

Peter B Becker

List of Publications by Year in descending order

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157
papers

14,672
citations

22153

59
h-index

20358

116
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170
all docs

170
docs citations

170
times ranked

10923
citing authors

#	ARTICLE	IF	CITATIONS
1	Self-organization of microtubules into bipolar spindles around artificial chromosomes in <i>Xenopus</i> egg extracts. <i>Nature</i> , 1996, 382, 420-425.	27.8	921
2	Histone acetylation: a switch between repressive and permissive chromatin. <i>EMBO Reports</i> , 2002, 3, 224-229.	4.5	813
3	ATP-Dependent Nucleosome Remodeling. <i>Annual Review of Biochemistry</i> , 2002, 71, 247-273.	11.1	681
4	ATP-dependent nucleosome disruption at a heat-shock promoter mediated by binding of GAGA transcription factor. <i>Nature</i> , 1994, 367, 525-532.	27.8	663
5	Chromatin-remodelling factor CHRAC contains the ATPases ISWI and topoisomerase II. <i>Nature</i> , 1997, 388, 598-602.	27.8	484
6	Activation of Transcription through Histone H4 Acetylation by MOF, an Acetyltransferase Essential for Dosage Compensation in <i>Drosophila</i> . <i>Molecular Cell</i> , 2000, 5, 367-375.	9.7	429
7	Molecular cloning and expression of a hexameric <i>Drosophila</i> heat shock factor subject to negative regulation. <i>Cell</i> , 1990, 63, 1085-1097.	28.9	372
8	Genomic footprinting reveals cell type-specific DNA binding of ubiquitous factors. <i>Cell</i> , 1987, 51, 435-443.	28.9	364
9	Chromodomains are protein-RNA interaction modules. <i>Nature</i> , 2000, 407, 405-409.	27.8	364
10	In vivo protein-DNA interactions in a glucocorticoid response element require the presence of the hormone. <i>Nature</i> , 1986, 324, 686-688.	27.8	346
11	Nucleosome Movement by CHRAC and ISWI without Disruption or trans-Displacement of the Histone Octamer. <i>Cell</i> , 1999, 97, 843-852.	28.9	314
12	A CAF-1-PCNA-Mediated Chromatin Assembly Pathway Triggered by Sensing DNA Damage. <i>Molecular and Cellular Biology</i> , 2000, 20, 1206-1218.	2.3	294
13	Nucleosome Remodeling and Epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a017905-a017905.	5.5	255
14	Crystal Structure and Functional Analysis of a Nucleosome Recognition Module of the Remodeling Factor ISWI. <i>Molecular Cell</i> , 2003, 12, 449-460.	9.7	239
15	The histone H4 acetyltransferase MOF uses a C2HC zinc finger for substrate recognition. <i>EMBO Reports</i> , 2001, 2, 113-118.	4.5	231
16	The DNA chaperone HMGB1 facilitates ACF/CHRAC-dependent nucleosome sliding. <i>EMBO Journal</i> , 2002, 21, 6865-6873.	7.8	219
17	ISWI Is an ATP-Dependent Nucleosome Remodeling Factor. <i>Molecular Cell</i> , 1999, 3, 239-245.	9.7	205
18	Dosage compensation: the beginning and end of generalization. <i>Nature Reviews Genetics</i> , 2007, 8, 47-57.	16.3	204

