

Peter B Becker

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1046162/peter-b-becker-publications-by-citations.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Self-organization of microtubules into bipolar spindles around artificial chromosomes in <i>Xenopus</i> egg extracts. <i>Nature</i> , 1996 , 382, 420-5	50.4	803
154	Histone acetylation: a switch between repressive and permissive chromatin. Second in review series on chromatin dynamics. <i>EMBO Reports</i> , 2002 , 3, 224-9	6.5	683
153	ATP-dependent nucleosome remodeling. <i>Annual Review of Biochemistry</i> , 2002 , 71, 247-73	29.1	625
152	ATP-dependent nucleosome disruption at a heat-shock promoter mediated by binding of GAGA transcription factor. <i>Nature</i> , 1994 , 367, 525-32	50.4	601
151	Chromatin-remodelling factor CHRAC contains the ATPases ISWI and topoisomerase II. <i>Nature</i> , 1997 , 388, 598-602	50.4	437
150	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, 367-75	17.6	380
149	Molecular cloning and expression of a hexameric <i>Drosophila</i> heat shock factor subject to negative regulation. <i>Cell</i> , 1990 , 63, 1085-97	56.2	345
148	Genomic footprinting reveals cell type-specific DNA binding of ubiquitous factors. <i>Cell</i> , 1987 , 51, 435-43	56.2	336
147	Chromodomains are protein-RNA interaction modules. <i>Nature</i> , 2000 , 407, 405-9	50.4	332
146	In vivo protein-DNA interactions in a glucocorticoid response element require the presence of the hormone. <i>Nature</i> , 1986 , 324, 686-8	50.4	317
145	Nucleosome movement by CHRAC and ISWI without disruption or trans-displacement of the histone octamer. <i>Cell</i> , 1999 , 97, 843-52	56.2	291
144	A CAF-1-PCNA-mediated chromatin assembly pathway triggered by sensing DNA damage. <i>Molecular and Cellular Biology</i> , 2000 , 20, 1206-18	4.8	256
143	Crystal structure and functional analysis of a nucleosome recognition module of the remodeling factor ISWI. <i>Molecular Cell</i> , 2003 , 12, 449-60	17.6	204
142	The histone H4 acetyltransferase MOF uses a C2HC zinc finger for substrate recognition. <i>EMBO Reports</i> , 2001 , 2, 113-8	6.5	198
141	The DNA chaperone HMGB1 facilitates ACF/CHRAC-dependent nucleosome sliding. <i>EMBO Journal</i> , 2002 , 21, 6865-73	13	193
140	ISWI is an ATP-dependent nucleosome remodeling factor. <i>Molecular Cell</i> , 1999 , 3, 239-45	17.6	191
139	Modulation of ISWI function by site-specific histone acetylation. <i>EMBO Reports</i> , 2002 , 3, 242-7	6.5	188

138	Critical role for the histone H4 N terminus in nucleosome remodeling by ISWI. <i>Molecular and Cellular Biology</i> , 2001 , 21, 875-83	4.8	178
137	Dosage compensation: the beginning and end of generalization. <i>Nature Reviews Genetics</i> , 2007 , 8, 47-57	30.1	175
136	Physical and functional association of SU(VAR)3-9 and HDAC1 in Drosophila. <i>EMBO Reports</i> , 2001 , 2, 915-9	10.5	173
135	Nucleosome remodeling and epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5,	10.2	171
134	The many colours of chromodomains. <i>BioEssays</i> , 2004 , 26, 133-40	4.1	148
133	Nucleosome mobilization and positioning by ISWI-containing chromatin-remodeling factors. <i>Journal of Cell Science</i> , 2001 , 114, 2561-2568	5.3	146
132	The chromosomal high-affinity binding sites for the Drosophila dosage compensation complex. <i>PLoS Genetics</i> , 2008 , 4, e1000302	6	136
