Peter B Becker

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

155 papers	12,709 citations	57 h-index	111 g-index
170 ext. papers	13,815 ext. citations	12.8 avg, IF	6.4 L-index

#	Paper	IF	Citations
155	Divergent evolution toward sex chromosome-specific gene regulation in. *Genes and Development*, **2021**, 35, 1055-1070	12.6	1
154	Cell-free genomics reveal intrinsic, cooperative and competitive determinants of chromatin interactions. *Nucleic Acids Research*, **2021**, 49, 7602-7617	20.1	1
153	Variation on a theme: Evolutionary strategies for H2A.Z exchange by SWR1-type remodelers. *Current Opinion in Cell Biology*, **2021**, 70, 1-9	9	7
152	Identification of Intrinsic RNA Binding Specificity of Purified Proteins by RNA Immunoprecipitation (vitRIP). *Bio-protocol*, **2021**, 11, e3946	0.9	
151	Two-step mechanism for selective incorporation of lncRNA into a chromatin modifier. *Nucleic Acids Research*, **2020**, 48, 7483-7501	20.1	6
150	Beads on a string-nucleosome array arrangements and folding of the chromatin fiber. *Nature Structural and Molecular Biology*, **2020**, 27, 109-118	17.6	41
149	SWR1 and NuA4 complexes are defined by DOMINO isoforms. *ELife*, **2020**, 9,	8.9	8
148	A Drosophila cell-free system that senses DNA breaks and triggers phosphorylation signalling. *Nucleic Acids Research*, **2019**, 47, 7444-7459	20.1	1
147	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of Drosophila helicase Maleless. *Nucleic Acids Research*, **2019**, 47, 4319-4333	20.1	7
146	Progressive dosage compensation during Drosophila embryogenesis is reflected by gene arrangement. *EMBO Reports*, **2019**, 20, e48138	6.5	6
145	JASPer controls interphase histone H3S10 phosphorylation by chromosomal kinase JIL-1 in Drosophila. *Nature Communications*, **2019**, 10, 5343	17.4	5
144	Factor cooperation for chromosome discrimination in Drosophila. *Nucleic Acids Research*, **2019**, 47, 1706-1724	20.1	13
143	Genome-wide measurement of local nucleosome array regularity and spacing by nanopore sequencing. *Nature Structural and Molecular Biology*, **2018**, 25, 894-901	17.6	38
142	CHRAC/ACF contribute to the repressive ground state of chromatin. *Life Science Alliance*, **2018**, 1, e201800024	5.8	14
141	Genome-wide Rules of Nucleosome Phasing in Drosophila. *Molecular Cell*, **2018**, 72, 661-672.e4	17.6	17
140	Ubiquitylation of the acetyltransferase MOF in Drosophila melanogaster. *PLoS ONE*, **2017**, 12, e0177408	3.7	7
139	Chromosome topology guides the Dosage Compensation Complex for target gene activation. *EMBO Reports*, **2017**,	6.5	26