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19	Critical Role for the Histone H4 N Terminus in Nucleosome Remodeling by ISWI. <i>Molecular and Cellular Biology</i> , 2001, 21, 875-883.	2.3	202
20	Modulation of ISWI function by site-specific histone acetylation. <i>EMBO Reports</i> , 2002, 3, 242-247.	4.5	202
21	Physical and functional association of SU(VAR)3 and HDAC1 in <i>Drosophila</i> . <i>EMBO Reports</i> , 2001, 2, 915-919.	4.5	186
22	Nucleosome mobilization and positioning by ISWI-containing chromatin-remodeling factors. <i>Journal of Cell Science</i> , 2001, 114, 2561-2568.	2.0	172
23	The many colours of chromodomains. <i>BioEssays</i> , 2004, 26, 133-140.	2.5	161
24	The Chromosomal High-Affinity Binding Sites for the <i>Drosophila</i> Dosage Compensation Complex. <i>PLoS Genetics</i> , 2008, 4, e1000302.	3.5	161
25	Active promoters and insulators are marked by the centrosomal protein 190. <i>EMBO Journal</i> , 2009, 28, 877-888.	7.8	145
26	Active promoters give rise to false positive "Phantom Peaks" in ChIP-seq experiments. <i>Nucleic Acids Research</i> , 2015, 43, 6959-6968.	14.5	144
27	ATP-dependent nucleosome remodelling: factors and functions. <i>Journal of Cell Science</i> , 2004, 117, 3707-3711.	2.0	143
28	Chromosome-wide gene-specific targeting of the <i>Drosophila</i> dosage compensation complex. <i>Genes and Development</i> , 2006, 20, 858-870.	5.9	142
29	A critical epitope for substrate recognition by the nucleosome remodeling ATPase ISWI. <i>Nucleic Acids Research</i> , 2002, 30, 649-655.	14.5	137
30	The dMi-2 chromodomains are DNA binding modules important for ATP-dependent nucleosome mobilization. <i>EMBO Journal</i> , 2002, 21, 2430-2440.	7.8	132
31	Chromatin-remodeling factors: machines that regulate?. <i>Current Opinion in Cell Biology</i> , 1998, 10, 346-353.	5.4	128
32	ISWI Induces Nucleosome Sliding on Nicked DNA. <i>Molecular Cell</i> , 2001, 8, 1085-1092.	9.7	125
33	Nucleosome remodeling: one mechanism, many phenomena?. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1677, 58-63.	2.4	123
34	Global and Specific Responses of the Histone Acetylome to Systematic Perturbation. <i>Molecular Cell</i> , 2015, 57, 559-571.	9.7	119
35	Life span extension by targeting a link between metabolism and histone acetylation in <i>Drosophila</i> . <i>EMBO Reports</i> , 2016, 17, 455-469.	4.5	116
36	Electrostatic Mechanism of Nucleosome Spacing. <i>Journal of Molecular Biology</i> , 1995, 252, 305-313.	4.2	115

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37	Two-Step Synergism between the Progesterone Receptor and the DNA-Binding Domain of Nuclear Factor 1 on MMTV Minichromosomes. <i>Molecular Cell</i> , 1999, 4, 45-54.	9.7	114
38	Functional integration of the histone acetyltransferase MOF into the dosage compensation complex. <i>EMBO Journal</i> , 2004, 23, 2258-2268.	7.8	108
39	Nucleosome Binding by the Bromodomain and PHD Finger of the Transcriptional Cofactor p300. <i>Journal of Molecular Biology</i> , 2004, 337, 773-788.	4.2	108
40	ACF1 improves the effectiveness of nucleosome mobilization by ISWI through PHD-histone contacts. <i>EMBO Journal</i> , 2004, 23, 4029-4039.	7.8	102
41	NEW EMBO MEMBER'S REVIEW: Nucleosome sliding: facts and fiction. <i>EMBO Journal</i> , 2002, 21, 4749-4753.	7.8	99
42	Functional Delineation of Three Groups of the ATP-dependent Family of Chromatin Remodeling Enzymes. <i>Journal of Biological Chemistry</i> , 2000, 275, 18864-18870.	3.4	95
43	Regulation of higher-order chromatin structures by nucleosome-remodelling factors. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 151-156.	3.3	94
44	Combined Use of RNAi and Quantitative Proteomics to Study Gene Function in <i>Drosophila</i> . <i>Molecular Cell</i> , 2008, 31, 762-772.	9.7	93
45	Nucleosome sliding mechanisms: new twists in a looped history. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1026-1032.	8.2	92
46	The <i>Drosophila</i> MSL complex activates the transcription of target genes. <i>Genes and Development</i> , 2005, 19, 2284-2288.	5.9	91
47	Beads on a string nucleosome array arrangements and folding of the chromatin fiber. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 109-118.	8.2	86
48	ATP-Dependent roX RNA Remodeling by the Helicase maleless Enables Specific Association of MSL Proteins. <i>Molecular Cell</i> , 2013, 51, 174-184.	9.7	84
49	The establishment of active promoters in chromatin. <i>BioEssays</i> , 1994, 16, 541-547.	2.5	81
50	Different chromatin interfaces of the <i>Drosophila</i> dosage compensation complex revealed by high-shear ChIP-seq. <i>Genome Research</i> , 2013, 23, 473-485.	5.5	78
51	The ATPase domain of ISWI is an autonomous nucleosome remodeling machine. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 82-89.	8.2	77
52	Recruitment of the Nucleolar Remodeling Complex NoRC Establishes Ribosomal DNA Silencing in Chromatin. <i>Molecular and Cellular Biology</i> , 2004, 24, 1791-1798.	2.3	76
53	Sequence-Specific Targeting of <i>Drosophila</i> roX Genes by the MSL Dosage Compensation Complex. <i>Molecular Cell</i> , 2003, 11, 977-986.	9.7	73
54	The Histone Fold Subunits of <i>Drosophila</i> CHRAC Facilitate Nucleosome Sliding through Dynamic DNA Interactions. <i>Molecular and Cellular Biology</i> , 2005, 25, 9886-9896.	2.3	71