131	Chromosome-wide gene-specific targeting of the Drosophila dosage compensation complex. <i>Genes and Development</i> , 2006 , 20, 858-70	12.6	134
130	ATP-dependent nucleosome remodelling: factors and functions. <i>Journal of Cell Science</i> , 2004 , 117, 3707-3713	3.1	131
129	Active promoters and insulators are marked by the centrosomal protein 190. <i>EMBO Journal</i> , 2009 , 28, 877-88	13	124
128	A critical epitope for substrate recognition by the nucleosome remodeling ATPase ISWI. <i>Nucleic Acids Research</i> , 2002 , 30, 649-55	20.1	123
127	The dMi-2 chromodomains are DNA binding modules important for ATP-dependent nucleosome mobilization. <i>EMBO Journal</i> , 2002 , 21, 2430-40	13	121
126	ISWI induces nucleosome sliding on nicked DNA. <i>Molecular Cell</i> , 2001 , 8, 1085-92	17.6	119
125	Chromatin-remodeling factors: machines that regulate?. <i>Current Opinion in Cell Biology</i> , 1998 , 10, 346-53	9	115
124	Nucleosome remodeling: one mechanism, many phenomena?. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004 , 1677, 58-63		115
123	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	17.6	110
122	Active promoters give rise to false positive Phantom Peaks in ChIP-seq experiments. <i>Nucleic Acids Research</i> , 2015 , 43, 6959-68	20.1	107
121	Nucleosome binding by the bromodomain and PHD finger of the transcriptional cofactor p300. <i>Journal of Molecular Biology</i> , 2004 , 337, 773-88	6.5	104

120	Electrostatic mechanism of nucleosome spacing. <i>Journal of Molecular Biology</i> , 1995 , 252, 305-13	6.5	104
119	Functional integration of the histone acetyltransferase MOF into the dosage compensation complex. <i>EMBO Journal</i> , 2004 , 23, 2258-68	13	97
118	Global and specific responses of the histone acetylome to systematic perturbation. <i>Molecular Cell</i> , 2015 , 57, 559-71	17.6	93
117	ACF1 improves the effectiveness of nucleosome mobilization by ISWI through PHD-histone contacts. <i>EMBO Journal</i> , 2004 , 23, 4029-39	13	93
116	Life span extension by targeting a link between metabolism and histone acetylation in Drosophila. <i>EMBO Reports</i> , 2016 , 17, 455-69	6.5	93
115	Regulation of higher-order chromatin structures by nucleosome-remodelling factors. <i>Current Opinion in Genetics and Development</i> , 2006 , 16, 151-6	4.9	89
114	Nucleosome sliding: facts and fiction. <i>EMBO Journal</i> , 2002 , 21, 4749-53	13	89
113	Combined use of RNAi and quantitative proteomics to study gene function in Drosophila. <i>Molecular Cell</i> , 2008 , 31, 762-72	17.6	87
112	Functional delineation of three groups of the ATP-dependent family of chromatin remodeling enzymes. <i>Journal of Biological Chemistry</i> , 2000 , 275, 18864-70	5.4	87
111	The Drosophila MSL complex activates the transcription of target genes. <i>Genes and Development</i> , 2005 , 19, 2284-8	12.6	81
110	Nucleosome sliding mechanisms: new twists in a looped history. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1026-32	17.6	77
109	The establishment of active promoters in chromatin. <i>BioEssays</i> , 1994 , 16, 541-7	4.1	71
108	Recruitment of the nucleolar remodeling complex NoRC establishes ribosomal DNA silencing in chromatin. <i>Molecular and Cellular Biology</i> , 2004 , 24, 1791-8	4.8	69
107	ATP-dependent roX RNA remodeling by the helicase maleless enables specific association of MSL proteins. <i>Molecular Cell</i> , 2013 , 51, 174-84	17.6	68
