Biophysics and Physicobiology</i> , 2018, 15, 251-254.	0.5	0
66	CHD3 helicase domain mutations cause a neurodevelopmental syndrome with macrocephaly and impaired speech and language. <i>Nature Communications</i> , 2018, 9, 4619.	5.8	70
67	Structural basis of the nucleosome transition during RNA polymerase II passage. <i>Science</i> , 2018, 362, 595-598.	6.0	157
68	Structural Diversity of Nucleosomes Characterized by Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 8217-8226.	3.2	15
69	Histone Methylation by SETD1A Protects Nascent DNA through the Nucleosome Chaperone Activity of FANCD2. <i>Molecular Cell</i> , 2018, 71, 25-41.e6.	4.5	87
70	Histone H2A variants confer specific properties to nucleosomes and impact on chromatin accessibility. <i>Nucleic Acids Research</i> , 2018, 46, 7675-7685.	6.5	65
71	Structural polymorphism of the <i>Escherichia coli</i> poly-L-glutamate synthetase RimK. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 385-390.	0.4	3
72	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.	6.5	58

#	ARTICLE	IF	CITATIONS
73	Methods for Preparing Nucleosomes Containing Histone Variants. <i>Methods in Molecular Biology</i> , 2018, 1832, 3-20.	0.4	47
74	Structural Basis of Homology-Directed DNA Repair Mediated by RAD52. <i>IScience</i> , 2018, 3, 50-62.	1.9	49
75	MNase, as a probe to study the sequence-dependent site exposures in the +1 nucleosomes of yeast. <i>Nucleic Acids Research</i> , 2018, 46, 7124-7137.	6.5	12
76	Testis-Specific Histone Variant H3t Gene Is Essential for Entry into Spermatogenesis. <i>Cell Reports</i> , 2017, 18, 593-600.	2.9	82
77	Identification of the amino acid residues responsible for stable nucleosome formation by histone H3.Y. <i>Nucleus</i> , 2017, 8, 239-248.	0.6	10
78	Xeroderma pigmentosum group C protein interacts with histones: regulation by acetylated states of histone H3. <i>Genes To Cells</i> , 2017, 22, 310-327.	0.5	22
79	Crystal structure of the overlapping dinucleosome composed of hexasome and octasome. <i>Science</i> , 2017, 356, 205-208.	6.0	77
80	Activation of the FA pathway mediated by phosphorylation and ubiquitination. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2017, 803-805, 89-95.	0.4	18
81	Structure and Dynamics of a 197Åbp Nucleosome in Complex with Linker Histone H1. <i>Molecular Cell</i> , 2017, 66, 384-397.e8.	4.5	225
82	Phosphorylation of CBX2 controls its nucleosome-binding specificity. <i>Journal of Biochemistry</i> , 2017, 162, 343-355.	0.9	31
83	Synthetic Posttranslational Modifications: Chemical Catalyst-Driven Regioselective Histone Acylation of Native Chromatin. <i>Journal of the American Chemical Society</i> , 2017, 139, 7568-7576.	6.6	60
84	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.	4.5	123
85	Synthetic Chromatin Acylation by an Artificial Catalyst System. <i>CheM</i> , 2017, 2, 840-859.	5.8	29
86	Histone Variant H2A.L2 Guides Transition Protein-Dependent Protamine Assembly in Male Germ Cells. <i>Molecular Cell</i> , 2017, 66, 89-101.e8.	4.5	116
87	Crystal Structure and Characterization of Novel Human Histone H3 Variants, H3.6, H3.7, and H3.8. <i>Biochemistry</i> , 2017, 56, 2184-2196.	1.2	20
88	Histone H3 Methylated at Arginine 17 Is Essential for Reprogramming the Paternal Genome in Zygotes. <i>Cell Reports</i> , 2017, 20, 2756-2765.	2.9	35
89	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.	3.1	56
90	<scp>SYCP</scp>3 regulates strand invasion activities of <scp>RAD</scp>51 and <scp>DMC</scp>1. <i>Genes To Cells</i> , 2017, 22, 799-809.	0.5	16