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55	Targeting Determinants of Dosage Compensation in Drosophila. <i>PLoS Genetics</i> , 2006, 2, e5.	3.5	71
56	Genome-wide measurement of local nucleosome array regularity and spacing by nanopore sequencing. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 894-901.	8.2	68
57	Chapter 12 Chromatin Assembly Extracts from Drosophila Embryos. <i>Methods in Cell Biology</i> , 1994, 44, 207-223.	1.1	67
58	Dosage compensation and the global re-balancing of aneuploid genomes. <i>Genome Biology</i> , 2010, 11, 216.	9.6	67
59	Structure of the RNA Helicase MLE Reveals the Molecular Mechanisms for Uridine Specificity and RNA-ATP Coupling. <i>Molecular Cell</i> , 2015, 60, 487-499.	9.7	67
60	Tramtrack69 interacts with the dMiã€2 subunit of theDrosophilaNuRD chromatin remodelling complex. <i>EMBO Reports</i> , 2001, 2, 1089-1094.	4.5	65
61	The DNA binding CXC domain of MSL2 is required for faithful targeting the Dosage Compensation Complex to the X chromosome. <i>Nucleic Acids Research</i> , 2010, 38, 3209-3221.	14.5	65
62	PionX sites mark the X chromosome for dosage compensation. <i>Nature</i> , 2016, 537, 244-248.	27.8	65
63	A finger on the mark. <i>Nature</i> , 2006, 442, 31-32.	27.8	64
64	The MOF-containing NSL complex associates globally with housekeeping genes, but activates only a defined subset. <i>Nucleic Acids Research</i> , 2012, 40, 1509-1522.	14.5	64
65	The Activation Potential of MOF Is Constrained for Dosage Compensation. <i>Molecular Cell</i> , 2010, 38, 815-826.	9.7	63
66	Role for hACF1 in the G2/M damage checkpoint. <i>Nucleic Acids Research</i> , 2011, 39, 8445-8456.	14.5	62
67	Ran Binds to Chromatin by Two Distinct Mechanisms. <i>Current Biology</i> , 2002, 12, 1151-1156.	3.9	58
68	Heat Shock Factor Increases the Reinitiation Rate from Potentiated Chromatin Templates. <i>Molecular and Cellular Biology</i> , 1998, 18, 361-367.	2.3	56
69	The Novel Transcription Factor e(y)2 Interacts with TAF II 40 and Potentiates Transcription Activation on Chromatin Templates. <i>Molecular and Cellular Biology</i> , 2001, 21, 5223-5231.	2.3	55
70	The variant histone H2A.V of Drosophilaã€”three roles, two guises. <i>Chromosoma</i> , 2013, 122, 245-258.	2.2	55
71	Global Analysis of the Relationship between JIL-1 Kinase and Transcription. <i>PLoS Genetics</i> , 2011, 7, e1001327.	3.5	55
72	Lifting a chromosome: dosage compensation in Drosophila melanogaster. <i>FEBS Letters</i> , 2004, 567, 8-14.	2.8	54

