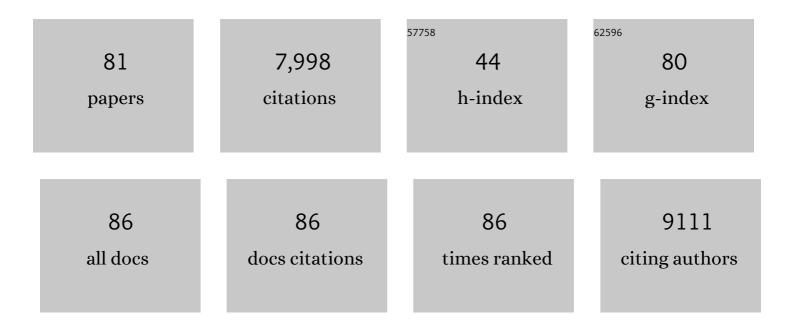
Asifa Akhtar

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1903766/publications.pdf Version: 2024-02-01



Δςιέλ Δκητλά

#	Article	IF	CITATIONS
1	Modulation of cellular processes by histone and non-histone protein acetylation. Nature Reviews Molecular Cell Biology, 2022, 23, 329-349.	37.0	239
2	Epigenetic Regulators as the Gatekeepers of Hematopoiesis. Trends in Genetics, 2021, 37, 125-142.	6.7	40
3	RNA nucleation by MSL2 induces selective X chromosome compartmentalization. Nature, 2021, 589, 137-142.	27.8	34
4	Functional mechanisms and abnormalities of the nuclear lamina. Nature Cell Biology, 2021, 23, 116-126.	10.3	52
5	Distinct mechanisms mediate X chromosome dosage compensation in <i>Anopheles</i> and <i>Drosophila</i> . Life Science Alliance, 2021, 4, e202000996.	2.8	13
6	Chemotherapy-induced transposable elements activate MDA5 to enhance haematopoietic regeneration. Nature Cell Biology, 2021, 23, 704-717.	10.3	40
7	Differential H4K16ac levels ensure a balance between quiescence and activation in hematopoietic stem cells. Science Advances, 2021, 7, .	10.3	11
8	Histone H4 lysine 16 acetylation controls central carbon metabolism and diet-induced obesity in mice. Nature Communications, 2021, 12, 6212.	12.8	16
9	FLASH: ultra-fast protocol to identify RNA–protein interactions in cells. Nucleic Acids Research, 2020, 48, e15-e15.	14.5	21
10	Nephronophthisis gene products display RNA-binding properties and are recruited to stress granules. Scientific Reports, 2020, 10, 15954.	3.3	13
11	Temporal expression of MOF acetyltransferase primes transcription factor networks for erythroid fate. Science Advances, 2020, 6, eaaz4815.	10.3	17
12	Evolutionary conserved NSL complex/BRD4 axis controls transcription activation via histone acetylation. Nature Communications, 2020, 11, 2243.	12.8	21
13	Neural metabolic imbalance induced by MOF dysfunction triggers pericyte activation and breakdown of vasculature. Nature Cell Biology, 2020, 22, 828-841.	10.3	27
14	Intergenerationally Maintained Histone H4 Lysine 16 Acetylation Is Instructive for Future Gene Activation. Cell, 2020, 182, 127-144.e23.	28.9	57
15	MAPCap allows high-resolution detection and differential expression analysis of transcription start sites. Nature Communications, 2019, 10, 3219.	12.8	16
16	Hi-C guided assemblies reveal conserved regulatory topologies on X and autosomes despite extensive genome shuffling. Genes and Development, 2019, 33, 1591-1612.	5.9	43
17	Systematic Identification of Cell-Cell Communication Networks in the Developing Brain. IScience, 2019, 21, 273-287.	4.1	37
18	The NSL complex maintains nuclear architecture stability via lamin A/C acetylation. Nature Cell Biology, 2019, 21, 1248-1260.	10.3	61

