

Hiroshi Kimura

List of Publications by Year in descending order

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Version: 2024-02-01

212
papers

10,660
citations

41323

49
h-index

45285

90
g-index

239
all docs

239
docs citations

239
times ranked

13536
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	Live imaging of transcription sites using an elongating RNA polymerase II-specific probe. <i>Journal of Cell Biology</i> , 2022, 221, .	2.3	22
3	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
4	Cryo-EM Analysis of Chromatin. <i>Nihon Kessho Gakkaishi</i> , 2022, 64, 65-68.	0.0	0
5	Imaging transcription elongation dynamics by new technologies unveils the organization of initiation and elongation in transcription factories. <i>Current Opinion in Cell Biology</i> , 2022, 74, 71-79.	2.6	11
6	A <i>Drosophila</i> toolkit for HA-tagged proteins unveils a block in autophagy flux in the last instar larval fat body. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	2
7	Characteristic H3 N-tail dynamics in the nucleosome core particle, nucleosome, and chromatosome. <i>IScience</i> , 2022, 25, 103937.	1.9	5
8	Single-cell profiling of transcriptome and histone modifications with EpiDamID. <i>Molecular Cell</i> , 2022, 82, 1956-1970.e14.	4.5	28
9	Locus-specific induction of gene expression from heterochromatin loci during cellular senescence. <i>Nature Aging</i> , 2022, 2, 31-45.	5.3	12
10	Contributions of Histone Variants in Nucleosome Structure and Function. <i>Journal of Molecular Biology</i> , 2021, 433, 166678.	2.0	49
11	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
12	Structural basis of nucleosomal histone H4 lysine 20 methylation by SET8 methyltransferase. <i>Life Science Alliance</i> , 2021, 4, e202000919.	1.3	17
13	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
14	Variable immersion microscopy with a high numerical aperture. <i>Optics Letters</i> , 2021, 46, 856.	1.7	1
15	Evidence for divergence of DNA methylation maintenance and a conserved inhibitory mechanism from DNA demethylation in chickens and mammals. <i>Genes and Genomics</i> , 2021, 43, 269-280.	0.5	3
16	Transcription organizes euchromatin via microphase separation. <i>Nature Communications</i> , 2021, 12, 1360.	5.8	83
17	Dynamics of transcription-mediated conversion from euchromatin to facultative heterochromatin at the Xist promoter by Tsix. <i>Cell Reports</i> , 2021, 34, 108912.	2.9	9
18	The SUN2-nesprin-2 LINC complex and KIF20A function in the Golgi dispersal. <i>Scientific Reports</i> , 2021, 11, 5358.	1.6	10

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19	RNA polymerase II condensate formation and association with Cajal and histone locus bodies in living human cells. <i>Genes To Cells</i> , 2021, 26, 298-312.	0.5	13
20	Attrition of X Chromosome Inactivation in Aged Hematopoietic Stem Cells. <i>Stem Cell Reports</i> , 2021, 16, 708-716.	2.3	10
21	Simple Fluorogenic Cellular Assay for Histone Deacetylase Inhibitors Based on Split-Yellow Fluorescent Protein and Intrabodies. <i>ACS Omega</i> , 2021, 6, 10039-10046.	1.6	3
22	Identification of Rpd3 as a novel epigenetic regulator of Drosophila FIG 4, a Charcot-Marie-Tooth disease-causing gene. <i>NeuroReport</i> , 2021, 32, 562-568.	0.6	1
23	A live imaging system to analyze spatiotemporal dynamics of RNA polymerase II modification in <i>Arabidopsis thaliana</i> . <i>Communications Biology</i> , 2021, 4, 580.	2.0	5
24	Chromatin structure-dependent histone incorporation revealed by a genome-wide deposition assay. <i>ELife</i> , 2021, 10, .	2.8	6
25	Ubiquitination-dependent and -independent repression of target genes by SETDB1 reveal a context-dependent role for its methyltransferase activity during adipogenesis. <i>Genes To Cells</i> , 2021, 26, 513-529.	0.5	6
26	Live-cell imaging reveals the spatiotemporal organization of endogenous RNA polymerase II phosphorylation at a single gene. <i>Nature Communications</i> , 2021, 12, 3158.	5.8	36
27	Live-cell imaging probes to track chromatin modification dynamics. <i>Microscopy (Oxford, England)</i> , 2021, 70, 415-422.	0.7	16
28	Cryptic promoter activation occurs by at least two different mechanisms in the <i>Arabidopsis</i> genome. <i>Plant Journal</i> , 2021, 108, 29-39.	2.8	3
29	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
30	Visualizing looping of two endogenous genomic loci using synthetic zinc-finger proteins with anti-FLAG and anti-HA frankenbodies in living cells. <i>Genes To Cells</i> , 2021, 26, 905-926.	0.5	15
31	Recent advances in single-cell epigenomics. <i>Current Opinion in Structural Biology</i> , 2021, 71, 116-122.	2.6	14
32	Cryo-EM structure of the CENP-A nucleosome in complex with phosphorylated CENP-C. <i>EMBO Journal</i> , 2021, 40, e105671.	3.5	35
33	Chromatin loading of MCM hexamers is associated with di-/tri-methylation of histone H4K20 toward S-phase entry. <i>Nucleic Acids Research</i> , 2021, 49, 12152-12166.	6.5	12
34	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
35	Modeling population size independent tissue epigenomes by ChIP-seq with single thin sections. <i>Molecular Systems Biology</i> , 2021, 17, e10323.	3.2	1
36	High-throughput single-cell epigenomic profiling by targeted insertion of promoters (TIP-seq). <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	19