138	PionX sites mark the X chromosome for dosage compensation. *Nature*, **2016**, 537, 244-248	50.4	43
137	High levels of histone H3 acetylation at the CMV promoter are predictive of stable expression in Chinese hamster ovary cells. *Biotechnology Progress*, **2016**, 32, 776-86	2.8	21
136	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. *Cell Systems*, **2016**, 2, 49-58	10.6	11
135	A role for tuned levels of nucleosome remodeler subunit ACF1 during Drosophila oogenesis. *Developmental Biology*, **2016**, 411, 217-230	3.1	11
134	Life span extension by targeting a link between metabolism and histone acetylation in Drosophila. *EMBO Reports*, **2016**, 17, 455-69	6.5	93
133	Splice variants of the SWR1-type nucleosome remodeling factor Domino have distinct functions during Drosophila melanogaster oogenesis. *Development (Cambridge)*, **2016**, 143, 3154-67	6.6	10
132	Active promoters give rise to false positive 'Phantom Peaks' in ChIP-seq experiments. *Nucleic Acids Research*, **2015**, 43, 6959-68	20.1	107
131	Beads-on-a-string on a bead: reconstitution and analysis of chromatin on a solid support. *Methods in Molecular Biology*, **2015**, 1288, 1-14	1.4	
130	Computational study of remodeling in a nucleosomal array. *European Physical Journal E*, **2015**, 38, 85	1.5	3
129	Structure of the RNA Helicase MLE Reveals the Molecular Mechanisms for Uridine Specificity and RNA-ATP Coupling. *Molecular Cell*, **2015**, 60, 487-99	17.6	47
128	Global and specific responses of the histone acetylome to systematic perturbation. *Molecular Cell*, **2015**, 57, 559-71	17.6	93
127	UNR facilitates the interaction of MLE with the lncRNA roX2 during Drosophila dosage compensation. *Nature Communications*, **2014**, 5, 4762	17.4	21
126	ISWI remodelling of physiological chromatin fibres acetylated at lysine 16 of histone H4. *PLoS ONE*, **2014**, 9, e88411	3.7	20
125	Rapid purification of recombinant histones. *PLoS ONE*, **2014**, 9, e104029	3.7	29
124	Structural basis of X chromosome DNA recognition by the MSL2 CXC domain during Drosophila dosage compensation. *Genes and Development*, **2014**, 28, 2652-62	12.6	19
123	The histone-fold protein CHRAC14 influences chromatin composition in response to DNA damage. *Cell Reports*, **2014**, 7, 321-330	10.6	20
122	ATP-dependent roX RNA remodeling by the helicase maleless enables specific association of MSL proteins. *Molecular Cell*, **2013**, 51, 174-84	17.6	68
121	The variant histone H2A.V of Drosophila--three roles, two guises. *Chromosoma*, **2013**, 122, 245-58	2.8	39

120	Nucleosome sliding mechanisms: new twists in a looped history. *Nature Structural and Molecular Biology*, **2013**, 20, 1026-32	17.6	77
119	Different chromatin interfaces of the Drosophila dosage compensation complex revealed by high-shear ChIP-seq. *Genome Research*, **2013**, 23, 473-85	9.7	59
118	Nucleosome remodeling and epigenetics. *Cold Spring Harbor Perspectives in Biology*, **2013**, 5,	10.2	171
117	The ATPase domain of ISWI is an autonomous nucleosome remodeling machine. *Nature Structural and Molecular Biology*, **2013**, 20, 82-9	17.6	61
116	Comment on "Drosophila dosage compensation involves enhanced Pol II recruitment to male X-linked promoters". *Science*, **2013**, 340, 273	33.3	14
115	Roles of long, non-coding RNA in chromosome-wide transcription regulation: lessons from two dosage compensation systems. *Biochimie*, **2012**, 94, 1490-8	4.6	20
114	MSL2 combines sensor and effector functions in homeostatic control of the Drosophila dosage compensation machinery. *Molecular Cell*, **2012**, 48, 647-54	17.6	21
113	The MOF-containing NSL complex associates globally with housekeeping genes, but activates only a defined subset. *Nucleic Acids Research*, **2012**, 40, 1509-22	20.1	52
112	Probing the conformation of the ISWI ATPase domain with genetically encoded photoreactive crosslinkers and mass spectrometry. *Molecular and Cellular Proteomics*, **2012**, 11, M111.012088	7.6	40
111	Nucleosome remodeler SNF2L suppresses cell proliferation and migration and attenuates Wnt signaling. *Molecular and Cellular Biology*, **2012**, 32, 2359-71	4.8	24
110	A defined in vitro system to study ATP-dependent remodeling of short chromatin fibers. *Methods in Molecular Biology*, **2012**, 833, 255-70	1.4	3
109	Nucleosome Remodelling and Epigenome Diversification. *Research and Perspectives in Neurosciences*, **2012**, 1-9		
108	Transcription modulation chromosome-wide: universal features and principles of dosage compensation in worms and flies. *Current Opinion in Genetics and Development*, **2011**, 21, 147-53	4.9	26
107	Role for hACF1 in the G2/M damage checkpoint. *Nucleic Acids Research*, **2011**, 39, 8445-56	20.1	53
106	Global analysis of the relationship between JIL-1 kinase and transcription. *PLoS Genetics*, **2011**, 7, e1001327	6	48
105	Developmental role for ACF1-containing nucleosome remodellers in chromatin organisation. *Development (Cambridge)*, **2010**, 137, 3513-22	6.6	21
104	The DNA binding CXC domain of MSL2 is required for faithful targeting the Dosage Compensation Complex to the X chromosome. *Nucleic Acids Research*, **2010**, 38, 3209-21	20.1	50
103	The activation potential of MOF is constrained for dosage compensation. *Molecular Cell*, **2010**, 38, 815-26	17.6	59