#	ARTICLE	IF	CITATIONS
91	Polymorphism of apyrimidinic DNA structures in the nucleosome. <i>Scientific Reports</i> , 2017, 7, 41783.	1.6	9
92	Influence of polynucleosome preparation methods on sedimentation velocity analysis of chromatin. <i>Journal of Biochemistry</i> , 2017, 161, 381-388.	0.9	5
93	InÂvitro reconstitution and biochemical analyses of the <i>Schizosaccharomyces pombe</i> nucleosome. <i>Biochemical and Biophysical Research Communications</i> , 2017, 482, 896-901.	1.0	10
94	Crystal Structure of Overlapping Dinucleosome, the New Basic Unit of Chromatin. <i>Seibutsu Butsuri</i> , 2017, 57, 309-311.	0.0	0
95	Parallel mapping with site-directed hydroxyl radicals and micrococcal nuclease reveals structural features of positioned nucleosomes in vivo. <i>PLoS ONE</i> , 2017, 12, e0186974.	1.1	5
96	Structure of the human DNA-repair protein RAD52 containing surface mutations. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 598-603.	0.4	5
97	Chromatin architecture may dictate the target site for DMC1, but not for RAD51, during homologous pairing. <i>Scientific Reports</i> , 2016, 6, 24228.	1.6	12
98	Structure and function of human histone H3.Y nucleosome. <i>Nucleic Acids Research</i> , 2016, 44, 6127-6141.	6.5	44
99	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. <i>Genome Biology</i> , 2016, 17, 36.	3.8	121
100	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.	6.5	44
101	The Flexible Ends of CENP-A Nucleosome Are Required for Mitotic Fidelity. <i>Molecular Cell</i> , 2016, 63, 674-685.	4.5	72
102	A Genetically Encoded Probe for Live-Cell Imaging of H4K20 Monomethylation. <i>Journal of Molecular Biology</i> , 2016, 428, 3885-3902.	2.0	52
103	Histone H3.5 forms an unstable nucleosome and accumulates around transcription start sites in human testis. <i>Epigenetics and Chromatin</i> , 2016, 9, 2.	1.8	53
104	Structural and biochemical analyses of monoubiquitinated human histones H2B and H4. <i>Open Biology</i> , 2016, 6, 160090.	1.5	35
105	Sequence-directed nucleosome-depletion is sufficient to activate transcription from a yeast core promoter in vivo. <i>Biochemical and Biophysical Research Communications</i> , 2016, 476, 57-62.	1.0	5
106	Relaxed Chromatin Formation and Weak Suppression of Homologous Pairing by the Testis-Specific Linker Histone H1T. <i>Biochemistry</i> , 2016, 55, 637-646.	1.2	8
107	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.	6.5	49
108	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.	0.5	21

#	ARTICLE	IF	CITATIONS
109	Crystal structure of the nucleosome containing ultraviolet light-induced cyclobutane pyrimidine dimer. <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 117-122.	1.0	17
110	Crystal structure of the nucleosome containing histone H3 with crotonylated lysine 122. <i>Biochemical and Biophysical Research Communications</i> , 2016, 469, 483-489.	1.0	17
111	Crystal structures of heterotypic nucleosomes containing histones H2A.Z and H2A. <i>Open Biology</i> , 2016, 6, 160127.	1.5	27
112	Structural basis of pyrimidine-pyrimidone (6â€“4) photoproduct recognition by UV-DDB in the nucleosome. <i>Scientific Reports</i> , 2015, 5, 16330.	1.6	39
113	Structure of RizA, an <i>L</i> -amino-acid ligase from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1125-1130.	0.4	11
114	Solution structure of variant H2A.Z.1 nucleosome investigated by small-angle X-ray and neutron scatterings. <i>Biochemistry and Biophysics Reports</i> , 2015, 4, 28-32.	0.7	10
