

Catherine A Musselman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6394412/publications.pdf>

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	Reprogramming CBX8-PRC1 function with a positive allosteric modulator. <i>Cell Chemical Biology</i> , 2022, 29, 555-571.e11.	2.5	12
2	Visualizing Conformational Ensembles of the Nucleosome by NMR. <i>ACS Chemical Biology</i> , 2022, 17, 495-502.	1.6	12
3	Characterization of functional disordered regions within chromatin-associated proteins. <i>IScience</i> , 2021, 24, 102070.	1.9	27
4	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
5	Nucleosome composition regulates the histone H3 tail conformational ensemble and accessibility. <i>Nucleic Acids Research</i> , 2021, 49, 4750-4767.	6.5	29
6	Histone Tail Conformations: A Fuzzy Affair with DNA. <i>Trends in Biochemical Sciences</i> , 2021, 46, 564-578.	3.7	56
7	Optimization of Ligands Using Focused DNA-Encoded Libraries To Develop a Selective, Cell-Permeable CBX8 Chromodomain Inhibitor. <i>ACS Chemical Biology</i> , 2020, 15, 112-131.	1.6	53
8	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
9	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
10	Chromatin and epigenetic signaling pathways. , 2019, , 1-23.		0
11	RNA Splicing of the BHC80 Gene Contributes to Neuroendocrine Prostate Cancer Progression. <i>European Urology</i> , 2019, 76, 157-166.	0.9	19
12	Strategies for Generating Modified Nucleosomes: Applications within Structural Biology Studies. <i>ACS Chemical Biology</i> , 2019, 14, 579-586.	1.6	9
13	Engagement of DNA and H3K27me3 by the CBX8 chromodomain drives chromatin association. <i>Nucleic Acids Research</i> , 2019, 47, 2289-2305.	6.5	27
14	The PHD finger of Spp1 mediates histone modification cross-talk. <i>Biochemical Journal</i> , 2019, 476, 2351-2354.	1.7	1
15	E-C coupling structural protein junctophilin-2 encodes a stress-adaptive transcription regulator. <i>Science</i> , 2018, 362, .	6.0	78
16	Reading More than Histones: The Prevalence of Nucleic Acid Binding among Reader Domains. <i>Molecules</i> , 2018, 23, 2614.	1.7	51
17	A histone reader becomes the readout. <i>Journal of Biological Chemistry</i> , 2018, 293, 7486-7487.	1.6	2
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	Rapid Detection of Urinary Tract Infections via Bacterial Nuclease Activity. <i>Molecular Therapy</i> , 2017, 25, 1353-1362.	3.7	18
21	Covalent Modifications of Histone H3K9 Promote Binding of CHD3. <i>Cell Reports</i> , 2017, 21, 455-466.	2.9	36
22	DNA binding drives the association of BRG1/hBRM bromodomains with nucleosomes. <i>Nature Communications</i> , 2017, 8, 16080.	5.8	61
23	Accessibility of the histone H3 tail in the nucleosome for binding of paired readers. <i>Nature Communications</i> , 2017, 8, 1489.	5.8	67
24	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
25	Preparation, Biochemical Analysis, and Structure Determination of Methyllysine Readers. <i>Methods in Enzymology</i> , 2016, 573, 345-362.	0.4	3
26	Structural Plasticity of Methyllysine Recognition by the Tandem Tudor Domain of 53BP1. <i>Structure</i> , 2015, 23, 312-321.	1.6	32
27	The structural basis of urea-induced protein unfolding in β^2 -catenin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2840-2847.	2.5	15
28	Inhibition of histone binding by supramolecular hosts. <i>Biochemical Journal</i> , 2014, 459, 505-512.	1.7	48
29	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
30	Towards understanding methyllysine readout. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 686-693.	0.9	51
31	Binding of PHF1 Tudor to H3K36me3 enhances nucleosome accessibility. <i>Nature Communications</i> , 2013, 4, 2969.	5.8	77
32	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
33	Perceiving the epigenetic landscape through histone readers. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1218-1227.	3.6	688
34	Emerging methodologies to investigate lipid-protein interactions. <i>Integrative Biology (United Kingdom)</i> , 2012, 4, 101-110.	0.6	35
35	Multivalent Recognition of Histone Tails by the PHD Fingers of CHD5. <i>Biochemistry</i> , 2012, 51, 6534-6544.	1.2	46
36	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

#	ARTICLE	IF	CITATIONS
37	Handpicking epigenetic marks with PHD fingers. <i>Nucleic Acids Research</i> , 2011, 39, 9061-9071.	6.5	175
38	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
39	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
40	Combinatorial profiling of chromatin binding modules reveals multisite discrimination. <i>Nature Chemical Biology</i> , 2010, 6, 283-290.	3.9	115
41	Referencing Strategy for the Direct Comparison of Nuclear Magnetic Resonance and Molecular Dynamics Motional Parameters in RNA. <i>Journal of Physical Chemistry B</i> , 2010, 114, 929-939.	1.2	18
42	Structural Insight into p53 Recognition by the 53BP1 Tandem Tudor Domain. <i>Journal of Molecular Biology</i> , 2010, 398, 489-496.	2.0	50
43	Molecular Mechanism of MLL PHD3 and RNA Recognition by the Cyp33 RRM Domain. <i>Journal of Molecular Biology</i> , 2010, 400, 145-154.	2.0	40
44	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
45	NMR assignments and histone specificity of the ING2 PHD finger. <i>Magnetic Resonance in Chemistry</i> , 2009, 47, 352-358.	1.1	9
46	Membrane insertion of the FYVE domain is modulated by pH. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 76, 852-860.	1.5	58
47	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
48	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
49	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
50	iRED Analysis of TAR RNA Reveals Motional Coupling, Long-Range Correlations, and a Dynamical Hinge. <i>Biophysical Journal</i> , 2007, 93, 411-422.	0.2	31
51	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
52	Impact of static and dynamic A-form heterogeneity on the determination of RNA global structural dynamics using NMR residual dipolar couplings. <i>Journal of Biomolecular NMR</i> , 2006, 36, 235-249.	1.6	54