102	Dosage compensation and the global re-balancing of aneuploid genomes. *Genome Biology*, **2010**, 11, 216	18.3	49
101	Form and function of dosage-compensated chromosomes--a chicken-and-egg relationship. *BioEssays*, **2010**, 32, 709-17	4.1	8
100	Phosphorylation of SU(VAR)3-9 by the chromosomal kinase JIL-1. *PLoS ONE*, **2010**, 5, e10042	3.7	18
99	Nucleosome dynamics and epigenetic stability. *Essays in Biochemistry*, **2010**, 48, 63-74	7.6	22
98	The dosage compensation complex shapes the conformation of the X chromosome in Drosophila. *Genes and Development*, **2009**, 23, 2490-5	12.6	50
97	Preparation of chromatin assembly extracts from preblastoderm Drosophila embryos. *Methods in Molecular Biology*, **2009**, 523, 1-10	1.4	4
96	Active promoters and insulators are marked by the centrosomal protein 190. *EMBO Journal*, **2009**, 28, 877-88	13	124
95	Drosophila ISWI regulates the association of histone H1 with interphase chromosomes in vivo. *Genetics*, **2009**, 182, 661-9	4	34
94	Analysis of reconstituted chromatin using a solid-phase approach. *Methods in Molecular Biology*, **2009**, 523, 11-25	1.4	1
93	ACF catalyses chromatosome movements in chromatin fibres. *EMBO Journal*, **2008**, 27, 817-26	13	43
92	ATP-dependent chromatosome remodeling. *Biological Chemistry*, **2008**, 389, 345-52	4.5	18
91	Combined use of RNAi and quantitative proteomics to study gene function in Drosophila. *Molecular Cell*, **2008**, 31, 762-72	17.6	87
90	DNA sequence and the organization of chromosomal domains. *Current Opinion in Genetics and Development*, **2008**, 18, 175-80	4.9	15
89	Structure-function analysis of the RNA helicase maleless. *Nucleic Acids Research*, **2008**, 36, 950-62	20.1	32
88	The chromosomal high-affinity binding sites for the Drosophila dosage compensation complex. *PLoS Genetics*, **2008**, 4, e1000302	6	136
87	Site-specific acetylation of ISWI by GCN5. *BMC Molecular Biology*, **2007**, 8, 73	4.5	33
86	Dosage compensation: the beginning and end of generalization. *Nature Reviews Genetics*, **2007**, 8, 47-57	30.1	175
85	Cumulative contributions of weak DNA determinants to targeting the Drosophila dosage compensation complex. *Nucleic Acids Research*, **2007**, 35, 3561-72	20.1	31