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73	The dosage compensation complex shapes the conformation of the X chromosome in <i>Drosophila</i> . <i>Genes and Development</i> , 2009, 23, 2490-2495.	5.9	54
74	Solid phase DNase I footprinting: quick and versatile. <i>Nucleic Acids Research</i> , 1994, 22, 1511-1512.	14.5	52
75	Dynamic chromatin: concerted nucleosome remodelling and acetylation. <i>Biological Chemistry</i> , 2005, 386, 745-51.	2.5	51
76	The MRG Domain Mediates the Functional Integration of MSL3 into the Dosage Compensation Complex. <i>Molecular and Cellular Biology</i> , 2005, 25, 5947-5954.	2.3	48
77	Dual regulation of the <i>Drosophila</i> hsp26 promoter in vitro. <i>Nucleic Acids Research</i> , 1995, 23, 2479-2487.	14.5	47
78	The Effect of Nucleosome Phasing Sequences and DNA Topology on Nucleosome Spacing. <i>Journal of Molecular Biology</i> , 1996, 260, 1-8.	4.2	47
79	The <i>Drosophila</i> Polycomb Protein Interacts with Nucleosomal Core Particles In Vitro via Its Repression Domain. <i>Molecular and Cellular Biology</i> , 1999, 19, 8451-8460.	2.3	47
80	ACF catalyses chromosome movements in chromatin fibres. <i>EMBO Journal</i> , 2008, 27, 817-826.	7.8	45
81	Probing the Conformation of the ISWI ATPase Domain With Genetically Encoded Photoreactive Crosslinkers and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.012088.	3.8	45
82	Rapid Purification of Recombinant Histones. <i>PLoS ONE</i> , 2014, 9, e104029.	2.5	45
83	HMG-D and Histone H1 Interplay during Chromatin Assembly and Early Embryogenesis. <i>Journal of Biological Chemistry</i> , 2001, 276, 37569-37576.	3.4	40
84	Site-specific acetylation of ISWI by GCN5. <i>BMC Molecular Biology</i> , 2007, 8, 73.	3.0	40
85	Structure-function analysis of the RNA helicase maleless. <i>Nucleic Acids Research</i> , 2008, 36, 950-962.	14.5	40
86	The bifunctional protein DCoH modulates interactions of the homeodomain transcription factor HNF1 with nucleic acids 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1997, 265, 20-29.	4.2	39
87	Chromosome topology guides the <i>Drosophila</i> Dosage Compensation Complex for target gene activation. <i>EMBO Reports</i> , 2017, 18, 1854-1868.	4.5	39
88	Stable chromosomal association of MSL2 defines a dosage-compensated nuclear compartment. <i>Chromosoma</i> , 2005, 114, 352-364.	2.2	34
89	Cumulative contributions of weak DNA determinants to targeting the <i>Drosophila</i> dosage compensation complex. <i>Nucleic Acids Research</i> , 2007, 35, 3561-3572.	14.5	34
90	<i>Drosophila</i> ISWI Regulates the Association of Histone H1 With Interphase Chromosomes <i>in Vivo</i> . <i>Genetics</i> , 2009, 182, 661-669.	2.9	34

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91	Modifications of the Histone N-Terminal Domains: Evidence for an "Epigenetic Code"?. <i>Molecular Biotechnology</i> , 2001, 17, 01-14.	2.4	33
92	High levels of histone H3 acetylation at the CMV promoter are predictive of stable expression in Chinese hamster ovary cells. <i>Biotechnology Progress</i> , 2016, 32, 776-786.	2.6	33
93	The glutamine-rich domain of the Drosophila GAGA factor is necessary for amyloid fibre formation in vitro , but not for chromatin remodelling 1 Edited by M. Yaniv. <i>Journal of Molecular Biology</i> , 1999, 285, 527-544.	4.2	32
94	Transcription modulation chromosome-wide: universal features and principles of dosage compensation in worms and flies. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 147-153.	3.3	31
95	MSL2 Combines Sensor and Effector Functions in Homeostatic Control of the Drosophila Dosage Compensation Machinery. <i>Molecular Cell</i> , 2012, 48, 647-654.	9.7	31
96	Genome-wide Rules of Nucleosome Phasing in Drosophila. <i>Molecular Cell</i> , 2018, 72, 661-672.e4.	9.7	31
97	Assembly of MMTV promoter minichromosomes with positioned nucleosomes precludes NF1 access but not restriction enzyme cleavage. <i>Nucleic Acids Research</i> , 1998, 26, 3657-3666.	14.5	30
98	The Histone-Fold Protein CHRAC14 Influences Chromatin Composition in Response to DNA Damage. <i>Cell Reports</i> , 2014, 7, 321-330.	6.4	30
99	UNR facilitates the interaction of MLE with the lncRNA roX2 during Drosophila dosage compensation. <i>Nature Communications</i> , 2014, 5, 4762.	12.8	30
100	Factor cooperation for chromosome discrimination in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2019, 47, 1706-1724.	14.5	30
101	An improved protocol for genomic sequencing and footprinting by ligation-mediated PCR. <i>Nucleic Acids Research</i> , 1993, 21, 2779-2781.	14.5	29
102	Nucleosome Remodeler SNF2L Suppresses Cell Proliferation and Migration and Attenuates Wnt Signaling. <i>Molecular and Cellular Biology</i> , 2012, 32, 2359-2371.	2.3	29
103	Structural basis of X chromosome DNA recognition by the MSL2 CXC domain during <i>Drosophila</i> dosage compensation. <i>Genes and Development</i> , 2014, 28, 2652-2662.	5.9	28
104	The Architecture of the Heat-inducible <i>Drosophila</i> hsp27 Promoter in Nuclei. <i>Journal of Molecular Biology</i> , 1996, 256, 249-263.	4.2	26
105	Dosage compensation in flies: Mechanism, models, mystery. <i>FEBS Letters</i> , 2005, 579, 3258-3263.	2.8	26
106	CHRAC/ACF contribute to the repressive ground state of chromatin. <i>Life Science Alliance</i> , 2018, 1, e201800024.	2.8	26
107	Developmental role for ACF1-containing nucleosome remodellers in chromatin organisation. <i>Development (Cambridge)</i> , 2010, 137, 3513-3522.	2.5	25
108	Nucleosome dynamics and epigenetic stability. <i>Essays in Biochemistry</i> , 2010, 48, 63-74.	4.7	25