115	Mutations in the Gene Encoding the E2 Conjugating Enzyme UBE2T Cause Fanconi Anemia. <i>American Journal of Human Genetics</i> , 2015, 96, 1001-1007.	2.6	100
116	Mass Spectrometric Approach for Characterizing the Disordered Tail Regions of the Histone H2A/H2B Dimer. <i>Analytical Chemistry</i> , 2015, 87, 2220-2227.	3.2	10
117	Human tNASP Promotes in Vitro Nucleosome Assembly with Histone H3.3. <i>Biochemistry</i> , 2015, 54, 1171-1179.	1.2	13
118	Chargeâ€“neutralization effect of the tail regions on the histone H ₂ A ₂ H ₂ B dimer structure. <i>Protein Science</i> , 2015, 24, 1224-1231.	3.1	4
119	Nucleosome organization and chromatin dynamics in telomeres. <i>Biomolecular Concepts</i> , 2015, 6, 67-75.	1.0	10
120	Human FAN1 promotes strand incision in 5â€“flapped DNA complexed with RPA. <i>Journal of Biochemistry</i> , 2015, 158, 263-270.	0.9	8
121	Cryogenic coherent x-ray diffraction imaging for biological non-crystalline particles using the KOTŒBUKI-1 diffraction apparatus at SACLA. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2015, 48, 184003.	0.6	32
122	Dynamic changes in CCAN organization through CENP-C during cell-cycle progression. <i>Molecular Biology of the Cell</i> , 2015, 26, 3768-3776.	0.9	62
123	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.	6.5	59
124	hCAS/CSE1L regulates RAD51 distribution and focus formation for homologous recombinational repair. <i>Genes To Cells</i> , 2015, 20, 681-694.	0.5	13
125	Influence of DNA methylation on positioning and DNA flexibility of nucleosomes with pericentric satellite DNA. <i>Open Biology</i> , 2015, 5, 150128.	1.5	22
126	Stable complex formation of CENP-B with the CENP-A nucleosome. <i>Nucleic Acids Research</i> , 2015, 43, 4909-4922.	6.5	59

#	ARTICLE	IF	CITATIONS
127	Two Arginine Residues Suppress the Flexibility of Nucleosomal DNA in the Canonical Nucleosome Core. PLoS ONE, 2015, 10, e0120635.	1.1	30
128	Evaluation of Chemical Fluorescent Dyes as a Protein Conjugation Partner for Live Cell Imaging. PLoS ONE, 2014, 9, e106271.	1.1	51
129	Defective FANCI Binding by a Fanconi Anemia-Related FANCD2 Mutant. PLoS ONE, 2014, 9, e114752.	1.1	5
130	The centromeric nucleosome-like CENPâ€“Tâ€“Wâ€“Sâ€“X complex induces positive supercoils into DNA. Nucleic Acids Research, 2014, 42, 1644-1655.	6.5	72
131	A method for evaluating nucleosome stability with a protein-binding fluorescent dye. Methods, 2014, 70, 119-126.	1.9	60
132	Sufficient Amounts of Functional HOP2/MND1 Complex Promote Interhomolog DNA Repair but Are Dispensable for Intersister DNA Repair during Meiosis in <i>Arabidopsis</i> . Plant Cell, 2014, 25, 4924-4940.	3.1	54
133	N-terminal phosphorylation of HP1± increases its nucleosome-binding specificity. Nucleic Acids Research, 2014, 42, 12498-12511.	6.5	63
134	Functional analyses of the C-terminal half of the <i>Saccharomyces cerevisiae</i> Rad52 protein. Nucleic Acids Research, 2014, 42, 941-951.	6.5	12
135	Telomeric repeats act as nucleosome-disfavouring sequences in vivo. Nucleic Acids Research, 2014, 42, 1541-1552.	6.5	20
136	Structure of human nucleosome containing the testis-specific histone variant TSH2B. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 444-449.	0.4	18
137	Compensatory Functions and Interdependency of the DNA-Binding Domain of BRCA2 with the BRCA1â€“PALB2â€“BRCA2 Complex. Cancer Research, 2014, 74, 797-807.	0.4	20
138	Expression and purification of human FANCI and FANCD2 using <i>Escherichia coli</i> cells. Protein Expression and Purification, 2014, 103, 8-15.	0.6	6