84	Acetylation increases access of remodelling complexes to their nucleosome targets to enhance initiation of V(D)J recombination. *Nucleic Acids Research*, **2007**, 35, 6311-21	20.1	17
83	Targeting determinants of dosage compensation in Drosophila. *PLoS Genetics*, **2006**, 2, e5	6	66
82	Chromosome-wide gene-specific targeting of the Drosophila dosage compensation complex. *Genes and Development*, **2006**, 20, 858-70	12.6	134
81	Wolfram Hörz 1944-2005. *Cell*, **2006**, 124, 13-4	56.2	2
80	Regulation of higher-order chromatin structures by nucleosome-remodelling factors. *Current Opinion in Genetics and Development*, **2006**, 16, 151-6	4.9	89
79	Gene regulation by histone H1: new links to DNA methylation. *Cell*, **2005**, 123, 1178-9	56.2	19
78	Dosage compensation in flies: mechanism, models, mystery. *FEBS Letters*, **2005**, 579, 3258-63	3.8	25
77	Dynamic chromatin: concerted nucleosome remodelling and acetylation. *Biological Chemistry*, **2005**, 386, 745-51	4.5	46
76	Stable chromosomal association of MSL2 defines a dosage-compensated nuclear compartment. *Chromosoma*, **2005**, 114, 352-64	2.8	31
75	MOF, an Acetyl Transferase Involved in Dosage Compensation in Drosophila, Uses a CCHC Finger for Substrate Recognition **2005**, 247-251		
74	The Drosophila MSL complex activates the transcription of target genes. *Genes and Development*, **2005**, 19, 2284-8	12.6	81
73	The histone fold subunits of Drosophila CHRAC facilitate nucleosome sliding through dynamic DNA interactions. *Molecular and Cellular Biology*, **2005**, 25, 9886-96	4.8	65
72	The MRG domain mediates the functional integration of MSL3 into the dosage compensation complex. *Molecular and Cellular Biology*, **2005**, 25, 5947-54	4.8	41
71	ATP-dependent nucleosome remodelling: factors and functions. *Journal of Cell Science*, **2004**, 117, 3707-11	5.3	131
70	Recruitment of the nucleolar remodeling complex NoRC establishes ribosomal DNA silencing in chromatin. *Molecular and Cellular Biology*, **2004**, 24, 1791-8	4.8	69
69	Functional integration of the histone acetyltransferase MOF into the dosage compensation complex. *EMBO Journal*, **2004**, 23, 2258-68	13	97
68	ACF1 improves the effectiveness of nucleosome mobilization by ISWI through PHD-histone contacts. *EMBO Journal*, **2004**, 23, 4029-39	13	93
67	Nucleosome remodeling: one mechanism, many phenomena?. *Biochimica Et Biophysica Acta Gene Regulatory Mechanisms*, **2004**, 1677, 58-63		115

66	The many colours of chromodomains. *BioEssays*, **2004**, 26, 133-40	4.1	148
65	A nucleosome sliding assay for chromatin remodeling factors. *Methods in Enzymology*, **2004**, 377, 344-53	1.7	19
64	Lifting a chromosome: dosage compensation in Drosophila melanogaster. *FEBS Letters*, **2004**, 567, 8-14	3.8	48
63	Nucleosome binding by the bromodomain and PHD finger of the transcriptional cofactor p300. *Journal of Molecular Biology*, **2004**, 337, 773-88	6.5	104
62	Analysis of activator-dependent transcription reinitiation in vitro. *Methods in Enzymology*, **2003**, 370, 487-501	1.7	3
61	Sequence-specific targeting of Drosophila roX genes by the MSL dosage compensation complex. *Molecular Cell*, **2003**, 11, 977-86	17.6	67
60	Crystal structure and functional analysis of a nucleosome recognition module of the remodeling factor ISWI. *Molecular Cell*, **2003**, 12, 449-60	17.6	204
59	Determination of Unknown Genomic Sequences Without Cloning **2003**, 373-383		
58	Ran binds to chromatin by two distinct mechanisms. *Current Biology*, **2002**, 12, 1151-6	6.3	56
57	Histone acetylation: a switch between repressive and permissive chromatin. Second in review series on chromatin dynamics. *EMBO Reports*, **2002**, 3, 224-9	6.5	683
56	The dMi-2 chromodomains are DNA binding modules important for ATP-dependent nucleosome mobilization. *EMBO Journal*, **2002**, 21, 2430-40	13	121
55	Nucleosome sliding: facts and fiction. *EMBO Journal*, **2002**, 21, 4749-53	13	89
54	The DNA chaperone HMGB1 facilitates ACF/CHRAC-dependent nucleosome sliding. *EMBO Journal*, **2002**, 21, 6865-73	13	193
53	A critical epitope for substrate recognition by the nucleosome remodeling ATPase ISWI. *Nucleic Acids Research*, **2002**, 30, 649-55	20.1	123
52	Modulation of ISWI function by site-specific histone acetylation. *EMBO Reports*, **2002**, 3, 242-7	6.5	188
51	ATP-dependent nucleosome remodeling. *Annual Review of Biochemistry*, **2002**, 71, 247-73	29.1	625
50	Modifications of the histone N-terminal domains. Evidence for an "epigenetic code"?. *Molecular Biotechnology*, **2001**, 17, 1-13	3	27
49	The histone H4 acetyltransferase MOF uses a C2HC zinc finger for substrate recognition. *EMBO Reports*, **2001**, 2, 113-8	6.5	198