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109	Gene Regulation by Histone H1: New Links to DNA Methylation. <i>Cell</i> , 2005, 123, 1178-1179.	28.9	24
110	ISWI Remodelling of Physiological Chromatin Fibres Acetylated at Lysine 16 of Histone H4. <i>PLoS ONE</i> , 2014, 9, e88411.	2.5	24
111	A Nucleosome Sliding Assay for Chromatin Remodeling Factors. <i>Methods in Enzymology</i> , 2003, 377, 344-353.	1.0	21
112	Phosphorylation of SU(VAR)3 ϵ 9 by the Chromosomal Kinase JIL-1. <i>PLoS ONE</i> , 2010, 5, e10042.	2.5	21
113	Roles of long, non-coding RNA in chromosome-wide transcription regulation: Lessons from two dosage compensation systems. <i>Biochimie</i> , 2012, 94, 1490-1498.	2.6	20
114	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. <i>Cell Systems</i> , 2016, 2, 49-58.	6.2	19
115	ATP-dependent chromatosome remodeling. <i>Biological Chemistry</i> , 2008, 389, 345-352.	2.5	18
116	DNA sequence and the organization of chromosomal domains. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 175-180.	3.3	18
117	JASPer controls interphase histone H3S10 phosphorylation by chromosomal kinase JIL-1 in <i>Drosophila</i> . <i>Nature Communications</i> , 2019, 10, 5343.	12.8	18
118	Transcription factor-mediated chromatin remodelling: mechanisms and models. <i>FEBS Letters</i> , 1995, 369, 118-121.	2.8	17
119	Biochemical Analysis of Chromatin Structure and Function Using <i>Drosophila</i> Embryo Extracts. <i>Methods</i> , 1997, 12, 28-35.	3.8	17
120	Acetylation increases access of remodelling complexes to their nucleosome targets to enhance initiation of V(D)J recombination. <i>Nucleic Acids Research</i> , 2007, 35, 6311-6321.	14.5	17
121	Splice variants of the SWR1-type nucleosome remodeling factor Domino have distinct functions during <i>Drosophila melanogaster</i> oogenesis. <i>Development (Cambridge)</i> , 2016, 143, 3154-3167.	2.5	17
122	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of <i>Drosophila</i> helicase Maleless. <i>Nucleic Acids Research</i> , 2019, 47, 4319-4333.	14.5	17
123	Variation on a theme: Evolutionary strategies for H2A.Z exchange by SWR1-type remodelers. <i>Current Opinion in Cell Biology</i> , 2021, 70, 1-9.	5.4	17
124	A role for tuned levels of nucleosome remodeler subunit ACF1 during <i>Drosophila</i> oogenesis. <i>Developmental Biology</i> , 2016, 411, 217-230.	2.0	16
125	Comment on <i>Drosophila</i> Dosage Compensation Involves Enhanced Pol II Recruitment to Male X-Linked Promoters. <i>Science</i> , 2013, 340, 273-273.	12.6	15
126	Nucleosome remodelers on track. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 732-733.	8.2	14

