

# Michael G Poirier

## List of Publications by Year in descending order

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47  
papers

2,851  
citations

236925

25  
h-index

214800

47  
g-index

52  
all docs

52  
docs citations

52  
times ranked

2951  
citing authors

#	ARTICLE	IF	CITATIONS
1	H1.0 C Terminal Domain Is Integral for Altering Transcription Factor Binding within Nucleosomes. <i>Biochemistry</i> , 2022, 61, 625-638.	2.5	10
2	High-Force Application by a Nanoscale DNA Force Spectrometer. <i>ACS Nano</i> , 2022, 16, 5682-5695.	14.6	20
3	Histone H4 Tails in Nucleosomes: a Fuzzy Interaction with DNA. <i>Angewandte Chemie</i> , 2021, 133, 6554-6561.	2.0	1
4	Histone H4 Tails in Nucleosomes: a Fuzzy Interaction with DNA. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 6480-6487.	13.8	24
5	Nucleosome composition regulates the histone H3 tail conformational ensemble and accessibility. <i>Nucleic Acids Research</i> , 2021, 49, 4750-4767.	14.5	29
6	Conformational Dynamics of Histone H3 Tails in Chromatin. <i>Journal of Physical Chemistry Letters</i> , 2021, 12, 6174-6181.	4.6	13
7	Structural and biophysical characterization of the nucleosome-binding PZP domain. <i>STAR Protocols</i> , 2021, 2, 100479.	1.2	5
8	The role of the PZP domain of AF10 in acute leukemia driven by AF10 translocations. <i>Nature Communications</i> , 2021, 12, 4130.	12.8	8
9	Protein cofactors and substrate influence Mg <sup>2+</sup> -dependent structural changes in the catalytic RNA of archaeal RNase P. <i>Nucleic Acids Research</i> , 2021, 49, 9444-9458.	14.5	6
10	A nanoscale DNA force spectrometer capable of applying tension and compression on biomolecules. <i>Nucleic Acids Research</i> , 2021, 49, 8987-8999.	14.5	24
11	Molecular Basis for the PZP Domain of BRPF1 Association with Chromatin. <i>Structure</i> , 2020, 28, 105-110.e3.	3.3	20
12	Molecular mechanism of the MORC4 ATPase activation. <i>Nature Communications</i> , 2020, 11, 5466.	12.8	14
13	DNA sequence influences hexasome orientation to regulate DNA accessibility. <i>Nucleic Acids Research</i> , 2019, 47, 5617-5633.	14.5	12
14	Quantitative Modeling of Nucleosome Unwrapping from Both Ends. <i>Biophysical Journal</i> , 2019, 117, 2204-2216.	0.5	15
15	The path towards functional nanoparticle-DNA origami composites. <i>Materials Science and Engineering Reports</i> , 2019, 138, 153-209.	31.8	15
16	Live-cell imaging reveals the interplay between transcription factors, nucleosomes, and bursting. <i>EMBO Journal</i> , 2019, 38, .	7.8	155
17	Biophysics of Chromatin Dynamics. <i>Annual Review of Biophysics</i> , 2019, 48, 321-345.	10.0	102
18	Mechanism for autoinhibition and activation of the MORC3 ATPase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6111-6119.	7.1	25