48	Physical and functional association of SU(VAR)3-9 and HDAC1 in Drosophila. *EMBO Reports*, **2001**, 2, 9154-65	8.5	173
47	Tramtrack69 interacts with the dMi-2 subunit of the Drosophila NuRD chromatin remodelling complex. *EMBO Reports*, **2001**, 2, 1089-94	6.5	60
46	HMG-D and histone H1 interplay during chromatin assembly and early embryogenesis. *Journal of Biological Chemistry*, **2001**, 276, 37569-76	5.4	37
45	Critical role for the histone H4 N terminus in nucleosome remodeling by ISWI. *Molecular and Cellular Biology*, **2001**, 21, 875-83	4.8	178
44	The novel transcription factor e(y)2 interacts with TAF(II)40 and potentiates transcription activation on chromatin templates. *Molecular and Cellular Biology*, **2001**, 21, 5223-31	4.8	52
43	ISWI induces nucleosome sliding on nicked DNA. *Molecular Cell*, **2001**, 8, 1085-92	17.6	119
42	Nucleosome mobilization and positioning by ISWI-containing chromatin-remodeling factors. *Journal of Cell Science*, **2001**, 114, 2561-2568	5.3	146
41	Chromodomains are protein-RNA interaction modules. *Nature*, **2000**, 407, 405-9	50.4	332
40	Functional delineation of three groups of the ATP-dependent family of chromatin remodeling enzymes. *Journal of Biological Chemistry*, **2000**, 275, 18864-70	5.4	87
39	A CAF-1-PCNA-mediated chromatin assembly pathway triggered by sensing DNA damage. *Molecular and Cellular Biology*, **2000**, 20, 1206-18	4.8	256
38	Activation of transcription through histone H4 acetylation by MOF, an acetyltransferase essential for dosage compensation in Drosophila. *Molecular Cell*, **2000**, 5, 367-75	17.6	380
37	A solid-phase approach for the analysis of reconstituted chromatin. *Methods in Molecular Biology*, **1999**, 119, 195-206	1.4	11
36	Reconstitution and analysis of hyperacetylated chromatin. *Methods in Molecular Biology*, **1999**, 119, 207-17	1.4	6
35	Analysis of modulators of chromatin structure in Drosophila. *Methods in Enzymology*, **1999**, 304, 742-57	1.7	12
34	Chromatin Protocols **1999**,		30
33	Two-step synergism between the progesterone receptor and the DNA-binding domain of nuclear factor 1 on MMTV minichromosomes. *Molecular Cell*, **1999**, 4, 45-54	17.6	110
32	ISWI is an ATP-dependent nucleosome remodeling factor. *Molecular Cell*, **1999**, 3, 239-45	17.6	191
31	Nucleosome movement by CHRAC and ISWI without disruption or trans-displacement of the histone octamer. *Cell*, **1999**, 97, 843-52	56.2	291