106	Sequence-specific targeting of Drosophila roX genes by the MSL dosage compensation complex. <i>Molecular Cell</i> , 2003 , 11, 977-86	17.6	67
105	Targeting determinants of dosage compensation in Drosophila. <i>PLoS Genetics</i> , 2006 , 2, e5	6	66
104	The histone fold subunits of Drosophila CHRAC facilitate nucleosome sliding through dynamic DNA interactions. <i>Molecular and Cellular Biology</i> , 2005 , 25, 9886-96	4.8	65
103	The ATPase domain of ISWI is an autonomous nucleosome remodeling machine. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 82-9	17.6	61

102	Tramtrack69 interacts with the dMi-2 subunit of the Drosophila NuRD chromatin remodelling complex. <i>EMBO Reports</i> , 2001 , 2, 1089-94	6.5	60
101	Different chromatin interfaces of the Drosophila dosage compensation complex revealed by high-shear CHIP-seq. <i>Genome Research</i> , 2013 , 23, 473-85	9.7	59
100	The activation potential of MOF is constrained for dosage compensation. <i>Molecular Cell</i> , 2010 , 38, 815-26	7.6	59
99	Chromatin assembly extracts from Drosophila embryos. <i>Methods in Cell Biology</i> , 1994 , 44, 207-23	1.8	59
98	Ran binds to chromatin by two distinct mechanisms. <i>Current Biology</i> , 2002 , 12, 1151-6	6.3	56
97	Heat shock factor increases the reinitiation rate from potentiated chromatin templates. <i>Molecular and Cellular Biology</i> , 1998 , 18, 361-7	4.8	56
96	Role for hACF1 in the G2/M damage checkpoint. <i>Nucleic Acids Research</i> , 2011 , 39, 8445-56	20.1	53
95	The MOF-containing NSL complex associates globally with housekeeping genes, but activates only a defined subset. <i>Nucleic Acids Research</i> , 2012 , 40, 1509-22	20.1	52
94	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, 5223-31	4.8	52
93	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, 3209-21	20.1	50
92	The dosage compensation complex shapes the conformation of the X chromosome in Drosophila. <i>Genes and Development</i> , 2009 , 23, 2490-5	12.6	50
91	Dosage compensation and the global re-balancing of aneuploid genomes. <i>Genome Biology</i> , 2010 , 11, 216	18.3	49
90	Lifting a chromosome: dosage compensation in Drosophila melanogaster. <i>FEBS Letters</i> , 2004 , 567, 8-14	3.8	48
89	Solid phase DNase I footprinting: quick and versatile. <i>Nucleic Acids Research</i> , 1994 , 22, 1511-2	20.1	48
88	Global analysis of the relationship between JIL-1 kinase and transcription. <i>PLoS Genetics</i> , 2011 , 7, e1001327	13.7	48
87	Structure of the RNA Helicase MLE Reveals the Molecular Mechanisms for Uridine Specificity and RNA-ATP Coupling. <i>Molecular Cell</i> , 2015 , 60, 487-99	17.6	47
86	Dynamic chromatin: concerted nucleosome remodelling and acetylation. <i>Biological Chemistry</i> , 2005 , 386, 745-51	4.5	46
85	PionX sites mark the X chromosome for dosage compensation. <i>Nature</i> , 2016 , 537, 244-248	50.4	43

84	ACF catalyses chromatosome movements in chromatin fibres. <i>EMBO Journal</i> , 2008 , 27, 817-26	13	43
83	Dual regulation of the <i>Drosophila</i> hsp26 promoter in vitro. <i>Nucleic Acids Research</i> , 1995 , 23, 2479-87	20.1	43
82	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, 8451-60	4.8	42
81	The effect of nucleosome phasing sequences and DNA topology on nucleosome spacing. <i>Journal of Molecular Biology</i> , 1996 , 260, 1-8	6.5	42
