

Felix Mueller-Planitz

List of Publications by Year in descending order

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1486
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#	ARTICLE	IF	CITATIONS
1	The Myosin Chaperone UNC-45 Is Organized in Tandem Modules to Support Myofilament Formation in <i>C.Âlegans</i> . <i>Cell</i> , 2013, 152, 183-195.	28.9	94
2	Nucleosome sliding mechanisms: new twists in a looped history. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1026-1032.	8.2	92
3	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
4	A Poly-ADP-Ribose Trigger Releases the Auto-Inhibition of a Chromatin Remodeling Oncogene. <i>Molecular Cell</i> , 2017, 68, 860-871.e7.	9.7	70
5	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
6	Regulation of a heterodimeric kinesin-2 through an unprocessive motor domain that is turned processive by its partner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10460-10465.	7.1	62
7	Nucleosome Spacing Generated by ISWI and CHD1 Remodelers Is Constant Regardless of Nucleosome Density. <i>Molecular and Cellular Biology</i> , 2015, 35, 1588-1605.	2.3	52
8	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
9	Rapid Purification of Recombinant Histones. <i>PLoS ONE</i> , 2014, 9, e104029.	2.5	45
10	Myosin Vaâ€™s adaptor protein melanophilin enforces track selection on the microtubule and actin networks in vitro. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4714-E4723.	7.1	28
11	Concerted regulation of ISWI by an autoinhibitory domain and the H4 N-terminal tail. <i>ELife</i> , 2017, 6, .	6.0	28
12	Kinesinâ€™2 motors adapt their stepping behavior for processive transport on axonemes and microtubules. <i>EMBO Reports</i> , 2017, 18, 1947-1956.	4.5	26
13	Nucleosome Positioning and Spacing: From Mechanism to Function. <i>Journal of Molecular Biology</i> , 2021, 433, 166847.	4.2	26
14	ISWI Remodelling of Physiological Chromatin Fibres Acetylated at Lysine 16 of Histone H4. <i>PLoS ONE</i> , 2014, 9, e88411.	2.5	24
15	DNA topoisomerase II selects DNA cleavage sites based on reactivity rather than binding affinity. <i>Nucleic Acids Research</i> , 2007, 35, 3764-3773.	14.5	23
16	Coupling between ATP Binding and DNA Cleavage by DNA Topoisomerase II. <i>Journal of Biological Chemistry</i> , 2008, 283, 17463-17476.	3.4	23
17	A critical role for linker DNA in higher-order folding of chromatin fibers. <i>Nucleic Acids Research</i> , 2021, 49, 2537-2551.	14.5	19
18	Interdomain Communication in DNA Topoisomerase II. <i>Journal of Biological Chemistry</i> , 2006, 281, 23395-23404.	3.4	18

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19	No need for a power stroke in ISWI-mediated nucleosome sliding. EMBO Reports, 2013, 14, 1092-1097.	4.5	18
20	Crossfinder-assisted mapping of protein crosslinks formed by site-specifically incorporated crosslinkers. Bioinformatics, 2015, 31, 2043-2045.	4.1	18
21	A case of convergent evolution: Several viral and bacterial pathogens hijack RSK kinases through a common linear motif. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	14
22	The biogenesis and function of nucleosome arrays. Nature Communications, 2021, 12, 7011.	12.8	12
23	Structural Architecture of the Nucleosome Remodeler ISWI Determined from Cross-Linking, Mass Spectrometry, SAXS, and Modeling. Structure, 2018, 26, 282-294.e6.	3.3	11
24	A CDK-regulated chromatin segregase promoting chromosome replication. Nature Communications, 2021, 12, 5224.	12.8	6
25	Remodeling and Repositioning of Nucleosomes in Nucleosomal Arrays. Methods in Molecular Biology, 2018, 1805, 349-370.	0.9	5
26	Integrative Modeling of the ISWI Chromatin Remodeling Enzyme from Cross-Linking/Mass Spectrometry and Saxes Data. Biophysical Journal, 2016, 110, 237a.	0.5	0