30	Preparation of chromatin assembly extracts from preblastoderm Drosophila embryos. *Methods in Molecular Biology*, **1999**, 119, 187-94	1.4	12
29	The glutamine-rich domain of the Drosophila GAGA factor is necessary for amyloid fibre formation in vitro, but not for chromatin remodelling. *Journal of Molecular Biology*, **1999**, 285, 527-44	6.5	27
28	The Drosophila polycomb protein interacts with nucleosomal core particles In vitro via its repression domain. *Molecular and Cellular Biology*, **1999**, 19, 8451-60	4.8	42
27	Chromatin-remodeling factors: machines that regulate?. *Current Opinion in Cell Biology*, **1998**, 10, 346-53	9	115
26	Structural and functional analysis of chromatin assembled from defined histones. *Methods*, **1998**, 15, 343-53	4.6	6
25	Assembly of MMTV promoter minichromosomes with positioned nucleosomes precludes NF1 access but not restriction enzyme cleavage. *Nucleic Acids Research*, **1998**, 26, 3657-66	20.1	29
24	Heat shock factor increases the reinitiation rate from potentiated chromatin templates. *Molecular and Cellular Biology*, **1998**, 18, 361-7	4.8	56
23	Solid phase technology improves coupled gel shift/footprinting analysis. *Nucleic Acids Research*, **1997**, 25, 453-4	20.1	6
22	The bifunctional protein DCoH modulates interactions of the homeodomain transcription factor HNF1 with nucleic acids. *Journal of Molecular Biology*, **1997**, 265, 20-9	6.5	36
21	Genomic footprinting of Drosophila embryo nuclei by linker tag selection LM-PCR. *Methods*, **1997**, 11, 171-9	4.6	5
20	Biochemical analysis of chromatin structure and function using Drosophila embryo extracts. *Methods*, **1997**, 12, 28-35	4.6	13
19	Chromatin-remodelling factor CHRAC contains the ATPases ISWI and topoisomerase II. *Nature*, **1997**, 388, 598-602	50.4	437
18	The architecture of the heat-inducible Drosophila hsp27 promoter in nuclei. *Journal of Molecular Biology*, **1996**, 256, 249-63	6.5	25
17	The effect of nucleosome phasing sequences and DNA topology on nucleosome spacing. *Journal of Molecular Biology*, **1996**, 260, 1-8	6.5	42
16	Self-organization of microtubules into bipolar spindles around artificial chromosomes in Xenopus egg extracts. *Nature*, **1996**, 382, 420-5	50.4	803
15	Determination of unknown genomic sequences without cloning. *Methods in Molecular Biology*, **1996**, 65, 119-31	1.4	
14	Drosophila chromatin and transcription. *Seminars in Cell Biology*, **1995**, 6, 185-90		11
13	Dual regulation of the Drosophila hsp26 promoter in vitro. *Nucleic Acids Research*, **1995**, 23, 2479-87	20.1	43

12	Electrostatic mechanism of nucleosome spacing. *Journal of Molecular Biology*, **1995**, 252, 305-13	6.5	104
11	Transcription factor-mediated chromatin remodelling: mechanisms and models. *FEBS Letters*, **1995**, 369, 118-21	3.8	17
10	Solid phase DNase I footprinting: quick and versatile. *Nucleic Acids Research*, **1994**, 22, 1511-2	20.1	48
9	Chromatin assembly extracts from Drosophila embryos. *Methods in Cell Biology*, **1994**, 44, 207-23	1.8	59
8	The establishment of active promoters in chromatin. *BioEssays*, **1994**, 16, 541-7	4.1	71
7	ATP-dependent nucleosome disruption at a heat-shock promoter mediated by binding of GAGA transcription factor. *Nature*, **1994**, 367, 525-32	50.4	601
6	An improved protocol for genomic sequencing and footprinting by ligation-mediated PCR. *Nucleic Acids Research*, **1993**, 21, 2779-81	20.1	29
5	Footprinting of DNA-binding proteins in intact cells. *Methods in Enzymology*, **1993**, 218, 568-87	1.7	4
4	Molecular cloning and expression of a hexameric Drosophila heat shock factor subject to negative regulation. *Cell*, **1990**, 63, 1085-97	56.2	345
3	Genomic footprinting reveals cell type-specific DNA binding of ubiquitous factors. *Cell*, **1987**, 51, 435-43	56.2	336
2	In vivo protein-DNA interactions in a glucocorticoid response element require the presence of the hormone. *Nature*, **1986**, 324, 686-8	50.4	317
1	Genome-wide rules of nucleosome phasing		1