

# Catherine A Musselman

## List of Publications by Year in descending order

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Version: 2024-02-01

52  
papers

3,284  
citations

172386

29  
h-index

189801

50  
g-index

58  
all docs

58  
docs citations

58  
times ranked

4568  
citing authors

#	ARTICLE	IF	CITATIONS
1	Perceiving the epigenetic landscape through histone readers. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1218-1227.	3.6	688
2	Tcf1 and Lef1 transcription factors establish CD8+ T cell identity through intrinsic HDAC activity. <i>Nature Immunology</i> , 2016, 17, 695-703.	7.0	188
3	Handpicking epigenetic marks with PHD fingers. <i>Nucleic Acids Research</i> , 2011, 39, 9061-9071.	6.5	175
4	Molecular basis for H3K36me3 recognition by the Tudor domain of PHF1. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1266-1272.	3.6	174
5	Plant Homeodomain (PHD) Fingers of CHD4 Are Histone H3-binding Modules with Preference for Unmodified H3K4 and Methylated H3K9. <i>Journal of Biological Chemistry</i> , 2011, 286, 11779-11791.	1.6	147
6	Combinatorial profiling of chromatin binding modules reveals multisite discrimination. <i>Nature Chemical Biology</i> , 2010, 6, 283-290.	3.9	115
7	Binding of the CHD4 PHD2 finger to histone H3 is modulated by covalent modifications. <i>Biochemical Journal</i> , 2009, 423, 179-187.	1.7	106
8	The conformation of the histone H3 tail inhibits association of the BPTF PHD finger with the nucleosome. <i>ELife</i> , 2018, 7, .	2.8	104
9	PHD Fingers: Epigenetic Effectors and Potential Drug Targets. <i>Molecular Interventions: Pharmacological Perspectives From Biology, Chemistry and Genomics</i> , 2009, 9, 314-323.	3.4	101
10	Bivalent recognition of nucleosomes by the tandem PHD fingers of the CHD4 ATPase is required for CHD4-mediated repression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 787-792.	3.3	96
11	Binding of the MLL PHD3 Finger to Histone H3K4me3 Is Required for MLL-Dependent Gene Transcription. <i>Journal of Molecular Biology</i> , 2010, 400, 137-144.	2.0	88
12	E-C coupling structural protein junctophilin-2 encodes a stress-adaptive transcription regulator. <i>Science</i> , 2018, 362, .	6.0	78
13	Binding of PHF1 Tudor to H3K36me3 enhances nucleosome accessibility. <i>Nature Communications</i> , 2013, 4, 2969.	5.8	77
14	Accessibility of the histone H3 tail in the nucleosome for binding of paired readers. <i>Nature Communications</i> , 2017, 8, 1489.	5.8	67
15	Characterizing Complex Dynamics in the Transactivation Response Element Apical Loop and Motional Correlations with the Bulge by NMR, Molecular Dynamics, and Mutagenesis. <i>Biophysical Journal</i> , 2008, 95, 3906-3915.	0.2	65
16	DNA binding drives the association of BRG1/hBRM bromodomains with nucleosomes. <i>Nature Communications</i> , 2017, 8, 16080.	5.8	61
17	Membrane insertion of the FYVE domain is modulated by pH. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 852-860.	1.5	58
18	Characterizing the relative orientation and dynamics of RNA A-form helices using NMR residual dipolar couplings. <i>Nature Protocols</i> , 2007, 2, 1536-1546.	5.5	56