139	FANCD2 Binds CtIP and Regulates DNA-End Resection during DNA Interstrand Crosslink Repair. Cell Reports, 2014, 7, 1039-1047.	2.9	73
140	Mislocalization of the Centromeric Histone Variant CenH3/CENP-A in Human Cells Depends on the Chaperone DAXX. Molecular Cell, 2014, 53, 631-644.	4.5	214
141	Distinct Features of the Histone Core Structure in Nucleosomes Containing the Histone H2A.B Variant. Biophysical Journal, 2014, 106, 2206-2213.	0.2	26
142	Green fluorescent protein fused to the C terminus of RAD51 specifically interferes with secondary DNA binding by the RAD51-ssDNA complex. Genes and Genetic Systems, 2014, 89, 169-179.	0.2	16
143	2SDA-01 Structural basis of chromatin dynamics regulated by histone variants(2SDA Studies of) Tj ETQq1 1 0.784314 rgBT /Overlock	0.0	0
144	Crystal structure and stable property of the cancer-associated heterotypic nucleosome containing CENP-A and H3.3. Scientific Reports, 2014, 4, 7115.	1.6	64

#	ARTICLE	IF	CITATIONS
145	Nap1 stimulates homologous recombination by RAD51 and RAD54 in higher-ordered chromatin containing histone H1. <i>Scientific Reports</i> , 2014, 4, 4863.	1.6	27
146	DNA Binding Properties of the Actin-Related Protein Arp8 and Its Role in DNA Repair. <i>PLoS ONE</i> , 2014, 9, e108354.	1.1	16
147	Genetically encoded system to track histone modification in vivo. <i>Scientific Reports</i> , 2013, 3, 2436.	1.6	96
148	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.	1.2	56
149	Contribution of histone N-terminal tails to the structure and stability of nucleosomes. <i>FEBS Open Bio</i> , 2013, 3, 363-369.	1.0	105
150	Current progress on structural studies of nucleosomes containing histone H3 variants. <i>Current Opinion in Structural Biology</i> , 2013, 23, 109-115.	2.6	32
151	Purification and characterization of the fission yeast telomere clustering factors, Bqt1 and Bqt2. <i>Protein Expression and Purification</i> , 2013, 88, 207-213.	0.6	6
152	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.	3.2	22
153	Conclusive Evidence of the Reconstituted Hexasome Proven by Native Mass Spectrometry. <i>Biochemistry</i> , 2013, 52, 5155-5157.	1.2	26
154	Nap1 regulates proper CENP-B binding to nucleosomes. <i>Nucleic Acids Research</i> , 2013, 41, 2869-2880.	6.5	19
155	Vertebrate Spt2 is a novel nucleolar histone chaperone that assists in ribosomal DNA transcription. <i>Journal of Cell Science</i> , 2013, 126, 1323-32.	1.2	24
156	Interaction between Basic Residues of Epstein-Barr Virus EBNA1 Protein and Cellular Chromatin Mediates Viral Plasmid Maintenance. <i>Journal of Biological Chemistry</i> , 2013, 288, 24189-24199.	1.6	15
157	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
158	Crystallization and preliminary X-ray diffraction analysis of the secreted protein Athe_0614 from <i>Caldicellulosiruptor bescii</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 438-440.	0.7	4
159	Structural basis of a nucleosome containing histone H2A.B/H2A.Bbd that transiently associates with reorganized chromatin. <i>Scientific Reports</i> , 2013, 3, 3510.	1.6	61
160	2SCP-02 Structural versatility of nucleosomes in higher order chromatin(2SCP Functional dynamics) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.0	0
161	Nucleosome Structure. , 2013, , 1552-1556.		1
162	Homologous Pairing Activities of Two Rice RAD51 Proteins, RAD51A1 and RAD51A2. <i>PLoS ONE</i> , 2013, 8, e75451.	1.1	18