80	Beads on a string-nucleosome array arrangements and folding of the chromatin fiber. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 109-118	17.6	41
79	The MRG domain mediates the functional integration of MSL3 into the dosage compensation complex. <i>Molecular and Cellular Biology</i> , 2005 , 25, 5947-54	4.8	41
78	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	7.6	40
77	The variant histone H2A.V of <i>Drosophila</i> --three roles, two guises. <i>Chromosoma</i> , 2013 , 122, 245-58	2.8	39
76	Genome-wide measurement of local nucleosome array regularity and spacing by nanopore sequencing. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 894-901	17.6	38
75	HMG-D and histone H1 interplay during chromatin assembly and early embryogenesis. <i>Journal of Biological Chemistry</i> , 2001 , 276, 37569-76	5.4	37
74	The bifunctional protein DCoH modulates interactions of the homeodomain transcription factor HNF1 with nucleic acids. <i>Journal of Molecular Biology</i> , 1997 , 265, 20-9	6.5	36
73	<i>Drosophila</i> ISWI regulates the association of histone H1 with interphase chromosomes in vivo. <i>Genetics</i> , 2009 , 182, 661-9	4	34
72	Site-specific acetylation of ISWI by GCN5. <i>BMC Molecular Biology</i> , 2007 , 8, 73	4.5	33
71	Structure-function analysis of the RNA helicase maleless. <i>Nucleic Acids Research</i> , 2008 , 36, 950-62	20.1	32
70	Cumulative contributions of weak DNA determinants to targeting the <i>Drosophila</i> dosage compensation complex. <i>Nucleic Acids Research</i> , 2007 , 35, 3561-72	20.1	31
69	Stable chromosomal association of MSL2 defines a dosage-compensated nuclear compartment. <i>Chromosoma</i> , 2005 , 114, 352-64	2.8	31
68	Chromatin Protocols 1999 ,		30
67	Rapid purification of recombinant histones. <i>PLoS ONE</i> , 2014 , 9, e104029	3.7	29

66	Assembly of MMTV promoter minichromosomes with positioned nucleosomes precludes NF1 access but not restriction enzyme cleavage. <i>Nucleic Acids Research</i> , 1998 , 26, 3657-66	20.1	29
65	An improved protocol for genomic sequencing and footprinting by ligation-mediated PCR. <i>Nucleic Acids Research</i> , 1993 , 21, 2779-81	20.1	29
64	Modifications of the histone N-terminal domains. Evidence for an "epigenetic code"?. <i>Molecular Biotechnology</i> , 2001 , 17, 1-13	3	27
63	The glutamine-rich domain of the Drosophila GAGA factor is necessary for amyloid fibre formation in vitro, but not for chromatin remodelling. <i>Journal of Molecular Biology</i> , 1999 , 285, 527-44	6.5	27
62	Chromosome topology guides the Dosage Compensation Complex for target gene activation. <i>EMBO Reports</i> , 2017 ,	6.5	26
61	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, 147-53	4.9	26
60	Dosage compensation in flies: mechanism, models, mystery. <i>FEBS Letters</i> , 2005 , 579, 3258-63	3.8	25
59	The architecture of the heat-inducible Drosophila hsp27 promoter in nuclei. <i>Journal of Molecular Biology</i> , 1996 , 256, 249-63	6.5	25
58	Nucleosome remodeler SNF2L suppresses cell proliferation and migration and attenuates Wnt signaling. <i>Molecular and Cellular Biology</i> , 2012 , 32, 2359-71	4.8	24
57	Nucleosome dynamics and epigenetic stability. <i>Essays in Biochemistry</i> , 2010 , 48, 63-74	7.6	22
56	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, 776-86	2.8	21
55	UNR facilitates the interaction of MLE with the lncRNA roX2 during Drosophila dosage compensation. <i>Nature Communications</i> , 2014 , 5, 4762	17.4	21