#	ARTICLE	IF	CITATIONS
19	Dissociation rate compensation mechanism for budding yeast pioneer transcription factors. <i>ELife</i> , 2019, 8, .	6.0	68
20	Hydrazide Mimics for Protein Lysine Acylation To Assess Nucleosome Dynamics and Deubiquitinase Action. <i>Journal of the American Chemical Society</i> , 2018, 140, 9478-9485.	13.7	33
21	Dynamic DNA Origami Device for Measuring Compressive Depletion Forces. <i>ACS Nano</i> , 2017, 11, 6566-6573.	14.6	59
22	PHF1 Tudor and N-terminal domains synergistically target partially unwrapped nucleosomes to increase DNA accessibility. <i>Nucleic Acids Research</i> , 2017, 45, gkw1320.	14.5	27
23	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. <i>Cell Reports</i> , 2017, 21, 455-466.	6.4	36
24	Accessibility of the histone H3 tail in the nucleosome for binding of paired readers. <i>Nature Communications</i> , 2017, 8, 1489.	12.8	67
25	Probing Nucleosome Stability with a DNA Origami Nanocaliper. <i>ACS Nano</i> , 2016, 10, 7073-7084.	14.6	90
26	Methods for Investigating DNA Accessibility with Single Nucleosomes. <i>Methods in Enzymology</i> , 2016, 581, 379-415.	1.0	9
27	Electron Paramagnetic Resonance of a Single NV Nanodiamond Attached to an Individual Biomolecule. <i>Biophysical Journal</i> , 2016, 110, 2044-2052.	0.5	12
28	Nanofiber-based paramagnetic probes for rapid, real-time biomedical oximetry. <i>Biomedical Microdevices</i> , 2016, 18, 38.	2.8	5
29	Bivalent interaction of the PZP domain of BRPF1 with the nucleosome impacts chromatin dynamics and acetylation. <i>Nucleic Acids Research</i> , 2016, 44, 472-484.	14.5	49
30	Aurora-A mediated histone H3 phosphorylation of threonine 118 controls condensin I and cohesin occupancy in mitosis. <i>ELife</i> , 2016, 5, e11402.	6.0	23
31	Linker histone H1 and H3K56 acetylation are antagonistic regulators of nucleosome dynamics. <i>Nature Communications</i> , 2015, 6, 10152.	12.8	39
32	Histone Acetylation near the Nucleosome Dyad Axis Enhances Nucleosome Disassembly by RSC and SWI/SNF. <i>Molecular and Cellular Biology</i> , 2015, 35, 4083-4092.	2.3	35
33	Histone Core Phosphorylation Regulates DNA Accessibility. <i>Journal of Biological Chemistry</i> , 2015, 290, 22612-22621.	3.4	76
34	Post-Translational Modifications of Histones That Influence Nucleosome Dynamics. <i>Chemical Reviews</i> , 2015, 115, 2274-2295.	47.7	384
35	Single molecule fluorescence methodologies for investigating transcription factor binding kinetics to nucleosomes and DNA. <i>Methods</i> , 2014, 70, 108-118.	3.8	31
36	Nucleosomes accelerate transcription factor dissociation. <i>Nucleic Acids Research</i> , 2014, 42, 3017-3027.	14.5	123

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37	Histone H3 and H4 N-Terminal Tails in Nucleosome Arrays at Cellular Concentrations Probed by Magic Angle Spinning NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2013, 135, 15278-15281.	13.7	80
38	Binding of PHF1 Tudor to H3K36me3 enhances nucleosome accessibility. <i>Nature Communications</i> , 2013, 4, 2969.	12.8	77
39	ATP-dependent nucleosome unwrapping catalyzed by human RAD51. <i>Nucleic Acids Research</i> , 2013, 41, 7302-7312.	14.5	11
40	Structural basis for high-affinity binding of LEDGF PWWP to mononucleosomes. <i>Nucleic Acids Research</i> , 2013, 41, 3924-3936.	14.5	182
41	Regulation of the nucleosome unwrapping rate controls DNA accessibility. <i>Nucleic Acids Research</i> , 2012, 40, 10215-10227.	14.5	104
42	Preparation of Fully Synthetic Histone H3 Reveals That Acetyl-Lysine 56 Facilitates Protein Binding Within Nucleosomes. <i>Journal of Molecular Biology</i> , 2011, 408, 187-204.	4.2	133
43	Histone fold modifications control nucleosome unwrapping and disassembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12711-12716.	7.1	172
44	A quantitative model of nucleosome dynamics. <i>Nucleic Acids Research</i> , 2011, 39, 8306-8313.	14.5	49
45	Acetylation of Histone H3 at the Nucleosome Dyad Alters DNA-Histone Binding. <i>Journal of Biological Chemistry</i> , 2009, 284, 23312-23321.	3.4	116
46	Dynamics and function of compact nucleosome arrays. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 938-944.	8.2	123
47	Spontaneous Access to DNA Target Sites in Folded Chromatin Fibers. <i>Journal of Molecular Biology</i> , 2008, 379, 772-786.	4.2	135