#	ARTICLE	IF	CITATIONS
163	DNA robustly stimulates FANCD2 monoubiquitylation in the complex with FANCI. <i>Nucleic Acids Research</i> , 2012, 40, 4553-4561.	6.5	79
164	Histone chaperone activity of Fanconi anemia proteins, FANCD2 and FANCI, is required for DNA crosslink repair. <i>EMBO Journal</i> , 2012, 31, 3524-3536.	3.5	61
165	RAD51 Plays a Crucial Role in Halting Cell Death Program Induced by Ionizing Radiation in Bovine Oocytes1. <i>Biology of Reproduction</i> , 2012, 86, 76.	1.2	17
166	Comparison between the CENP-A and histone H3 structures in nucleosomes. <i>Nucleus</i> , 2012, 3, 6-11.	0.6	27
167	ATR ATRIP Kinase Complex Triggers Activation of the Fanconi Anemia DNA Repair Pathway. <i>Cancer Research</i> , 2012, 72, 1149-1156.	0.4	62
168	Human PSF concentrates DNA and stimulates duplex capture in DMC1-mediated homologous pairing. <i>Nucleic Acids Research</i> , 2012, 40, 3031-3041.	6.5	7
169	Structural Analysis of the Hexasome, Lacking One Histone H2A/H2B Dimer from the Conventional Nucleosome. <i>Biochemistry</i> , 2012, 51, 3302-3309.	1.2	101
170	Chd2 interacts with H3.3 to determine myogenic cell fate. <i>EMBO Journal</i> , 2012, 31, 2994-3007.	3.5	117
171	Structure and Function of Centromeric Nucleosomes Containing CENP-A. <i>Seibutsu Butsuri</i> , 2012, 52, 220-225.	0.0	0
172	Purification of the Human SMN GEMIN2 Complex and Assessment of Its Stimulation of RAD51-Mediated DNA Recombination Reactions. <i>Biochemistry</i> , 2011, 50, 6797-6805.	1.2	20
173	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.	1.2	37
174	Crystal structure of the human centromeric nucleosome containing CENP-A. <i>Nature</i> , 2011, 476, 232-235.	13.7	336
175	Structure of the CENP-A nucleosome and its implications for centromeric chromatin architecture. <i>Genes and Genetic Systems</i> , 2011, 86, 357-364.	0.2	7
176	Halenaquinone, a chemical compound that specifically inhibits the secondary DNA binding of RAD51. <i>Genes To Cells</i> , 2011, 16, 427-436.	0.5	39
177	Structural and biochemical analyses of the human PAD4 variant encoded by a functional haplotype gene. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 112-118.	2.5	14
178	Structures of human nucleosomes containing major histone H3 variants. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 578-583.	2.5	96
179	Structural basis for the DNA-binding activity of the bacterial $\hat{\nu}^2$ -propeller protein YncE. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 1045-1053.	2.5	13
180	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.	3.3	169

#	ARTICLE	IF	CITATIONS
181	Biochemical analysis of the human ENA/VASP-family proteins, MENA, VASP and EVL, in homologous recombination. <i>Journal of Biochemistry</i> , 2011, 149, 721-729.	0.9	3
182	Tracking epigenetic histone modifications in single cells using Fab-based live endogenous modification labeling. <i>Nucleic Acids Research</i> , 2011, 39, 6475-6488.	6.5	219
183	Vital Roles of the Second DNA-binding Site of Rad52 Protein in Yeast Homologous Recombination. <i>Journal of Biological Chemistry</i> , 2011, 286, 17607-17617.	1.6	18
184	Direct Inhibition of TNF- β Promoter Activity by Fanconi Anemia Protein FANCD2. <i>PLoS ONE</i> , 2011, 6, e23324.	1.1	29
185	Deimination stabilizes histone H2A/H2B dimers as revealed by electrospray ionization mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2010, 45, 900-908.	0.7	20
186	Dynamics in the transmission of genetic information: from meiosis to postmeiotic events. <i>FEBS Journal</i> , 2010, 277, 564-564.	2.2	0