#	Article	IF	CITATIONS
19	CAPRI enables comparison of evolutionarily conserved RNA interacting regions. Nature Communications, 2019, 10, 2682.	12.8	39
20	The nonâ€specific lethal (<scp>NSL</scp>) complex at the crossroads of transcriptional control and cellular homeostasis. EMBO Reports, 2019, 20, e47630.	4.5	63
21	The NSL complex-mediated nucleosome landscape is required to maintain transcription fidelity and suppression of transcription noise. Genes and Development, 2019, 33, 452-465.	5.9	12
22	Cofactor Analogues as Active Site Probes in Lysine Acetyltransferases. Journal of Medicinal Chemistry, 2019, 62, 2582-2597.	6.4	8
23	The many lives of KATs — detectors, integrators and modulators of the cellular environment. Nature Reviews Genetics, 2019, 20, 7-23.	16.3	129
24	Repetitive Elements Enhance Hematopoietic Regeneration Via Activation of the Innate Immune Receptor MDA5. Blood, 2019, 134, 818-818.	1.4	0
25	Dosage Compensation of the X Chromosome: A Complex Epigenetic Assignment Involving Chromatin Regulators and Long Noncoding RNAs. Annual Review of Biochemistry, 2018, 87, 323-350.	11.1	106
26	High-resolution TADs reveal DNA sequences underlying genome organization in flies. Nature Communications, 2018, 9, 189.	12.8	652
27	uvCLAP is a fast and non-radioactive method to identify in vivo targets of RNA-binding proteins. Nature Communications, 2018, 9, 1142.	12.8	22
28	Finding your way through the science maze. Nature Cell Biology, 2018, 20, 1000-1000.	10.3	0
29	De novo mutations in MSL3 cause an X-linked syndrome marked by impaired histone H4 lysine 16 acetylation. Nature Genetics, 2018, 50, 1442-1451.	21.4	28
30	Facultative dosage compensation of developmental genes on autosomes in Drosophila and mouse embryonic stem cells. Nature Communications, 2018, 9, 3626.	12.8	21
31	DHX9 suppresses RNA processing defects originating from the Alu invasion of the human genome. Nature, 2017, 544, 115-119.	27.8	415
32	A mutually exclusive stem–loop arrangement in roX2 RNA is essential for X-chromosome regulation in <i>Drosophila</i> . Genes and Development, 2017, 31, 1973-1987.	5.9	24
33	Functional interplay between MSL1 and CDK7 controls RNA polymerase II Ser5 phosphorylation. Nature Structural and Molecular Biology, 2016, 23, 580-589.	8.2	19
34	MOF Acetyl Transferase Regulates Transcription and Respiration in Mitochondria. Cell, 2016, 167, 722-738.e23.	28.9	130
35	Rapid evolutionary turnover underlies conserved lncRNA–genome interactions. Genes and Development, 2016, 30, 191-207.	5.9	152
36	An epigenetic regulator emerges as microtubule minus-end binding and stabilizing factor in mitosis. Nature Communications, 2015, 6, 7889.	12.8	48

#	Article	IF	CITATIONS
37	The MSL complex: juggling RNA–protein interactions for dosage compensation and beyond. Current Opinion in Genetics and Development, 2015, 31, 1-11.	3.3	55
38	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in Drosophila. Molecular Cell, 2015, 60, 146-162.	9.7	70
39	Revealing long noncoding RNA architecture and functions using domain-specific chromatin isolation by RNA purification. Nature Biotechnology, 2014, 32, 933-940.	17.5	161
40	Structural analysis of the KANSL1/WDR5/KANSL2 complex reveals that WDR5 is required for efficient assembly and chromatin targeting of the NSL complex. Genes and Development, 2014, 28, 929-942.	5.9	88
41	Considerations when investigating IncRNA function in vivo. ELife, 2014, 3, e03058.	6.0	309
42	MOF-associated complexes ensure stem cell identity and Xist repression. ELife, 2014, 3, e02024.	6.0	76
43	Tandem Stem-Loops in roX RNAs Act Together to Mediate X Chromosome Dosage Compensation in Drosophila. Molecular Cell, 2013, 51, 156-173.	9.7	152
44	The NSL Complex Regulates Housekeeping Genes in Drosophila. PLoS Genetics, 2012, 8, e1002736.	3.5	80
45	The MOF Chromobarrel Domain Controls Genome-wide H4K16 Acetylation and Spreading of the MSL Complex. Developmental Cell, 2012, 22, 610-624.	7.0	63
46	<i>Drosophila</i> Dosage Compensation Involves Enhanced Pol II Recruitment to Male X-Linked Promoters. Science, 2012, 337, 742-746.	12.6	69
47	Msl1-Mediated Dimerization of the Dosage Compensation Complex Is Essential for Male X-Chromosome Regulation in Drosophila. Molecular Cell, 2012, 48, 587-600.	9.7	42
48	Dosage compensation in Drosophila melanogaster: epigenetic fine-tuning of chromosome-wide transcription. Nature Reviews Genetics, 2012, 13, 123-134.	16.3	232
49	The nucleus and gene expression: the center of the cyclone. Current Opinion in Cell Biology, 2012, 24, 293-295.	5.4	1
50	A decade of molecular cell biology: achievements and challenges. Nature Reviews Molecular Cell Biology, 2011, 12, 669-674.	37.0	20
51	Structural basis for MOF and MSL3 recruitment into the dosage compensation complex by MSL1. Nature Structural and Molecular Biology, 2011, 18, 142-149.	8.2	98
52	Multiple facets of nuclear periphery in gene expression control. Current Opinion in Cell Biology, 2011, 23, 346-353.	5.4	51
53	Drosophila dosage compensation. Fly, 2011, 5, 147-154.	1.7	26
54	Nuclear Pore Proteins Nup153 and Megator Define Transcriptionally Active Regions in the Drosophila Genome. PLoS Genetics, 2010, 6, e1000846.	3.5	218

