Karoline Schnizer-Luger

List of Publications by Year
in descending order

105 papers	19,380 citations	44069 48 h-index	34986 98 g-index
140 all docs	140 docs citations	140 times ranked	14124 citing authors

#	Article	IF	Citations
1	Inhibitors of PARP: Number crunching and structure gazing. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2121979119.	7.1	52
2	PARP inhibitors trap PARP2 and alter the mode of recruitment of PARP2 at DNA damage sites. Nucleic Acids Research, 2022, 50, 3958-3973.	14.5	24
3	CENP-N promotes the compaction of centromeric chromatin. Nature Structural and Molecular Biology, 2022, 29, 403-413.	8.2	32
4	Spn1 and Its Dynamic Interactions with Spt6, Histones and Nucleosomes. Journal of Molecular Biology, 2022, 434, 167630.	4.2	5
5	Nucleosomes Meet Their Remodeler Match. Trends in Biochemical Sciences, 2021, 46, 41-50.	7.5	23
6	Histone Parylation factor 1 contributes to the inhibition of PARP1 by cancer drugs. Nature Communications, 2021, 12, 736.	12.8	40
7	HPF1 and nucleosomes mediate a dramatic switch in activity of PARP1 from polymerase to hydrolase. ELife, 2021, 10, .	6.0	43
8	Archaeal chromatin â€˜slinkiesâ€™ are inherently dynamic complexes with deflected DNA wrapping pathways. ELife, 2021, 10, .	6.0	36
9	Archaea: The Final Frontier of Chromatin. Journal of Molecular Biology, 2021, 433, 166791.	4.2	26
10	Solution structure(s) of trinucleosomes from contrast variation SAXS. Nucleic Acids Research, 2021, 49, 5028-5037.	14.5	3
11	Virus-encoded histone doublets are essential and form nucleosome-like structures. Cell, 2021, 184, 4237-4250.e19.	28.9	47
12	SMARCAD1 is an ATP-dependent histone octamer exchange factor with de novo nucleosome assembly activity. Science Advances, 2021, 7, eabk2380.	10.3	13
13	The BRCT domain of PARP1 binds intact DNA and mediates intrastrand transfer. Molecular Cell, 2021, 81, 4994-5006.e5.	9.7	44
14	FACT caught in the act of manipulating the nucleosome. Nature, 2020, 577, 426-431.	27.8	160
15	Histone chaperone FACT FAcilitates Chromatin Transcription: mechanistic and structural insights. Current Opinion in Structural Biology, 2020, 65, 26-32.	5.7	36
16	The secret life of histones. Science, 2020, 369, 33-33.	12.6	4
17	Picking a nucleosome lock: Sequence- and structure-specific recognition of the nucleosome. Journal of Biosciences, 2020, 45, 1.	1.1	9
18	Probing the Conformational Changes Associated with DNA Binding to PARP1. Biochemistry, 2020, 59, 2003-2011.	2.5	19

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19	Analytical Ultracentrifugation (AUC): An Overview of the Application of Fluorescence and Absorbance AUC to the Study of Biological Macromolecules. Current Protocols in Molecular Biology, 2020, 133, e131.	2.9	21
20	Bridging of nucleosome-proximal DNA double-strand breaks by PARP2 enhances its interaction with HPF1. PLoS ONE, 2020, 15, e0240932.	2.5	33
21	Navigating the structure of COMPASS. ELife, 2020, 9, .	6.0	1
22	Picking a nucleosome lock: Sequence- and structure-specific recognition of the nucleosome. Journal of Biosciences, 2020, 45, .	1.1	2
23	Title is missing!. , 2020, 15, e0240932.		0
24	Title is missing!. , 2020, 15, e0240932.		0
25	Title is missing!. , 2020, 15, e0240932.		0
26	Title is missing!. , 2020, 15, e0240932.		0
27	Quantitating repair protein accumulation at DNA lesions: Past, present, and future. DNA Repair, 2019, 81, 102650.	2.8	12
28	Kinetics of DNAâ€“protein association and dissociation by stopped-flow spectroscopy. Methods in Enzymology, 2019, 625, 135-156.	1.0	2
29	EvoChromo: towards a synthesis of chromatin biology and evolution. Development (Cambridge), 2019, 146, .	2.5	16
30	Q-FADD: A Mechanistic Approach for Modeling the Accumulation of Proteins at Sites of DNA Damage. Biophysical Journal, 2019, 116, 2224-2233.	0.5	16
31	Nonspecific Binding of RNA to PARP1 and PARP2 Does Not Lead to Catalytic Activation. Biochemistry, 2019, 58, 5107-5111.	2.5	18
32	Single and double box HMGB proteins differentially destabilize nucleosomes. Nucleic Acids Research, 2019, 47, 666-678.	14.5	122
33	Nucleosome structure and dynamics are coming of age. Nature Structural and Molecular Biology, 2019, 26, 3-13.	8.2	233
34	The elongation factor Spn1 is a multi-functional chromatin binding protein. Nucleic Acids Research, 2018, 46, 2321-2334.	14.5	19
35	Investigating the Dynamics of Destabilized Nucleosomes Using Methyl-TROSY NMR. Journal of the American Chemical Society, 2018, 140, 4774-4777.	13.7	42
36	Replication Stress Shapes a Protective Chromatin Environment across Fragile Genomic Regions. Molecular Cell, 2018, 69, 36-47.e7.	9.7	75