187	From meiosis to postmeiotic events: Uncovering the molecular roles of the meiosis-specific recombinase Dmc1. <i>FEBS Journal</i> , 2010, 277, 590-598.	2.2	40
188	Holliday junction-binding activity of human SPF45. <i>Genes To Cells</i> , 2010, 15, 373-383.	0.5	6
189	Enhancing Survival of Mouse Oocytes Following Chemotherapy or Aging by Targeting Bax and Rad51. <i>PLoS ONE</i> , 2010, 5, e9204.	1.1	51
190	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.	3.3	72
191	GEMIN2 promotes accumulation of RAD51 at double-strand breaks in homologous recombination. <i>Nucleic Acids Research</i> , 2010, 38, 5059-5074.	6.5	27
192	Single-stranded DNA catenation mediated by human EVL and a type I topoisomerase. <i>Nucleic Acids Research</i> , 2010, 38, 7579-7586.	6.5	4
193	The putative nuclear localization signal of the human RAD52 protein is a potential sumoylation site. <i>Journal of Biochemistry</i> , 2010, 147, 833-842.	0.9	16
194	Nucleosome Formation Activity of Human Somatic Nuclear Autoantigenic Sperm Protein (sNASP). <i>Journal of Biological Chemistry</i> , 2010, 285, 11913-11921.	1.6	54
195	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.	3.3	195
196	Human PSF binds to RAD51 and modulates its homologous-pairing and strand-exchange activities. <i>Nucleic Acids Research</i> , 2009, 37, 4296-4307.	6.5	51
197	Recombination Activator Function of the Novel RAD51- and RAD51B-binding Protein, Human EVL. <i>Journal of Biological Chemistry</i> , 2009, 284, 14326-14336.	1.6	17
198	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.	6.5	22

#	ARTICLE	IF	CITATIONS
199	Biochemical analysis of the human DMC1 Δ 37N polymorphism. FEBS Journal, 2009, 276, 457-465.	2.2	7
200	Biochemical analysis of the human EVL domains in homologous recombination. FEBS Journal, 2009, 276, 5841-5848.	2.2	2
201	c-ABL tyrosine kinase stabilizes RAD51 chromatin association. Biochemical and Biophysical Research Communications, 2009, 382, 286-291.	1.0	27
202	DIDS, a chemical compound that inhibits RAD51-mediated homologous pairing and strand exchange. Nucleic Acids Research, 2009, 37, 3367-3376.	6.5	59
203	The Lys313 residue of the human Rad51 protein negatively regulates the strand Δ exchange activity. Genes To Cells, 2008, 13, 91-103.	0.5	23
204	Inhibition of filament formation of human Rad51 protein by a small peptide derived from the BRCA Δ motif of the BRCA2 protein. Genes To Cells, 2008, 13, 471-481.	0.5	41
205	The actin-related protein hAtp8 accumulates on the mitotic chromosomes and functions in chromosome alignment. Experimental Cell Research, 2008, 314, 859-868.	1.2	28
206	Structural Analysis of the Human Rad51 Protein Δ DNA Complex Filament by Tryptophan Fluorescence Scanning Analysis: Transmission of Allosteric Effects between ATP Binding and DNA Binding. Journal of Molecular Biology, 2008, 383, 575-587.	2.0	9
207	A Common Mechanism for the ATP-DnaA-dependent Formation of Open Complexes at the Replication Origin. Journal of Biological Chemistry, 2008, 283, 8351-8362.	1.6	123
208	Filament formation and robust strand exchange activities of the rice DMC1A and DMC1B proteins. Nucleic Acids Research, 2008, 36, 4266-4276.	6.5	23
209	Nucleosome formation with the testis-specific histone H3 variant, H3t, by human nucleosome assembly proteins in vitro. Nucleic Acids Research, 2008, 36, 2208-2218.	6.5	78
210	Structural and functional analyses of the DMC1-M200V polymorphism found in the human population. Nucleic Acids Research, 2008, 36, 4181-4190.	6.5	33