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37	Spatiotemporal dynamics of SETD5-containing NCoR ¹ HDAC3 complex determines enhancer activation for adipogenesis. <i>Nature Communications</i> , 2021, 12, 7045.	5.8	10
38	Cryo-EM Structures of Centromeric Tri-nucleosomes Containing a Central CENP-A Nucleosome. <i>Structure</i> , 2020, 28, 44-53.e4.	1.6	47
39	CENP-B creates alternative epigenetic chromatin states permissive for CENP-A or heterochromatin assembly. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	32
40	Subnuclear gene positioning through lamina association affects copper tolerance. <i>Nature Communications</i> , 2020, 11, 5914.	5.8	37
41	Essentiality of CENP-A Depends on Its Binding Mode to HJURP. <i>Cell Reports</i> , 2020, 33, 108388.	2.9	9
42	Transcription-dependent cohesin repositioning rewires chromatin loops in cellular senescence. <i>Nature Communications</i> , 2020, 11, 6049.	5.8	42
43	Single-molecule imaging reveals control of parental histone recycling by free histones during DNA replication. <i>Science Advances</i> , 2020, 6, .	4.7	43
44	Structural basis for the inhibition of cGAS by nucleosomes. <i>Science</i> , 2020, 370, 455-458.	6.0	149
45	Chromatin integration labeling for mapping DNA-binding proteins and modifications with low input. <i>Nature Protocols</i> , 2020, 15, 3334-3360.	5.5	12
46	Genome-wide kinetic properties of transcriptional bursting in mouse embryonic stem cells. <i>Science Advances</i> , 2020, 6, eaaz6699.	4.7	66
47	Coordinated demethylation of H3K9 and H3K27 is required for rapid inflammatory responses of endothelial cells. <i>EMBO Journal</i> , 2020, 39, e103949.	3.5	37
48	Histone modification dynamics as revealed by a multicolor immunofluorescence-based single-cell analysis. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	19
49	H3K9me3 maintenance on a Human Artificial Chromosome is required for segregation but not centromere epigenetic memory. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	15
50	Kinase inhibition profiles as a tool to identify kinases for specific phosphorylation sites. <i>Nature Communications</i> , 2020, 11, 1684.	5.8	22
51	G9a is involved in the regulation of cranial bone formation through activation of Runx2 function during development. <i>Bone</i> , 2020, 137, 115332.	1.4	15
52	Synthetic hyperacetylation of nucleosomal histones. <i>RSC Chemical Biology</i> , 2020, 1, 56-59.	2.0	12
53	Cohesin and condensin extrude DNA loops in a cell cycle-dependent manner. <i>ELife</i> , 2020, 9, .	2.8	158
54	Biochemical analysis of nucleosome targeting by Tn5 transposase. <i>Open Biology</i> , 2019, 9, 190116.	1.5	14

