

Peter B Becker

List of Publications by Year in descending order

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157
papers

14,672
citations

22153

59
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20358

116
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170
all docs

170
docs citations

170
times ranked

10923
citing authors

#	ARTICLE	IF	CITATIONS
1	LncRNA <i>linc-RUS</i> shapes the gene expression program towards neurogenesis. <i>Life Science Alliance</i> , 2022, 5, e202201504.	2.8	5
2	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
3	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
4	Divergent evolution toward sex chromosome-specific gene regulation in <i>Drosophila</i> . <i>Genes and Development</i> , 2021, 35, 1055-1070.	5.9	12
5	Cell-free genomics reveal intrinsic, cooperative and competitive determinants of chromatin interactions. <i>Nucleic Acids Research</i> , 2021, 49, 7602-7617.	14.5	5
6	Two-step mechanism for selective incorporation of lncRNA into a chromatin modifier. <i>Nucleic Acids Research</i> , 2020, 48, 7483-7501.	14.5	12
7	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
8	<i>Drosophila</i> SWR1 and NuA4 complexes are defined by DOMINO isoforms. <i>ELife</i> , 2020, 9, .	6.0	14
9	Loss of nucleosome remodelers CHRAC/ACF does not sensitize early embryos to X-rays. <i>MicroPublication Biology</i> , 2020, 2020, .	0.1	0
10	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
11	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
12	Progressive dosage compensation during <i>Drosophila</i> embryogenesis is reflected by gene arrangement. <i>EMBO Reports</i> , 2019, 20, e48138.	4.5	9
13	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
14	Factor cooperation for chromosome discrimination in <i>Drosophila</i> . <i>Nucleic Acids Research</i> , 2019, 47, 1706-1724.	14.5	30
15	Genome-wide Rules of Nucleosome Phasing in <i>Drosophila</i> . <i>Molecular Cell</i> , 2018, 72, 661-672.e4.	9.7	31
16	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
17	CHRAC/ACF contribute to the repressive ground state of chromatin. <i>Life Science Alliance</i> , 2018, 1, e201800024.	2.8	26
18	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

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19	Ubiquitylation of the acetyltransferase MOF in <i>Drosophila melanogaster</i> . PLoS ONE, 2017, 12, e0177408.	2.5	11
20	Life span extension by targeting a link between metabolism and histone acetylation in <i>Drosophila</i> . EMBO Reports, 2016, 17, 455-469.	4.5	116
21	Splice variants of the SWR1-type nucleosome remodeling factor Domino have distinct functions during <i>Drosophila melanogaster</i> oogenesis. Development (Cambridge), 2016, 143, 3154-3167.	2.5	17
22	PionX sites mark the X chromosome for dosage compensation. Nature, 2016, 537, 244-248.	27.8	65
23	High levels of histone H ₃ acetylation at the CMV promoter are predictive of stable expression in Chinese hamster ovary cells. Biotechnology Progress, 2016, 32, 776-786.	2.6	33
24	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. Cell Systems, 2016, 2, 49-58.	6.2	19
25	A role for tuned levels of nucleosome remodeler subunit ACF1 during <i>Drosophila</i> oogenesis. Developmental Biology, 2016, 411, 217-230.	2.0	16
26	Global and Specific Responses of the Histone Acetylome to Systematic Perturbation. Molecular Cell, 2015, 57, 559-571.	9.7	119
27	Active promoters give rise to false positive "Phantom Peaks"™ in ChIP-seq experiments. Nucleic Acids Research, 2015, 43, 6959-6968.	14.5	144
28	Beads-on-a-String on a Bead: Reconstitution and Analysis of Chromatin on a Solid Support. Methods in Molecular Biology, 2015, 1288, 1-14.	0.9	0
29	Computational study of remodeling in a nucleosomal array. European Physical Journal E, 2015, 38, 85.	1.6	4
30	Structure of the RNA Helicase MLE Reveals the Molecular Mechanisms for Uridine Specificity and RNA-ATP Coupling. Molecular Cell, 2015, 60, 487-499.	9.7	67
31	ISWI Remodelling of Physiological Chromatin Fibres Acetylated at Lysine 16 of Histone H4. PLoS ONE, 2014, 9, e88411.	2.5	24
32	Rapid Purification of Recombinant Histones. PLoS ONE, 2014, 9, e104029.	2.5	45
33	Structural basis of X chromosome DNA recognition by the MSL2 CXC domain during <i>Drosophila</i> dosage compensation. Genes and Development, 2014, 28, 2652-2662.	5.9	28
34	The Histone-Fold Protein CHRAC14 Influences Chromatin Composition in Response to DNA Damage. Cell Reports, 2014, 7, 321-330.	6.4	30
35	UNR facilitates the interaction of MLE with the lncRNA roX2 during <i>Drosophila</i> dosage compensation. Nature Communications, 2014, 5, 4762.	12.8	30
36	ATP-Dependent roX RNA Remodeling by the Helicase maleless Enables Specific Association of MSL Proteins. Molecular Cell, 2013, 51, 174-184.	9.7	84