#	ARTICLE	IF	CITATIONS
19	Histone Tail Conformations: A Fuzzy Affair with DNA. Trends in Biochemical Sciences, 2021, 46, 564-578.	3.7	56
20	Impact of static and dynamic A-form heterogeneity on the determination of RNA global structural dynamics using NMR residual dipolar couplings. Journal of Biomolecular NMR, 2006, 36, 235-249.	1.6	54
21	Optimization of Ligands Using Focused DNA-Encoded Libraries To Develop a Selective, Cell-Permeable CBX8 Chromodomain Inhibitor. ACS Chemical Biology, 2020, 15, 112-131.	1.6	53
22	Towards understanding methyllysine readout. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 686-693.	0.9	51
23	Reading More than Histones: The Prevalence of Nucleic Acid Binding among Reader Domains. Molecules, 2018, 23, 2614.	1.7	51
24	Structural Insight into p53 Recognition by the 53BP1 Tandem Tudor Domain. Journal of Molecular Biology, 2010, 398, 489-496.	2.0	50
25	Inhibition of histone binding by supramolecular hosts. Biochemical Journal, 2014, 459, 505-512.	1.7	48
26	Multivalent Recognition of Histone Tails by the PHD Fingers of CHD5. Biochemistry, 2012, 51, 6534-6544.	1.2	46
27	Molecular Mechanism of MLL PHD3 and RNA Recognition by the Cyp33 RRM Domain. Journal of Molecular Biology, 2010, 400, 145-154.	2.0	40
28	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. Cell Reports, 2017, 21, 455-466.	2.9	36
29	Emerging methodologies to investigate lipid-protein interactions. Integrative Biology (United Tj ETQq1 1 0.784314 rgBT /Overlock 11	0.6	35
30	Structural Plasticity of Methyllysine Recognition by the Tandem Tudor Domain of 53BP1. Structure, 2015, 23, 312-321.	1.6	32
31	iRED Analysis of TAR RNA Reveals Motional Coupling, Long-Range Correlations, and a Dynamical Hinge. Biophysical Journal, 2007, 93, 411-422.	0.2	31
32	Nucleosome composition regulates the histone H3 tail conformational ensemble and accessibility. Nucleic Acids Research, 2021, 49, 4750-4767.	6.5	29
33	Engagement of DNA and H3K27me3 by the CBX8 chromodomain drives chromatin association. Nucleic Acids Research, 2019, 47, 2289-2305.	6.5	27
34	Characterization of functional disordered regions within chromatin-associated proteins. IScience, 2021, 24, 102070.	1.9	27
35	RNA Splicing of the BHC80 Gene Contributes to Neuroendocrine Prostate Cancer Progression. European Urology, 2019, 76, 157-166.	0.9	19
36	Referencing Strategy for the Direct Comparison of Nuclear Magnetic Resonance and Molecular Dynamics Motional Parameters in RNA. Journal of Physical Chemistry B, 2010, 114, 929-939.	1.2	18

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37	Rapid Detection of Urinary Tract Infections via Bacterial Nuclease Activity. <i>Molecular Therapy</i> , 2017, 25, 1353-1362.	3.7	18
38	The EZH2 SANT1 domain is a histone reader providing sensitivity to the modification state of the H4 tail. <i>Scientific Reports</i> , 2019, 9, 987.	1.6	18
39	The structural basis of urea-induced protein unfolding in $\hat{\text{I}}^2$ -catenin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2840-2847.	2.5	15
40	The molecular basis of selective DNA binding by the BRG1 AT-hook and bromodomain. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194566.	0.9	13
41	Reprogramming CBX8-PRC1 function with a positive allosteric modulator. <i>Cell Chemical Biology</i> , 2022, 29, 555-571.e11.	2.5	12
42	Visualizing Conformational Ensembles of the Nucleosome by NMR. <i>ACS Chemical Biology</i> , 2022, 17, 495-502.	1.6	12
43	NMR assignments and histone specificity of the ING2 PHD finger. <i>Magnetic Resonance in Chemistry</i> , 2009, 47, 352-358.	1.1	9
44	Strategies for Generating Modified Nucleosomes: Applications within Structural Biology Studies. <i>ACS Chemical Biology</i> , 2019, 14, 579-586.	1.6	9
45	Evolutionary Conservation of Structural and Functional Coupling between the BRM AT-Hook and Bromodomain. <i>Journal of Molecular Biology</i> , 2021, 433, 166845.	2.0	4
46	Methyl fingerprinting of the nucleosome reveals the molecular mechanism of high-mobility group nucleosomal-2 (HMGN2) association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12189-12190.	3.3	3
47	Preparation, Biochemical Analysis, and Structure Determination of Methyllysine Readers. <i>Methods in Enzymology</i> , 2016, 573, 345-362.	0.4	3
48	A histone reader becomes the readout. <i>Journal of Biological Chemistry</i> , 2018, 293, 7486-7487.	1.6	2
49	Photoactive spatial proximity probes for binding pairs with epigenetic marks. <i>Journal of Photochemistry and Photobiology A: Chemistry</i> , 2014, 290, 101-108.	2.0	1
50	The PHD finger of Spp1 mediates histone modification cross-talk. <i>Biochemical Journal</i> , 2019, 476, 2351-2354.	1.7	1
51	The EZH2 SANT1 Domain is a Histone Reader Providing Sensitivity to the Modification State of the H4 Tail. <i>Biophysical Journal</i> , 2018, 114, 445a.	0.2	0
52	Chromatin and epigenetic signaling pathways. , 2019, , 1-23.		0