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37	Constitutive centromere-associated network contacts confer differential stability on CENP-A nucleosomes in vitro and in the cell. Molecular Biology of the Cell, 2018, 29, 751-762.	2.1	27
38	Measuring Nucleosome Assembly Activity in vitro with the Nucleosome Assembly and Quantification (NAQ) Assay. Bio-protocol, 2018, 8, .	0.4	4
39	Mechanistic insights into histone deposition and nucleosome assembly by the chromatin assembly factor-1. Nucleic Acids Research, 2018, 46, 9907-9917.	14.5	67
40	Archaeal <scp>DNA</scp> on the histone merryâ€goâ€round. FEBS Journal, 2018, 285, 3168-3174.	4.7	13
41	FRET-based Stoichiometry Measurements of Protein Complexes in vitro. Bio-protocol, 2018, 8, .	0.4	7
42	The histone chaperone FACT modulates nucleosome structure by tethering its components. Life Science Alliance, 2018, 1, e201800107.	2.8	68
43	Poly(ADP-ribose) polymerase 1 searches DNA via a â€˜monkey barâ€™ mechanism. ELife, 2018, 7, .	6.0	56
44	PARP1 and Sox2: An Unlikely Team of Pioneers to Conquer the Nucleosome. Molecular Cell, 2017, 65, 581-582.	9.7	2
45	The Cac2 subunit is essential for productive histone binding and nucleosome assembly in CAF-1. Scientific Reports, 2017, 7, 46274.	3.3	30
46	Structure of histone-based chromatin in Archaea. Science, 2017, 357, 609-612.	12.6	149
47	Decoding the centromeric nucleosome through CENP-N. ELife, 2017, 6, .	6.0	101
48	Yeast CAF-1 assembles histone (H3-H4) 2 tetramers prior to DNA deposition. Nucleic Acids Research, 2017, 45, 9811-9812.	14.5	3
49	Biochemical and Biophysical Methods for Analysis of Poly(ADP-Ribose) Polymerase 1 and Its Interactions with Chromatin. Methods in Molecular Biology, 2017, 1608, 231-253.	0.9	2
50	DNA-mediated association of two histone-bound complexes of yeast Chromatin Assembly Factor-1 (CAF-1) drives tetrasome assembly in the wake of DNA replication. ELife, 2017, 6, .	6.0	71
51	A quantitative investigation of linker histone interactions with nucleosomes and chromatin. Scientific Reports, 2016, 6, 19122.	3.3	59
52	Coordinated Action of Nap1 and RSC in Disassembly of Tandem Nucleosomes. Molecular and Cellular Biology, 2016, 36, 2262-2271.	2.3	13
53	Bivalent interaction of the PZP domain of BRPF1 with the nucleosome impacts chromatin dynamics and acetylation. Nucleic Acids Research, 2016, 44, 472-484.	14.5	49
54	Histone Chaperone Nap1 Is a Major Regulator of Histone H2A-H2B Dynamics at the Inducible GAL Locus. Molecular and Cellular Biology, 2016, 36, 1287-1296.	2.3	24