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37	The variant histone H2A.V of <i>Drosophila</i> —three roles, two guises. <i>Chromosoma</i> , 2013, 122, 245-258.	2.2	55
38	Nucleosome sliding mechanisms: new twists in a looped history. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1026-1032.	8.2	92
39	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
40	Nucleosome Remodeling and Epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a017905-a017905.	5.5	255
41	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
42	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
43	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
44	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
45	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
46	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
47	MSL2 Combines Sensor and Effector Functions in Homeostatic Control of the <i>Drosophila</i> Dosage Compensation Machinery. <i>Molecular Cell</i> , 2012, 48, 647-654.	9.7	31
48	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
49	Nucleosome Remodelling and Epigenome Diversification. <i>Research and Perspectives in Neurosciences</i> , 2012, , 1-9.	0.4	0
50	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
51	Role for hACF1 in the G2/M damage checkpoint. <i>Nucleic Acids Research</i> , 2011, 39, 8445-8456.	14.5	62
52	Global Analysis of the Relationship between JIL-1 Kinase and Transcription. <i>PLoS Genetics</i> , 2011, 7, e1001327.	3.5	55
53	Form and function of dosage-compensated chromosomes—a chicken-and-egg relationship. <i>BioEssays</i> , 2010, 32, 709-717.	2.5	9
54	Developmental role for ACF1-containing nucleosome remodellers in chromatin organisation. <i>Development (Cambridge)</i> , 2010, 137, 3513-3522.	2.5	25

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55	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
56	The Activation Potential of MOF Is Constrained for Dosage Compensation. <i>Molecular Cell</i> , 2010, 38, 815-826.	9.7	63
57	Dosage compensation and the global re-balancing of aneuploid genomes. <i>Genome Biology</i> , 2010, 11, 216.	9.6	67
58	Nucleosome dynamics and epigenetic stability. <i>Essays in Biochemistry</i> , 2010, 48, 63-74.	4.7	25
59	Phosphorylation of SU(VAR)3 $\hat{=}$ 9 by the Chromosomal Kinase JIL-1. <i>PLoS ONE</i> , 2010, 5, e10042.	2.5	21
60	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
61	Preparation of Chromatin Assembly Extracts from Preblastoderm <i>Drosophila</i> Embryos. <i>Methods in Molecular Biology</i> , 2009, 523, 1-10.	0.9	10
62	Active promoters and insulators are marked by the centrosomal protein 190. <i>EMBO Journal</i> , 2009, 28, 877-888.	7.8	145
63	<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
64	Analysis of Reconstituted Chromatin Using a Solid-Phase Approach. <i>Methods in Molecular Biology</i> , 2009, 523, 11-25.	0.9	1
65	ACF catalyses chromatosome movements in chromatin fibres. <i>EMBO Journal</i> , 2008, 27, 817-826.	7.8	45
66	ATP-dependent chromatosome remodeling. <i>Biological Chemistry</i> , 2008, 389, 345-352.	2.5	18
67	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
68	DNA sequence and the organization of chromosomal domains. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 175-180.	3.3	18
69	Structure-function analysis of the RNA helicase maleless. <i>Nucleic Acids Research</i> , 2008, 36, 950-962.	14.5	40
70	The Chromosomal High-Affinity Binding Sites for the <i>Drosophila</i> Dosage Compensation Complex. <i>PLoS Genetics</i> , 2008, 4, e1000302.	3.5	161
71	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
72	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

