

# Ali Hamiche

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

5,425  
citations

126708

33  
h-index

133063

59  
g-index

62  
all docs

62  
docs citations

62  
times ranked

6930  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tannin extract from maritime pine bark exhibits anticancer properties by targeting the epigenetic UHRF1/DNMT1 tandem leading to the re-expression of <i>TP73</i> . <i>Food and Function</i> , 2022, 13, 316-326.	2.1	5
2	Dual role of histone variant H3.3B in spermatogenesis: positive regulation of piRNA transcription and implication in X-chromosome inactivation. <i>Nucleic Acids Research</i> , 2022, 50, 7350-7366.	6.5	5
3	CpG Islands Shape the Epigenome Landscape. <i>Journal of Molecular Biology</i> , 2021, 433, 166659.	2.0	16
4	The NANOTUMOR consortium “Towards the Tumor Cell Atlas. <i>Biology of the Cell</i> , 2021, 113, 272-280.	0.7	1
5	Thymoquinone Is a Multitarget Single Epidrug That Inhibits the UHRF1 Protein Complex. <i>Genes</i> , 2021, 12, 622.	1.0	14
6	MeCP2 is a microsatellite binding protein that protects CA repeats from nucleosome invasion. <i>Science</i> , 2021, 372, .	6.0	36
7	TIP60 governs the auto-ubiquitination of UHRF1 through USP7 dissociation from the UHRF1/USP7 complex. <i>International Journal of Oncology</i> , 2021, 59, .	1.4	7
8	The Role of Histone Variants in the Epithelial-To-Mesenchymal Transition. <i>Cells</i> , 2020, 9, 2499.	1.8	2
9	Cryo-electron microscopy of the chromatin fiber. <i>Current Opinion in Structural Biology</i> , 2020, 64, 97-103.	2.6	13
10	H2A.Z is dispensable for both basal and activated transcription in post-mitotic mouse muscles. <i>Nucleic Acids Research</i> , 2020, 48, 4601-4613.	6.5	18
11	Phase-plate cryo-EM structure of the Widom 601 CENP-A nucleosome core particle reveals differential flexibility of the DNA ends. <i>Nucleic Acids Research</i> , 2020, 48, 5735-5748.	6.5	27
12	Generation of Remosomes by the SWI/SNF Chromatin Remodeler Family. <i>Scientific Reports</i> , 2019, 9, 14212.	1.6	4
13	CENP-A nucleosome clusters form rosette-like structures around HJURP during G1. <i>Nature Communications</i> , 2019, 10, 4436.	5.8	25
14	Coordinated Dialogue between UHRF1 and DNMT1 to Ensure Faithful Inheritance of Methylated DNA Patterns. <i>Genes</i> , 2019, 10, 65.	1.0	73
15	Centromeric and ectopic assembly of CENP-A chromatin in health and cancer: old marks and new tracks. <i>Nucleic Acids Research</i> , 2019, 47, 1051-1069.	6.5	51
16	3DClusterViSu: 3D clustering analysis of super-resolution microscopy data by 3D Voronoi tessellations. <i>Bioinformatics</i> , 2018, 34, 3004-3012.	1.8	37
17	Identification of Deregulated Signaling Pathways in Jurkat Cells in Response to a Novel Acylspermidine Analogue-N4-Erucoyl Spermidine. <i>Epigenetics Insights</i> , 2018, 11, 251686571881454.	0.6	12
18	Structure of an H1-Bound 6-Nucleosome Array Reveals an Untwisted Two-Start Chromatin Fiber Conformation. <i>Molecular Cell</i> , 2018, 72, 902-915.e7.	4.5	93

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19	Thymoquinone challenges UHRF1 to commit auto-ubiquitination: a key event for apoptosis induction in cancer cells. <i>Oncotarget</i> , 2018, 9, 28599-28611.	0.8	25
20	Histone H3.3 regulates mitotic progression in mouse embryonic fibroblasts. <i>Biochemistry and Cell Biology</i> , 2017, 95, 491-499.	0.9	9
21	Structure and Dynamics of a 197Åbp Nucleosome in Complex with Linker Histone H1. <i>Molecular Cell</i> , 2017, 66, 384-397.e8.	4.5	225
22	The <i>Drosophila</i> DAXX-Like Protein (DLP) Cooperates with ASF1 for H3.3 Deposition and Heterochromatin Formation. <i>Molecular and Cellular Biology</i> , 2017, 37, .	1.1	15
23	Combinatorial DNA methylation codes at repetitive elements. <i>Genome Research</i> , 2017, 27, 934-946.	2.4	44
24	The epigenetic integrator UHRF1: on the road to become a universal biomarker for cancer. <i>Oncotarget</i> , 2017, 8, 51946-51962.	0.8	91
25	The Flexible Ends of CENP-A Nucleosome Are Required for Mitotic Fidelity. <i>Molecular Cell</i> , 2016, 63, 674-685.	4.5	72
26	Molecular basis and specificity of H2A.Z-H2B recognition and deposition by the histone chaperone YL1. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 309-316.	3.6	67
27	FACT Assists Base Excision Repair by Boosting the Remodeling Activity of RSC. <i>PLoS Genetics</i> , 2016, 12, e1006221.	1.5	39
28	Structure and function insights into the NuRD chromatin remodeling complex. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 2491-2507.	2.4	165
29	Cracking the ANP32 whips: Important functions, unequal requirement, and hints at disease implications. <i>BioEssays</i> , 2014, 36, 1062-1071.	1.2	90
30	ANP32E is a histone chaperone that removes H2A.Z from chromatin. <i>Nature</i> , 2014, 505, 648-653.	13.7	217
31	Epigallocatechin-3-gallate up-regulates tumor suppressor gene expression via a reactive oxygen species-dependent down-regulation of UHRF1. <i>Biochemical and Biophysical Research Communications</i> , 2013, 430, 208-212.	1.0	64
32	Phosphorylation of the CENP-A amino-terminus in mitotic centromeric chromatin is required for kinetochore function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8579-8584.	3.3	55
33	Cancer cell death and selection: Unexpected putative roles for pRb2/p130, BORIS and CTCF in endoplasmic stress response maintained by the T-antigen. <i>Cell Cycle</i> , 2012, 11, 2052-2052.	1.3	0
34	Chaperoning the histone H3 family. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2012, 1819, 230-237.	0.9	30
35	Argonaute proteins couple chromatin silencing to alternative splicing. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 998-1004.	3.6	245
36	Transcription cofactors TRIM24, TRIM28, and TRIM33 associate to form regulatory complexes that suppress murine hepatocellular carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8212-8217.	3.3	178