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55	The right place at the right time: chaperoning core histone variants. EMBO Reports, 2015, 16, 1454-1466.	4.5	55
56	Histone Acetylation near the Nucleosome Dyad Axis Enhances Nucleosome Disassembly by RSC and SWI/SNF. Molecular and Cellular Biology, 2015, 35, 4083-4092.	2.3	35
57	Histone Core Phosphorylation Regulates DNA Accessibility. Journal of Biological Chemistry, 2015, 290, 22612-22621.	3.4	76
58	A Multilaboratory Comparison of Calibration Accuracy and the Performance of External References in Analytical Ultracentrifugation. PLoS ONE, 2015, 10, e0126420.	2.5	71
59	Putting numbers on chromatin and its interacting partners. Methods, 2014, 70, 75-76.	3.8	0
60	Scm3 deposits a (Cse4â€"H4)2 tetramer onto DNA through a Cse4â€"H4 dimer intermediate. Nucleic Acids Research, 2014, 42, 5532-5542.	14.5	14
61	Automodification switches PARP-1 function from chromatin architectural protein to histone chaperone. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12752-12757.	7.1	127
62	Editorial overview: Nucleic acid movers and shakers. Current Opinion in Structural Biology, 2014, 24, v-vii.	5.7	0
63	The Histone Variant H2A.W Defines Heterochromatin and Promotes Chromatin Condensation in Arabidopsis. Cell, 2014, 158, 98-109.	28.9	257
64	Torque modulates nucleosome stability and facilitates H2A/H2B dimer loss. Nature Communications, 2013, 4, 2579.	12.8	116
65	Chaperone Nap1 Shields Histone Surfaces Used in a Nucleosome and Can Put H2A-H2B in an Unconventional Tetrameric Form. Molecular Cell, 2013, 51, 662-677.	9.7	69
66	The role of the nucleosome acidic patch in modulating higher order chromatin structure. Journal of the Royal Society Interface, 2013, 10, 20121022.	3.4	200
67	Histone chaperone FACT action during transcription through chromatin by RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7654-7659.	7.1	182
68	Assembly of Nucleosomal Arrays from Recombinant Core Histones and Nucleosome Positioning DNA. Journal of Visualized Experiments, 2013, , .	0.3	25
69	Quantifying Chromatin-Associated Interactions. Methods in Enzymology, 2012, 512, 243-274.	1.0	28
70	Alternative Modes of Binding of Poly(ADP-ribose) Polymerase 1 to Free DNA and Nucleosomes. Journal of Biological Chemistry, 2012, 287, 32430-32439.	3.4	78
71	Yeast CAF-1 assembles histone (H3-H4)2 tetramers prior to DNA deposition. Nucleic Acids Research, 2012, 40, 10139-10149.	14.5	66
72	Fluorescence strategies for high-throughput quantification of protein interactions. Nucleic Acids Research, 2012, 40, e33-e33.	14.5	53