54	MSL2 combines sensor and effector functions in homeostatic control of the Drosophila dosage compensation machinery. <i>Molecular Cell</i> , 2012 , 48, 647-54	17.6	21
53	Developmental role for ACF1-containing nucleosome remodellers in chromatin organisation. <i>Development (Cambridge)</i> , 2010 , 137, 3513-22	6.6	21
52	ISWI remodelling of physiological chromatin fibres acetylated at lysine 16 of histone H4. <i>PLoS ONE</i> , 2014 , 9, e88411	3.7	20
51	The histone-fold protein CHRAC14 influences chromatin composition in response to DNA damage. <i>Cell Reports</i> , 2014 , 7, 321-330	10.6	20
50	Roles of long, non-coding RNA in chromosome-wide transcription regulation: lessons from two dosage compensation systems. <i>Biochimie</i> , 2012 , 94, 1490-8	4.6	20
49	Structural basis of X chromosome DNA recognition by the MSL2 CXC domain during Drosophila dosage compensation. <i>Genes and Development</i> , 2014 , 28, 2652-62	12.6	19

48	Gene regulation by histone H1: new links to DNA methylation. <i>Cell</i> , 2005 , 123, 1178-9	56.2	19
47	A nucleosome sliding assay for chromatin remodeling factors. <i>Methods in Enzymology</i> , 2004 , 377, 344-53	1.7	19
46	ATP-dependent chromosome remodeling. <i>Biological Chemistry</i> , 2008 , 389, 345-52	4.5	18
45	Phosphorylation of SU(VAR)3-9 by the chromosomal kinase JIL-1. <i>PLoS ONE</i> , 2010 , 5, e10042	3.7	18
44	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, 6311-21	20.1	17
43	Transcription factor-mediated chromatin remodelling: mechanisms and models. <i>FEBS Letters</i> , 1995 , 369, 118-21	3.8	17
42	Genome-wide Rules of Nucleosome Phasing in Drosophila. <i>Molecular Cell</i> , 2018 , 72, 661-672.e4	17.6	17
41	DNA sequence and the organization of chromosomal domains. <i>Current Opinion in Genetics and Development</i> , 2008 , 18, 175-80	4.9	15
40	Comment on "Drosophila dosage compensation involves enhanced Pol II recruitment to male X-linked promoters". <i>Science</i> , 2013 , 340, 273	33.3	14
39	CHRAC/ACF contribute to the repressive ground state of chromatin. <i>Life Science Alliance</i> , 2018 , 1, e20180024	9.0	14
38	Biochemical analysis of chromatin structure and function using Drosophila embryo extracts. <i>Methods</i> , 1997 , 12, 28-35	4.6	13
37	Factor cooperation for chromosome discrimination in Drosophila. <i>Nucleic Acids Research</i> , 2019 , 47, 1706-1724	17.2	13
36	Analysis of modulators of chromatin structure in Drosophila. <i>Methods in Enzymology</i> , 1999 , 304, 742-57	1.7	12
35	Preparation of chromatin assembly extracts from preblastoderm Drosophila embryos. <i>Methods in Molecular Biology</i> , 1999 , 119, 187-94	1.4	12
34	Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. <i>Cell Systems</i> , 2016 , 2, 49-58	10.6	11
33	A role for tuned levels of nucleosome remodeler subunit ACF1 during Drosophila oogenesis. <i>Developmental Biology</i> , 2016 , 411, 217-230	3.1	11
32	A solid-phase approach for the analysis of reconstituted chromatin. <i>Methods in Molecular Biology</i> , 1999 , 119, 195-206	1.4	11
31	Drosophila chromatin and transcription. <i>Seminars in Cell Biology</i> , 1995 , 6, 185-90		11

30	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, 3154-67	6.6	10
29	Form and function of dosage-compensated chromosomes—a chicken-and-egg relationship. <i>BioEssays</i> , 2010 , 32, 709-17	4.1	8