211	Biochemical analysis of the N-terminal domain of human RAD54B. Nucleic Acids Research, 2008, 36, 5441-5450.	6.5	11
212	Identification of a Second DNA Binding Site in the Human Rad52 Protein. Journal of Biological Chemistry, 2008, 283, 24264-24273.	1.6	69
213	In Vivo and in Vitro Footprinting of Nucleosomes and Transcriptional Activators Using an Infrared-Fluorescence DNA Sequencer. Biological and Pharmaceutical Bulletin, 2008, 31, 187-192.	0.6	3
214	The interaction of DiaA and DnaA regulates the replication cycle in <i>E. coli</i> by directly promoting ATP Δ DnaA-specific initiation complexes. Genes and Development, 2007, 21, 2083-2099.	2.7	127
215	Altered DNA Binding by the Human Rad51-R150Q Mutant Found in Breast Cancer Patients. Biological and Pharmaceutical Bulletin, 2007, 30, 1374-1378.	0.6	14
216	HIV-1 Vpr induces ATM-dependent cellular signal with enhanced homologous recombination. Oncogene, 2007, 26, 477-486.	2.6	50

#	ARTICLE	IF	CITATIONS
217	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.	5.0	55
218	Roles of the human Rad51 L1 and L2 loops in DNA binding. <i>FEBS Journal</i> , 2006, 273, 3148-3159.	2.2	52
219	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.	0.5	33
220	Stimulation of Dmc1-mediated DNA strand exchange by the human Rad54B protein. <i>Nucleic Acids Research</i> , 2006, 34, 4429-4437.	6.5	20
221	HIV-1 Vpr Induces DNA Double-Strand Breaks. <i>Cancer Research</i> , 2006, 66, 627-631.	0.4	69
222	Stimulation of DNA Strand Exchange by the Human TBPIP/Hop2-Mnd1 Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 5575-5581.	1.6	49
223	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.	2.3	230
224	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.	1.6	22
225	Human Centromere Protein B Induces Translational Positioning of Nucleosomes on α -Satellite Sequences. <i>Journal of Biological Chemistry</i> , 2005, 280, 41609-41618.	1.6	53
226	A FancD2-Monoubiquitin Fusion Reveals Hidden Functions of Fanconi Anemia Core Complex in DNA Repair. <i>Molecular Cell</i> , 2005, 19, 841-847.	4.5	134
227	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.	6.5	84
228	Structural and biochemical analyses of hemimethylated DNA binding by the SeqA protein. <i>Nucleic Acids Research</i> , 2004, 32, 82-92.	6.5	28
229	Positive Role of the Mammalian TBPIP/HOP2 Protein in DMC1-mediated Homologous Pairing. <i>Journal of Biological Chemistry</i> , 2004, 279, 35263-35272.	1.6	43
230	CpG methylation of the CENP-B box reduces human CENP-B binding. <i>FEBS Journal</i> , 2004, 272, 282-289.	2.2	35
231	Mutational analyses of the human Rad51-Tyr315 residue, a site for phosphorylation in leukaemia cells. <i>Genes To Cells</i> , 2004, 9, 781-790.	0.5	24
232	Expression and purification of recombinant human histones. <i>Methods</i> , 2004, 33, 3-11.	1.9	153
233	Location of Tyrosine 315, a Target for Phosphorylation by cAbl Tyrosine Kinase, at the Edge of the Subunit-Subunit Interface of the Human Rad51 Filament. <i>Journal of Molecular Biology</i> , 2004, 339, 797-804.	2.0	27
234	Structural Basis for Octameric Ring Formation and DNA Interaction of the Human Homologous-Pairing Protein Dmc1. <i>Molecular Cell</i> , 2004, 14, 363-374.	4.5	99

#	ARTICLE	IF	CITATIONS
235	Identification of functional domains of the Escherichia coli SeqA protein. <i>Biochemical and Biophysical Research Communications</i> , 2003, 300, 699-705.	1.0	9
236	Incorporation of DUF/FACT into chromatin enhances the accessibility of nucleosomal DNA. <i>Biochemical and Biophysical Research Communications</i> , 2003, 303, 8-13.	1.0	6