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127	Drosophila SWR1 and NuA4 complexes are defined by DOMINO isoforms. <i>ELife</i> , 2020, 9, .	6.0	14
128	Drosophilachromatin and transcription. <i>Seminars in Cell Biology</i> , 1995, 6, 185-190.	3.4	12
129	Analysis of modulators of chromatin structure in <i>Drosophila</i> . <i>Methods in Enzymology</i> , 1999, 304, 742-757.	1.0	12
130	Preparation of Chromatin Assembly Extracts from Preblastoderm <i>Drosophila</i> Embryos. , 1999, 119, 187-194.		12
131	Two-step mechanism for selective incorporation of lncRNA into a chromatin modifier. <i>Nucleic Acids Research</i> , 2020, 48, 7483-7501.	14.5	12
132	Divergent evolution toward sex chromosome-specific gene regulation in <i>Drosophila</i> . <i>Genes and Development</i> , 2021, 35, 1055-1070.	5.9	12
133	A Solid-Phase Approach for the Analysis of Reconstituted Chromatin. , 1999, 119, 195-206.		11
134	Ubiquitylation of the acetyltransferase MOF in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2017, 12, e0177408.	2.5	11
135	Solid phase technology improves coupled gel shift/footprinting analysis. <i>Nucleic Acids Research</i> , 1997, 25, 453-454.	14.5	10
136	Preparation of Chromatin Assembly Extracts from Preblastoderm <i>Drosophila</i> Embryos. <i>Methods in Molecular Biology</i> , 2009, 523, 1-10.	0.9	10
137	Form and function of dosage-compensated chromosomes – a chicken-and-egg relationship. <i>BioEssays</i> , 2010, 32, 709-717.	2.5	9
138	Progressive dosage compensation during <i>Drosophila</i> embryogenesis is reflected by gene arrangement. <i>EMBO Reports</i> , 2019, 20, e48138.	4.5	9
139	[40] Footprinting of DNA-binding proteins in intact cells. <i>Methods in Enzymology</i> , 1993, 218, 568-587.	1.0	6
140	Structural and Functional Analysis of Chromatin Assembled from Defined Histones. <i>Methods</i> , 1998, 15, 343-353.	3.8	6
141	Reconstitution and Analysis of Hyperacetylated Chromatin. , 1999, 119, 207-218.		6
142	Genomic Footprinting of <i>Drosophila</i> Embryo Nuclei by Linker Tag Selection LM-PCR. <i>Methods</i> , 1997, 11, 171-179.	3.8	5
143	Cell-free genomics reveal intrinsic, cooperative and competitive determinants of chromatin interactions. <i>Nucleic Acids Research</i> , 2021, 49, 7602-7617.	14.5	5
144	lncRNA <i>RUS</i> shapes the gene expression program towards neurogenesis. <i>Life Science Alliance</i> , 2022, 5, e202201504.	2.8	5

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145	Computational study of remodeling in a nucleosomal array. <i>European Physical Journal E</i> , 2015, 38, 85.	1.6	4
146	A <i>Drosophila</i> cell-free system that senses DNA breaks and triggers phosphorylation signalling. <i>Nucleic Acids Research</i> , 2019, 47, 7444-7459.	14.5	4
147	Analysis of Activator-Dependent Transcription Reinitiation In Vitro. <i>Methods in Enzymology</i> , 2003, 370, 487-501.	1.0	3
148	A Defined In Vitro System to Study ATP-Dependent Remodeling of Short Chromatin Fibers. <i>Methods in Molecular Biology</i> , 2012, 833, 255-270.	0.9	3
149	Wolfram HÃ¶rz 1944â€“2005. <i>Cell</i> , 2006, 124, 13-14.	28.9	2
150	Analysis of Reconstituted Chromatin Using a Solid-Phase Approach. <i>Methods in Molecular Biology</i> , 2009, 523, 11-25.	0.9	1
151	Determination of Unknown Genomic Sequences Without Cloning. , 1996, 65, 119-132.		0
152	MOF, an Acetyl Transferase Involved in Dosage Compensation in <i>Drosophila</i> , Uses a CCHC Finger for Substrate Recognition. , 2005, , 247-251.		0
153	Beads-on-a-String on a Bead: Reconstitution and Analysis of Chromatin on a Solid Support. <i>Methods in Molecular Biology</i> , 2015, 1288, 1-14.	0.9	0
154	Identification of Intrinsic RNA Binding Specificity of Purified Proteins by in vitro RNA Immunoprecipitation (vitRIP). <i>Bio-protocol</i> , 2021, 11, e3946.	0.4	0
155	Determination of Unknown Genomic Sequences Without Cloning. , 2003, , 373-383.		0
156	Nucleosome Remodelling and Epigenome Diversification. <i>Research and Perspectives in Neurosciences</i> , 2012, , 1-9.	0.4	0
157	Loss of nucleosome remodelers CHRAC/ACF does not sensitize early embryos to X-rays. <i>MicroPublication Biology</i> , 2020, 2020, .	0.1	0