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55	Intrabody-based FRET probe to visualize endogenous histone acetylation. <i>Scientific Reports</i> , 2019, 9, 10188.	1.6	10
56	Cyclization of Single-Chain Fv Antibodies Markedly Suppressed Their Characteristic Aggregation Mediated by Inter-Chain VH-VL Interactions. <i>Molecules</i> , 2019, 24, 2620.	1.7	20
57	A genetically encoded probe for imaging nascent and mature HA-tagged proteins in vivo. <i>Nature Communications</i> , 2019, 10, 2947.	5.8	72
58	Reduction of Rpd3 suppresses defects in locomotive ability and neuronal morphology induced by the knockdown of <i>Drosophila</i> SLC25A46 via an epigenetic pathway. <i>Experimental Cell Research</i> , 2019, 385, 111673.	1.2	7
59	Preparation of single-chain Fv antibodies in the cytoplasm of <i>Escherichia coli</i> by simplified and systematic chaperone optimization. <i>Journal of Biochemistry</i> , 2019, 166, 455-462.	0.9	8
60	The NSL complex maintains nuclear architecture stability via lamin A/C acetylation. <i>Nature Cell Biology</i> , 2019, 21, 1248-1260.	4.6	61
61	Pathogenic Epigenetic Consequences of Genetic Alterations in IDH-Wild-Type Diffuse Astrocytic Gliomas. <i>Cancer Research</i> , 2019, 79, 4814-4827.	0.4	6
62	Identification of a chemical modulator of EZH2-mediated silencing by cell-based high-throughput screening assay. <i>Journal of Biochemistry</i> , 2019, 166, 41-50.	0.9	10
63	A mosaic of old and young nucleoporins. <i>Journal of Cell Biology</i> , 2019, 218, 385-386.	2.3	0
64	Effect of mycalolides isolated from a marine sponge <i>Mycale aff. nullarosette</i> on actin in living cells. <i>Scientific Reports</i> , 2019, 9, 7540.	1.6	9
65	Single nucleosome imaging reveals loose genome chromatin networks via active RNA polymerase II. <i>Journal of Cell Biology</i> , 2019, 218, 1511-1530.	2.3	162
66	The CENP-A centromere targeting domain facilitates H4K20 monomethylation in the nucleosome by structural polymorphism. <i>Nature Communications</i> , 2019, 10, 576.	5.8	28
67	A truncated form of a transcription factor Mamo activates vasa in <i>Drosophila</i> embryos. <i>Communications Biology</i> , 2019, 2, 422.	2.0	5
68	Heterochromatin suppresses gross chromosomal rearrangements at centromeres by repressing Tfs1/TFIIS-dependent transcription. <i>Communications Biology</i> , 2019, 2, 17.	2.0	24
69	Pioneer Factor NeuroD1 Rearranges Transcriptional and Epigenetic Profiles to Execute Microglia-Neuron Conversion. <i>Neuron</i> , 2019, 101, 472-485.e7.	3.8	161
70	A chromatin integration labelling method enables epigenomic profiling with lower input. <i>Nature Cell Biology</i> , 2019, 21, 287-296.	4.6	121
71	Histone demethylase JMJD1A coordinates acute and chronic adaptation to cold stress via thermogenic phospho-switch. <i>Nature Communications</i> , 2018, 9, 1566.	5.8	68
72	Histone H3.3 sub-variant H3mm7 is required for normal skeletal muscle regeneration. <i>Nature Communications</i> , 2018, 9, 1400.	5.8	23