237	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.	1.6	26
238	Region and amino acid residues required for Rad51C binding in the human Xrcc3 protein. <i>Nucleic Acids Research</i> , 2003, 31, 4041-4050.	6.5	16
239	Holliday Junction Binding Activity of the Human Rad51B Protein. <i>Journal of Biological Chemistry</i> , 2003, 278, 2767-2772.	1.6	54
240	Structural basis of replication origin recognition by the DnaA protein. <i>Nucleic Acids Research</i> , 2003, 31, 2077-2086.	6.5	183
241	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.	6.5	48
242	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.	1.6	72
243	Structural and functional analyses of proteins involved in translation, DNA recombination, chromosome architecture, and signal transduction. <i>Progress in Biotechnology</i> , 2002, 22, 169-180.	0.2	0
244	Crystal Structure of the Homologous-Pairing Domain from the Human Rad52 Recombinase in the Undecameric Form. <i>Molecular Cell</i> , 2002, 10, 359-371.	4.5	210
245	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.	3.5	97
246	Homologous Pairing Promoted by the Human Rad52 Protein. <i>Journal of Biological Chemistry</i> , 2001, 276, 35201-35208.	1.6	142
247	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.	3.3	123
248	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.	3.3	64
249	Structural genomics projects in Japan. <i>Progress in Biophysics and Molecular Biology</i> , 2000, 73, 363-376.	1.4	49
250	Specific defects in double-stranded DNA unwinding and homologous pairing of a mutant RecA protein. <i>FEBS Letters</i> , 2000, 477, 129-134.	1.3	8
251	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.	2.0	134
252	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.	2.0	71

#	ARTICLE	IF	CITATIONS
253	The Mutant RecA Proteins, RecAR243Q and RecAK245N, Exhibit Defective DNA Binding in Homologous Pairing. Archives of Biochemistry and Biophysics, 1999, 365, 83-91.	1.4	29
254	The Nucleosome: A Powerful Regulator of Transcription. Progress in Molecular Biology and Translational Science, 1998, 61, 379-422.	1.9	92
255	An interaction between a specified surface of the C-terminal domain of RecA protein and double-stranded DNA for homologous pairing. Journal of Molecular Biology, 1997, 274, 213-221.	2.0	80
256	Histone acetylation: influence on transcription, nucleosome mobility and positioning, and linker histone-dependent transcriptional repression. EMBO Journal, 1997, 16, 2096-2107.	3.5	207
257	Functional domains for assembly of histones H3 and H4 into the chromatin of Xenopus embryos. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 12780-12785.	3.3	42
258	A Possible Role of the C-terminal Domain of the RecA Protein. Journal of Biological Chemistry, 1996, 271, 33515-33524.	1.6	72
259	Solution structure of the DNA binding domain of a nucleoid-associated protein, H-NS, from Escherichia coli. FEBS Letters, 1995, 360, 125-131.	1.3	121
260	A chimeric Rec-A protein that implicates non-Watson-Crick interactions in homologous pairing. Nucleic Acids Research, 1994, 22, 3387-3391.	6.5	16
261	Proton NMR Study on a Histone-like Protein, HU.ALPHA., from Escherichia coli and Its Complex with Oligo DNAs.. Biological and Pharmaceutical Bulletin, 1993, 16, 437-443.	0.6	5
262	Specific and nonspecific interactions of integration host factor with oligo DNAs as revealed by circular dichroism spectroscopy and filter binding assay. Archives of Biochemistry and Biophysics, 1992, 295, 297-301.	1.4	4