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73	New insights into nucleosome and chromatin structure: an ordered state or a disordered affair?. Nature Reviews Molecular Cell Biology, 2012, 13, 436-447.	37.0	573
74	The Linker Region of MacroH2A Promotes Self-association of Nucleosomal Arrays. Journal of Biological Chemistry, 2011, 286, 23852-23864.	3.4	47
75	Nucleosome accessibility governed by the dimer/tetramer interface. Nucleic Acids Research, 2011, 39, 3093-3102.	14.5	175
76	Biophysical analysis and small-angle X-ray scattering-derived structures of MeCP2â€“nucleosome complexes. Nucleic Acids Research, 2011, 39, 4122-4135.	14.5	49
77	The Histone Chaperone FACT: Structural Insights and Mechanisms for Nucleosome Reorganization. Journal of Biological Chemistry, 2011, 286, 18369-18374.	3.4	181
78	Histone Chaperone FACT Coordinates Nucleosome Interaction through Multiple Synergistic Binding Events. Journal of Biological Chemistry, 2011, 286, 41883-41892.	3.4	129
79	Structural and Biophysical Studies of Human PARP-1 in Complex with Damaged DNA. Journal of Molecular Biology, 2010, 395, 983-994.	4.2	60
80	The Transcription Factor Spn1 Regulates Gene Expression via a Highly Conserved Novel Structural Motif. Journal of Molecular Biology, 2010, 404, 1-15.	4.2	22
81	Nucleosome thermodynamics, histone modifications, and histone chaperone function. FASEB Journal, 2010, 24, 310.2.	0.5	0
82	Nucleosome-binding affinity as a primary determinant of the nuclear mobility of the pioneer transcription factor FoxA. Genes and Development, 2009, 23, 804-809.	5.9	190
83	Histone chaperone specificity in Rtt109 activation. Nature Structural and Molecular Biology, 2008, 15, 957-964.	8.2	62
84	A Thermodynamic Model for Nap1-Histone Interactions. Journal of Biological Chemistry, 2008, 283, 32412-32418.	3.4	83
85	A charged and contoured surface on the nucleosome regulates chromatin compaction. Nature Structural and Molecular Biology, 2007, 14, 1105-1107.	8.2	99
86	The Nucleosomal Surface as a Docking Station for Kaposi's Sarcoma Herpesvirus LANA. Science, 2006, 311, 856-861.	12.6	469
87	Dynamic nucleosomes. Chromosome Research, 2006, 14, 5-16.	2.2	149
88	The structure of nucleosome assembly protein 1. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1248-1253.	7.1	178
89	Nucleosome and chromatin fiber dynamics. Current Opinion in Structural Biology, 2005, 15, 188-196.	5.7	191
90	The Core Histone N-terminal Tail Domains Function Independently and Additively during Salt-dependent Oligomerization of Nucleosomal Arrays. Journal of Biological Chemistry, 2005, 280, 33701-33706.	3.4	123

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91	Nucleosomes in Solution Exist as a Mixture of Twist-defect States. Journal of Molecular Biology, 2005, 345, 103-114.	4.2	52
92	A New Fluorescence Resonance Energy Transfer Approach Demonstrates That the Histone Variant H2AZ Stabilizes the Histone Octamer within the Nucleosome. Journal of Biological Chemistry, 2004, 279, 24274-24282.	3.4	193
93	Structural determinants for generating centromeric chromatin. Nature, 2004, 430, 578-582.	27.8	364
94	From The Cover: Molecular recognition of the nucleosomal "supergroove". Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6864-6869.	7.1	90
95	Reconstitution of Nucleosome Core Particles from Recombinant Histones and DNA. Methods in Enzymology, 2003, 375, 23-44.	1.0	709
96	Crystal Structures of Nucleosome Core Particles in Complex with Minor Groove DNA-binding Ligands. Journal of Molecular Biology, 2003, 326, 371-380.	4.2	147
97	Structure and dynamic behavior of nucleosomes. Current Opinion in Genetics and Development, 2003, 13, 127-135.	3.3	270
98	Solvent Mediated Interactions in the Structure of the Nucleosome Core Particle at 1.9Ã… Resolution. Journal of Molecular Biology, 2002, 319, 1097-1113.	4.2	1,340
99	Energetics and Affinity of the Histone Octamer for Defined DNA Sequences. Biochemistry, 2001, 40, 10927-10933.	2.5	74
100	Structure of the yeast nucleosome core particle reveals fundamental changes in internucleosome interactions. EMBO Journal, 2001, 20, 5207-5218.	7.8	360
101	Role of the Loop Containing Residue 115 in the Induced-Fit Mechanism of the Bacterial Cell Wall Biosynthetic Enzyme MurAâ€¡. Biochemistry, 2000, 39, 2164-2173.	2.5	47
102	Preparation of nucleosome core particle from recombinant histones. Methods in Enzymology, 1999, 304, 3-19.	1.0	671
103	The histone tails of the nucleosome. Current Opinion in Genetics and Development, 1998, 8, 140-146.	3.3	460
104	DNA binding within the nucleosome core. Current Opinion in Structural Biology, 1998, 8, 33-40.	5.7	275
105	Crystal structure of the nucleosome core particle at 2.8â€‰Ã… resolution. Nature, 1997, 389, 251-260.	27.8	8,091