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73	HELLS and CDCA7 comprise a bipartite nucleosome remodeling complex defective in ICF syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E876-E885.	3.3	88
74	Structural Basis of Heterochromatin Formation by Human HP1. <i>Molecular Cell</i> , 2018, 69, 385-397.e8.	4.5	196
75	Loss of Sfpq Causes Long-Gene Transcriptopathy in the Brain. <i>Cell Reports</i> , 2018, 23, 1326-1341.	2.9	75
76	Combined Loss of JMJD1A and JMJD1B Reveals Critical Roles for H3K9 Demethylation in the Maintenance of Embryonic Stem Cells and Early Embryogenesis. <i>Stem Cell Reports</i> , 2018, 10, 1340-1354.	2.3	23
77	Roles of histone H3.5 in human spermatogenesis and spermatogenic disorders. <i>Andrology</i> , 2018, 6, 158-165.	1.9	19
78	H3S10ph broadly marks early-replicating domains in interphase ESCs and shows reciprocal antagonism with H3K9me2. <i>Genome Research</i> , 2018, 28, 37-51.	2.4	43
79	Visualizing the Dynamics of Inactive X Chromosomes in Living Cells Using Antibody-Based Fluorescent Probes. <i>Methods in Molecular Biology</i> , 2018, 1861, 91-102.	0.4	15
80	JQ1 affects BRD2-dependent and independent transcription regulation without disrupting H4-hyperacetylated chromatin states. <i>Epigenetics</i> , 2018, 13, 410-431.	1.3	32
81	Methods for Preparing Nucleosomes Containing Histone Variants. <i>Methods in Molecular Biology</i> , 2018, 1832, 3-20.	0.4	47
82	Modular Redesign of a Cationic Lytic Peptide To Promote the Endosomal Escape of Biomacromolecules. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 12771-12774.	7.2	28
83	Modular Redesign of a Cationic Lytic Peptide To Promote the Endosomal Escape of Biomacromolecules. <i>Angewandte Chemie</i> , 2018, 130, 12953-12956.	1.6	5
84	Testis-Specific Histone Variant H3t Gene Is Essential for Entry into Spermatogenesis. <i>Cell Reports</i> , 2017, 18, 593-600.	2.9	82
85	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
86	Histone H3 Lysine 27 Trimethylation Leads to Loss of Mesendodermal Competence During Gastrulation in Zebrafish Ectodermal Cells. <i>Zoological Science</i> , 2017, 34, 64.	0.3	5
87	Differential lactate and cholesterol synthetic activities in XY and XX Sertoli cells. <i>Scientific Reports</i> , 2017, 7, 41912.	1.6	4
88	Live imaging of H3K9 acetylation in plant cells. <i>Scientific Reports</i> , 2017, 7, 45894.	1.6	15
89	Essential roles of G9a in cell proliferation and differentiation during tooth development. <i>Experimental Cell Research</i> , 2017, 357, 202-210.	1.2	11
90	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

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91	Synthetic Chromatin Acylation by an Artificial Catalyst System. <i>CheM</i> , 2017, 2, 840-859.	5.8	29
92	Global histone modification fingerprinting in human cells using epigenetic reverse phase protein array. <i>Cell Death Discovery</i> , 2017, 3, 16077.	2.0	12
93	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
94	Reduction in chromosome mobility accompanies nuclear organization during early embryogenesis in <i>Caenorhabditis elegans</i> . <i>Scientific Reports</i> , 2017, 7, 3631.	1.6	24
95	Epigenetic regulation of starvation-induced autophagy in <i>Drosophila</i> by histone methyltransferase G9a. <i>Scientific Reports</i> , 2017, 7, 7343.	1.6	31
96	Ser7 of RNAPII-CTD facilitates heterochromatin formation by linking ncRNA to RNAi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11208-E11217.	3.3	13
97	Influence of polynucleosome preparation methods on sedimentation velocity analysis of chromatin. <i>Journal of Biochemistry</i> , 2017, 161, 381-388.	0.9	5
98	Inhibition of RIF1 by SCAI Allows BRCA1-Mediated Repair. <i>Cell Reports</i> , 2017, 20, 297-307.	2.9	24
99	Impact of nucleic acid and methylated H3K9 binding activities of Suv39h1 on its heterochromatin assembly. <i>ELife</i> , 2017, 6, .	2.8	61
100	Targeted DNA methylation in pericentromeres with genome editing-based artificial DNA methyltransferase. <i>PLoS ONE</i> , 2017, 12, e0177764.	1.1	28
101	Semi-quantitative Analysis of H4K20me1 Levels in Living Cells Using Mintbody. <i>Bio-protocol</i> , 2017, 7, e2276.	0.2	3
102	Identification of Immunoglobulin Gene Sequences from a Small Read Number of mRNA-Seq Using Hybridomas. <i>PLoS ONE</i> , 2016, 11, e0165473.	1.1	11
103	The Histone Deacetylase Gene Rpd3 Is Required for Starvation Stress Resistance. <i>PLoS ONE</i> , 2016, 11, e0167554.	1.1	14
104	Genome-wide genetic screen identified the link between dG9a and epidermal growth factor receptor signaling pathway in vivo. <i>Experimental Cell Research</i> , 2016, 346, 53-64.	1.2	4
105	Targeting the Notch-regulated non-coding RNA TUG1 for glioma treatment. <i>Nature Communications</i> , 2016, 7, 13616.	5.8	267
106	Structure and function of human histone H3.Y nucleosome. <i>Nucleic Acids Research</i> , 2016, 44, 6127-6141.	6.5	44
107	Setdb1 maintains hematopoietic stem and progenitor cells by restricting the ectopic activation of nonhematopoietic genes. <i>Blood</i> , 2016, 128, 638-649.	0.6	61
108	Polycomb-dependent nucleolus localization of Jumonji/Jarid2 during <i>Drosophila</i> spermatogenesis. <i>Spermatogenesis</i> , 2016, 6, e1232023.	0.8	3