28	SWR1 and NuA4 complexes are defined by DOMINO isoforms. <i>ELife</i> , 2020 , 9,	8.9	8
27	Ubiquitylation of the acetyltransferase MOF in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2017 , 12, e0177408	3.7	7
26	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	20.1	7
25	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	9	7
24	Two-step mechanism for selective incorporation of lncRNA into a chromatin modifier. <i>Nucleic Acids Research</i> , 2020 , 48, 7483-7501	20.1	6
23	Solid phase technology improves coupled gel shift/footprinting analysis. <i>Nucleic Acids Research</i> , 1997 , 25, 453-4	20.1	6
22	Structural and functional analysis of chromatin assembled from defined histones. <i>Methods</i> , 1998 , 15, 343-53	4.6	6
21	Reconstitution and analysis of hyperacetylated chromatin. <i>Methods in Molecular Biology</i> , 1999 , 119, 207-17	1.7	6
20	Progressive dosage compensation during <i>Drosophila</i> embryogenesis is reflected by gene arrangement. <i>EMBO Reports</i> , 2019 , 20, e48138	6.5	6
19	Genomic footprinting of <i>Drosophila</i> embryo nuclei by linker tag selection LM-PCR. <i>Methods</i> , 1997 , 11, 171-9	4.6	5
18	JASPer controls interphase histone H3S10 phosphorylation by chromosomal kinase JIL-1 in <i>Drosophila</i> . <i>Nature Communications</i> , 2019 , 10, 5343	17.4	5
17	Preparation of chromatin assembly extracts from preblastoderm <i>Drosophila</i> embryos. <i>Methods in Molecular Biology</i> , 2009 , 523, 1-10	1.4	4
16	Footprinting of DNA-binding proteins in intact cells. <i>Methods in Enzymology</i> , 1993 , 218, 568-87	1.7	4
15	Computational study of remodeling in a nucleosomal array. <i>European Physical Journal E</i> , 2015 , 38, 85	1.5	3
14	Analysis of activator-dependent transcription reinitiation in vitro. <i>Methods in Enzymology</i> , 2003 , 370, 487-501	1.7	3
13	A defined in vitro system to study ATP-dependent remodeling of short chromatin fibers. <i>Methods in Molecular Biology</i> , 2012 , 833, 255-70	1.4	3

12	Wolfram Hitz 1944-2005. <i>Cell</i> , 2006 , 124, 13-4	56.2	2
11	A Drosophila cell-free system that senses DNA breaks and triggers phosphorylation signalling. <i>Nucleic Acids Research</i> , 2019 , 47, 7444-7459	20.1	1
10	Genome-wide rules of nucleosome phasing		1
9	Analysis of reconstituted chromatin using a solid-phase approach. <i>Methods in Molecular Biology</i> , 2009 , 523, 11-25	1.4	1
8	Divergent evolution toward sex chromosome-specific gene regulation in. <i>Genes and Development</i> , 2021 , 35, 1055-1070	12.6	1
7	Cell-free genomics reveal intrinsic, cooperative and competitive determinants of chromatin interactions. <i>Nucleic Acids Research</i> , 2021 , 49, 7602-7617	20.1	1
6	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	1.4	
5	MOF, an Acetyl Transferase Involved in Dosage Compensation in Drosophila, Uses a CCHC Finger for Substrate Recognition 2005 , 247-251		
4	Determination of unknown genomic sequences without cloning. <i>Methods in Molecular Biology</i> , 1996 , 65, 119-31	1.4	
3	Determination of Unknown Genomic Sequences Without Cloning 2003 , 373-383		
2	Nucleosome Remodelling and Epigenome Diversification. <i>Research and Perspectives in Neurosciences</i> , 2012 , 1-9		
1	Identification of Intrinsic RNA Binding Specificity of Purified Proteins by RNA Immunoprecipitation (vitRIP). <i>Bio-protocol</i> , 2021 , 11, e3946	0.9	