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37	The docking domain of histone H2A is required for H1 binding and RSC-mediated nucleosome remodeling. <i>Nucleic Acids Research</i> , 2011, 39, 2559-2570.	6.5	56
38	The structural plasticity of SCA7 domains defines their differential nucleosome-binding properties. <i>EMBO Reports</i> , 2010, 11, 612-618.	2.0	28
39	HJURP binds CENP-A via a highly conserved N-terminal domain and mediates its deposition at centromeres. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1349-1354.	3.3	170
40	The death-associated protein DAXX is a novel histone chaperone involved in the replication-independent deposition of H3.3. <i>Genes and Development</i> , 2010, 24, 1253-1265.	2.7	552
41	Physical and Functional Interaction between Heterochromatin Protein 1 and the RNA-binding Protein Heterogeneous Nuclear Ribonucleoprotein U. <i>Journal of Biological Chemistry</i> , 2009, 284, 27974-27979.	1.6	15
42	Histone Deacetylase Inhibitors Promote the Tumoricidal Effect of HAMLET. <i>Cancer Research</i> , 2007, 67, 11327-11334.	0.4	20
43	ATP-Dependent Chromatin Remodeling Is Required for Base Excision Repair in Conventional but Not in Variant H2A.Bbd Nucleosomes. <i>Molecular and Cellular Biology</i> , 2007, 27, 5949-5956.	1.1	103
44	Nucleolin is a histone chaperone with FACT-like activity and assists remodeling of nucleosomes. <i>EMBO Journal</i> , 2006, 25, 1669-1679.	3.5	219
45	Dissection of the unusual structural and functional properties of the variant H2A.Bbd nucleosome. <i>EMBO Journal</i> , 2006, 25, 4234-4244.	3.5	103
46	The histone variant mH2A1.1 interferes with transcription by down-regulating PARP-1 enzymatic activity. <i>Genes and Development</i> , 2006, 20, 3324-3336.	2.7	149
47	The NH 2 Tail of the Novel Histone Variant H2BFWT Exhibits Properties Distinct from Conventional H2B with Respect to the Assembly of Mitotic Chromosomes. <i>Molecular and Cellular Biology</i> , 2006, 26, 1518-1526.	1.1	53
48	Mechanism of Polymerase II Transcription Repression by the Histone Variant macroH2A. <i>Molecular and Cellular Biology</i> , 2006, 26, 1156-1164.	1.1	129
49	SWI/SNF remodeling and p300-dependent transcription of histone variant H2ABbd nucleosomal arrays. <i>EMBO Journal</i> , 2004, 23, 3815-3824.	3.5	66
50	Methods for chromatin assembly and remodeling. <i>Methods</i> , 2004, 33, 12-17.	1.9	7
51	Methods for Analysis of Nucleosome Sliding by Drosophila NURF. <i>Methods in Enzymology</i> , 2003, 377, 353-363.	0.4	6
52	HAMLET Interacts with Histones and Chromatin in Tumor Cell Nuclei. <i>Journal of Biological Chemistry</i> , 2003, 278, 42131-42135.	1.6	106
53	GAL4 directs nucleosome sliding induced by NURF. <i>EMBO Journal</i> , 2002, 21, 1406-1413.	3.5	38
54	Dual Functions of Largest NURF Subunit NURF301 in Nucleosome Sliding and Transcription Factor Interactions. <i>Molecular Cell</i> , 2001, 8, 531-543.	4.5	229

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55	A chromatin remodelling complex involved in transcription and DNA processing. Nature, 2000, 406, 541-544.	13.7	723
56	ATP-Dependent Histone Octamer Sliding Mediated by the Chromatin Remodeling Complex NURF. Cell, 1999, 97, 833-842.	13.5	302
57	The Switch in the Helical Handedness of the Histone (H3-H4) <sub>2</sub> Tetramer within a Nucleoprotein Particle Requires a Reorientation of the H3-H3 Interface. Journal of Biological Chemistry, 1998, 273, 9261-9269.	1.6	44
58	Linker Histone-dependent DNA Structure in Linear Mononucleosomes. Journal of Molecular Biology, 1996, 257, 30-42.	2.0	166
59	Octamer displacement and redistribution in transcription of single nucleosomes. Nucleic Acids Research, 1994, 22, 937-945.	6.5	50
60	Chromatin reconstitution on small DNA rings. Journal of Molecular Biology, 1992, 228, 327-337.	2.0	16