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109	KAT7/HBO1/MYST2 Regulates CENP-A Chromatin Assembly by Antagonizing Suv39h1-Mediated Centromere Inactivation. <i>Developmental Cell</i> , 2016, 37, 413-427.	3.1	78
110	Pericentric H3K9me3 Formation by HP1 Interaction-defective Histone Methyltransferase Suv39h1. <i>Cell Structure and Function</i> , 2016, 41, 145-152.	0.5	15
111	Histone H4 lysine 20 acetylation is associated with gene repression in human cells. <i>Scientific Reports</i> , 2016, 6, 24318.	1.6	40
112	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
113	<i>In vivo</i> tracking of histone H3 lysine 9 acetylation in <i>Xenopus laevis</i> during tail regeneration. <i>Genes To Cells</i> , 2016, 21, 358-369.	0.5	29
114	Epigenetic engineering shows that a human centromere resists silencing mediated by H3K27me3/K9me3. <i>Molecular Biology of the Cell</i> , 2016, 27, 177-196.	0.9	30
115	Histone H3K36 trimethylation is essential for multiple silencing mechanisms in fission yeast. <i>Nucleic Acids Research</i> , 2016, 44, 4147-4162.	6.5	44
116	Chromatin-prebound Crm1 recruits Nup98-HoxA9 fusion to induce aberrant expression of Hox cluster genes. <i>ELife</i> , 2016, 5, e09540.	2.8	45
117	Genomewide identification of target genes of histone methyltransferase dG9a during <i>Drosophila</i> embryogenesis. <i>Genes To Cells</i> , 2015, 20, 902-914.	0.5	12
118	Histone Acetylation on <i>Drosophila</i> Polytene Chromosomes Visualized by Mintbody. <i>Cytologia</i> , 2015, 80, 383-384.	0.2	8
119	Histone H4 acetylation required for chromatin decompaction during DNA replication. <i>Scientific Reports</i> , 2015, 5, 12720.	1.6	31
120	Tissue-specific expression of histone H3 variants diversified after species separation. <i>Epigenetics and Chromatin</i> , 2015, 8, 35.	1.8	51
121	The histone chaperone DAXX maintains the structural organization of heterochromatin domains. <i>Epigenetics and Chromatin</i> , 2015, 8, 44.	1.8	24
122	CENP-C and CENP-I are key connecting factors for kinetochore and CENP-A assembly. <i>Journal of Cell Science</i> , 2015, 128, 4572-87.	1.2	58
123	SUV420H2 suppresses breast cancer cell invasion through down regulation of the SH2 domain-containing focal adhesion protein tensin-3. <i>Experimental Cell Research</i> , 2015, 334, 90-99.	1.2	37
124	H3K36 Trimethylation-Mediated Epigenetic Regulation is Activated by Bam and Promotes Germ Cell Differentiation During Early Oogenesis in <i>Drosophila</i> . <i>Biology Open</i> , 2015, 4, 119-124.	0.6	11
125	Incorporation of histone H3.1 suppresses the lineage potential of skeletal muscle. <i>Nucleic Acids Research</i> , 2015, 43, 775-786.	6.5	34
126	Coordinated expression of H3K9 histone methyltransferases during tooth development in mice. <i>Histochemistry and Cell Biology</i> , 2015, 143, 259-266.	0.8	18