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73	Site-specific acetylation of ISWI by GCN5. <i>BMC Molecular Biology</i> , 2007, 8, 73.	3.0	40
74	Dosage compensation: the beginning and end of generalization. <i>Nature Reviews Genetics</i> , 2007, 8, 47-57.	16.3	204
75	Wolfram HÄr rz 1944â€“2005. <i>Cell</i> , 2006, 124, 13-14.	28.9	2
76	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
77	A finger on the mark. <i>Nature</i> , 2006, 442, 31-32.	27.8	64
78	Targeting Determinants of Dosage Compensation in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2006, 2, e5.	3.5	71
79	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
80	Nucleosome remodelers on track. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 732-733.	8.2	14
81	Stable chromosomal association of MSL2 defines a dosage-compensated nuclear compartment. <i>Chromosoma</i> , 2005, 114, 352-364.	2.2	34
82	MOF, an Acetyl Transferase Involved in Dosage Compensation in <i>Drosophila</i> , Uses a CCHC Finger for Substrate Recognition. , 2005, , 247-251.		0
83	The <i>Drosophila</i> MSL complex activates the transcription of target genes. <i>Genes and Development</i> , 2005, 19, 2284-2288.	5.9	91
84	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
85	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
86	Gene Regulation by Histone H1: New Links to DNA Methylation. <i>Cell</i> , 2005, 123, 1178-1179.	28.9	24
87	Dosage compensation in flies: Mechanism, models, mystery. <i>FEBS Letters</i> , 2005, 579, 3258-3263.	2.8	26
88	Dynamic chromatin: concerted nucleosome remodelling and acetylation. <i>Biological Chemistry</i> , 2005, 386, 745-51.	2.5	51
89	ATP-dependent nucleosome remodelling: factors and functions. <i>Journal of Cell Science</i> , 2004, 117, 3707-3711.	2.0	143
90	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

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91	Functional integration of the histone acetyltransferase MOF into the dosage compensation complex. EMBO Journal, 2004, 23, 2258-2268.	7.8	108
92	ACF1 improves the effectiveness of nucleosome mobilization by ISWI through PHD-histone contacts. EMBO Journal, 2004, 23, 4029-4039.	7.8	102
93	Nucleosome remodeling: one mechanism, many phenomena?. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2004, 1677, 58-63.	2.4	123
94	The many colours of chromodomains. BioEssays, 2004, 26, 133-140.	2.5	161
95	Lifting a chromosome: dosage compensation in Drosophila melanogaster. FEBS Letters, 2004, 567, 8-14.	2.8	54
96	Nucleosome Binding by the Bromodomain and PHD Finger of the Transcriptional Cofactor p300. Journal of Molecular Biology, 2004, 337, 773-788.	4.2	108
97	A Nucleosome Sliding Assay for Chromatin Remodeling Factors. Methods in Enzymology, 2003, 377, 344-353.	1.0	21
98	Sequence-Specific Targeting of Drosophila roX Genes by the MSL Dosage Compensation Complex. Molecular Cell, 2003, 11, 977-986.	9.7	73
99	Crystal Structure and Functional Analysis of a Nucleosome Recognition Module of the Remodeling Factor ISWI. Molecular Cell, 2003, 12, 449-460.	9.7	239
100	Analysis of Activator-Dependent Transcription Reinitiation In Vitro. Methods in Enzymology, 2003, 370, 487-501.	1.0	3
101	Determination of Unknown Genomic Sequences Without Cloning. , 2003, , 373-383.		0
102	A critical epitope for substrate recognition by the nucleosome remodeling ATPase ISWI. Nucleic Acids Research, 2002, 30, 649-655.	14.5	137
103	Modulation of ISWI function by site-specific histone acetylation. EMBO Reports, 2002, 3, 242-247.	4.5	202
104	ATP-Dependent Nucleosome Remodeling. Annual Review of Biochemistry, 2002, 71, 247-273.	11.1	681
105	Ran Binds to Chromatin by Two Distinct Mechanisms. Current Biology, 2002, 12, 1151-1156.	3.9	58
106	Histone acetylation: a switch between repressive and permissive chromatin. EMBO Reports, 2002, 3, 224-229.	4.5	813
107	The dMi-2 chromodomains are DNA binding modules important for ATP-dependent nucleosome mobilization. EMBO Journal, 2002, 21, 2430-2440.	7.8	132
108	NEW EMBO MEMBER'S REVIEW: Nucleosome sliding: facts and fiction. EMBO Journal, 2002, 21, 4749-4753.	7.8	99