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127	Phenotype Specific Analyses Reveal Distinct Regulatory Mechanism for Chronically Activated p53. <i>PLoS Genetics</i> , 2015, 11, e1005053.	1.5	47
128	Mammalian NET-Seq Reveals Genome-wide Nascent Transcription Coupled to RNA Processing. <i>Cell</i> , 2015, 161, 526-540.	13.5	466
129	H3K9MTase G9a is essential for the differentiation and growth of tenocytes in vitro. <i>Histochemistry and Cell Biology</i> , 2015, 144, 13-20.	0.8	14
130	Quantitative Dynamics of Chromatin Remodeling during Germ Cell Specification from Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2015, 16, 517-532.	5.2	166
131	Highly condensed chromatins are formed adjacent to subtelomeric and decondensed silent chromatin in fission yeast. <i>Nature Communications</i> , 2015, 6, 7753.	5.8	64
132	JMJD1A is a signal-sensing scaffold that regulates acute chromatin dynamics via SWI/SNF association for thermogenesis. <i>Nature Communications</i> , 2015, 6, 7052.	5.8	87
133	Stable complex formation of CENP-B with the CENP-A nucleosome. <i>Nucleic Acids Research</i> , 2015, 43, 4909-4922.	6.5	59
134	STAT5 Orchestrates Local Epigenetic Changes for Chromatin Accessibility and Rearrangements by Direct Binding to the TCRI ³ Locus. <i>Journal of Immunology</i> , 2015, 195, 1804-1814.	0.4	16
135	Distribution of histone H4 modifications as revealed by a panel of specific monoclonal antibodies. <i>Chromosome Research</i> , 2015, 23, 753-766.	1.0	49
136	Visualizing posttranslational and epigenetic modifications of endogenous proteins in vivo. <i>Histochemistry and Cell Biology</i> , 2015, 144, 101-109.	0.8	49
137	H3K4/H3K9me3 Bivalent Chromatin Domains Targeted by Lineage-Specific DNA Methylation Pauses Adipocyte Differentiation. <i>Molecular Cell</i> , 2015, 60, 584-596.	4.5	180
138	Visualization of Epigenetic Modifications in Preimplantation Embryos. <i>Methods in Molecular Biology</i> , 2015, 1222, 127-147.	0.4	12
139	An Insulator Element Located at the Cyclin B1 Interacting Protein 1 Gene Locus Is Highly Conserved among Mammalian Species. <i>PLoS ONE</i> , 2015, 10, e0131204.	1.1	6
140	Methylation of RNA polymerase II non-consensus Lysine residues marks early transcription in mammalian cells. <i>ELife</i> , 2015, 4, .	2.8	34
141	Evaluation of Chemical Fluorescent Dyes as a Protein Conjugation Partner for Live Cell Imaging. <i>PLoS ONE</i> , 2014, 9, e106271.	1.1	51
142	Quantifying histone and RNA polymerase II post-translational modification dynamics in mother and daughter cells. <i>Methods</i> , 2014, 70, 77-88.	1.9	16
143	A method for evaluating nucleosome stability with a protein-binding fluorescent dye. <i>Methods</i> , 2014, 70, 119-126.	1.9	60
144	Loss of histone H4K20 trimethylation predicts poor prognosis in breast cancer and is associated with invasive activity. <i>Breast Cancer Research</i> , 2014, 16, R66.	2.2	75

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145	Regulation of RNA polymerase II activation by histone acetylation in single living cells. <i>Nature</i> , 2014, 516, 272-275.	13.7	237
146	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.	4.5	214
147	Heterochromatin Dynamics during the Differentiation Process Revealed by the DNA Methylation Reporter Mouse, MethylRO. <i>Stem Cell Reports</i> , 2014, 2, 910-924.	2.3	40
148	Histone modifications for human epigenome analysis. <i>Journal of Human Genetics</i> , 2013, 58, 439-445.	1.1	371
149	Epigenetics of eu- and heterochromatin in inverted and conventional nuclei from mouse retina. <i>Chromosome Research</i> , 2013, 21, 535-554.	1.0	53
150	Predominant expression of H3K9 methyltransferases in prehypertrophic and hypertrophic chondrocytes during mouse growth plate cartilage development. <i>Gene Expression Patterns</i> , 2013, 13, 84-90.	0.3	17
151	Genetically encoded system to track histone modification in vivo. <i>Scientific Reports</i> , 2013, 3, 2436.	1.6	96
152	Hinge and Chromoshadow of HP1± Participate in Recognition of K9 Methylated Histone H3 in Nucleosomes. <i>Journal of Molecular Biology</i> , 2013, 425, 54-70.	2.0	44
153	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
154	Redistribution of the Lamin B1 genomic binding profile affects rearrangement of heterochromatic domains and SAHF formation during senescence. <i>Genes and Development</i> , 2013, 27, 1800-1808.	2.7	259
155	Lamin B Receptor Recognizes Specific Modifications of Histone H4 in Heterochromatin Formation. <i>Journal of Biological Chemistry</i> , 2012, 287, 42654-42663.	1.6	95
156	Reliable detection of epigenetic histone marks and nuclear proteins in tissue cryosections. <i>Chromosome Research</i> , 2012, 20, 849-858.	1.0	22
157	Independence of Repressive Histone Marks and Chromatin Compaction during Senescent Heterochromatic Layer Formation. <i>Molecular Cell</i> , 2012, 47, 203-214.	4.5	258
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