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109	The DNA chaperone HMGB1 facilitates ACF/CHRAC-dependent nucleosome sliding. <i>EMBO Journal</i> , 2002, 21, 6865-6873.	7.8	219
110	ISWI Induces Nucleosome Sliding on Nicked DNA. <i>Molecular Cell</i> , 2001, 8, 1085-1092.	9.7	125
111	Modifications of the Histone N-Terminal Domains: Evidence for an "Epigenetic Code"?. <i>Molecular Biotechnology</i> , 2001, 17, 01-14.	2.4	33
112	The histone H4 acetyltransferase MOF uses a C2HC zinc finger for substrate recognition. <i>EMBO Reports</i> , 2001, 2, 113-118.	4.5	231
113	Physical and functional association of SU(VAR)3 ϵ and HDAC1 in <i>Drosophila</i> . <i>EMBO Reports</i> , 2001, 2, 915-919.	4.5	186
114	Tramtrack69 interacts with the dMi ϵ 2 subunit of the <i>Drosophila</i> NuRD chromatin remodelling complex. <i>EMBO Reports</i> , 2001, 2, 1089-1094.	4.5	65
115	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
116	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
117	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
118	Nucleosome mobilization and positioning by ISWI-containing chromatin-remodeling factors. <i>Journal of Cell Science</i> , 2001, 114, 2561-2568.	2.0	172
119	Chromodomains are protein-RNA interaction modules. <i>Nature</i> , 2000, 407, 405-409.	27.8	364
120	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
121	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
122	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
123	A Solid-Phase Approach for the Analysis of Reconstituted Chromatin. , 1999, 119, 195-206.		11
124	Reconstitution and Analysis of Hyperacetylated Chromatin. , 1999, 119, 207-218.		6
125	Analysis of modulators of chromatin structure in <i>Drosophila</i> . <i>Methods in Enzymology</i> , 1999, 304, 742-757.	1.0	12
126	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

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127	ISWI Is an ATP-Dependent Nucleosome Remodeling Factor. <i>Molecular Cell</i> , 1999, 3, 239-245.	9.7	205
128	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
129	Preparation of Chromatin Assembly Extracts from Preblastoderm <i>Drosophila</i> Embryos. , 1999, 119, 187-194.		12
130	The glutamine-rich domain of the <i>Drosophila</i> 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
131	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
132	Chromatin-remodeling factors: machines that regulate?. <i>Current Opinion in Cell Biology</i> , 1998, 10, 346-353.	5.4	128
133	Structural and Functional Analysis of Chromatin Assembled from Defined Histones. <i>Methods</i> , 1998, 15, 343-353.	3.8	6
134	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
135	Heat Shock Factor Increases the Reinitiation Rate from Potentiated Chromatin Templates. <i>Molecular and Cellular Biology</i> , 1998, 18, 361-367.	2.3	56
136	Solid phase technology improves coupled gel shift/footprinting analysis. <i>Nucleic Acids Research</i> , 1997, 25, 453-454.	14.5	10
137	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
138	Genomic Footprinting of <i>Drosophila</i> Embryo Nuclei by Linker Tag Selection LM-PCR. <i>Methods</i> , 1997, 11, 171-179.	3.8	5
139	Biochemical Analysis of Chromatin Structure and Function Using <i>Drosophila</i> Embryo Extracts. <i>Methods</i> , 1997, 12, 28-35.	3.8	17
140	Chromatin-remodelling factor CHRAC contains the ATPases ISWI and topoisomerase II. <i>Nature</i> , 1997, 388, 598-602.	27.8	484
141	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
142	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
143	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
144	Determination of Unknown Genomic Sequences Without Cloning. , 1996, 65, 119-132.		0

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145	Drosophilachromatin and transcription. Seminars in Cell Biology, 1995, 6, 185-190.	3.4	12
146	Dual regulation of theDrosophillahsp26 promoterin vitro. Nucleic Acids Research, 1995, 23, 2479-2487.	14.5	47
147	Electrostatic Mechanism of Nucleosome Spacing. Journal of Molecular Biology, 1995, 252, 305-313.	4.2	115
148	Transcription factor-mediated chromatin remodelling: mechanisms and models. FEBS Letters, 1995, 369, 118-121.	2.8	17
149	Solid phase DNase I footprinting: quick and versatile. Nucleic Acids Research, 1994, 22, 1511-1512.	14.5	52
150	Chapter 12 Chromatin Assembly Extracts from Drosophila Embryos. Methods in Cell Biology, 1994, 44, 207-223.	1.1	67
151	The establishment of active promoters in chromatin. BioEssays, 1994, 16, 541-547.	2.5	81
152	ATP-dependent nucleosome disruption at a heat-shock promoter mediated by binding of GAGA transcription factor. Nature, 1994, 367, 525-532.	27.8	663
153	An improved protocol for genomic sequencing and footprinting by ligation-mediated PCR. Nucleic Acids Research, 1993, 21, 2779-2781.	14.5	29
154	[40] Footprinting of DNA-binding proteins in intact cells. Methods in Enzymology, 1993, 218, 568-587.	1.0	6
155	Molecular cloning and expression of a hexameric Drosophila heat shock factor subject to negative regulation. Cell, 1990, 63, 1085-1097.	28.9	372
156	Genomic footprinting reveals cell type-specific DNA binding of ubiquitous factors. Cell, 1987, 51, 435-443.	28.9	364
157	In vivo proteinâ€“DNA interactions in a glucocorticoid response element require the presence of the hormone. Nature, 1986, 324, 686-688.	27.8	346