#	Article	IF	CITATIONS
55	<i>Drosophila</i> MCRS2 Associates with RNA Polymerase II Complexes To Regulate Transcription. Molecular and Cellular Biology, 2010, 30, 4744-4755.	2.3	20
56	The Nonspecific Lethal Complex Is a Transcriptional Regulator in Drosophila. Molecular Cell, 2010, 38, 827-841.	9.7	131
57	The MSL complex: X chromosome and beyond. Current Opinion in Genetics and Development, 2010, 20, 171-178.	3.3	26
58	roX RNAs: Non-coding regulators of the male X chromosome in flies. RNA Biology, 2009, 6, 113-121.	3.1	45
59	X chromosomal regulation in flies: when less is more. Chromosome Research, 2009, 17, 603-19.	2.2	19
60	Reversible acetylation of the chromatin remodelling complex NoRC is required for non-coding RNA-dependent silencing. Nature Cell Biology, 2009, 11, 1010-1016.	10.3	109
61	Genome-wide Analysis Reveals MOF as a Key Regulator of Dosage Compensation and Gene Expression in Drosophila. Cell, 2008, 133, 813-828.	28.9	144
62	The histone acetyltransferase hMOF is frequently downregulated in primary breast carcinoma and medulloblastoma and constitutes a biomarker for clinical outcome in medulloblastoma. International Journal of Cancer, 2008, 122, 1207-1213.	5.1	146
63	Transcription-Coupled Methylation of Histone H3 at Lysine 36 Regulates Dosage Compensation by Enhancing Recruitment of the MSL Complex in <i>Drosophila melanogaster</i> . Molecular and Cellular Biology, 2008, 28, 3401-3409.	2.3	64
64	Cotranscriptional recruitment of the dosage compensation complex to X-linked target genes. Genes and Development, 2007, 21, 2030-2040.	5.9	52
65	The nuclear envelope and transcriptional control. Nature Reviews Genetics, 2007, 8, 507-517.	16.3	396
66	The right dose for every sex. Chromosoma, 2007, 116, 95-106.	2.2	44
67	Nuclear Pore Components Are Involved in the Transcriptional Regulation of Dosage Compensation in Drosophila. Molecular Cell, 2006, 21, 811-823.	9.7	368
68	A general precursor ion-like scanning mode on quadrupole-TOF instruments compatible with chromatographic separation. Proteomics, 2006, 6, 41-53.	2.2	32
69	Xâ€chromosome targeting and dosage compensation are mediated by distinct domains in MSLâ€3. EMBO Reports, 2006, 7, 531-538.	4.5	29
70	X-chromosome-wide profiling of MSL-1 distribution and dosage compensation in Drosophila. Genes and Development, 2006, 20, 871-883.	5.9	88
71	The Epigenome Network of Excellence. PLoS Biology, 2005, 3, e177.	5.6	18
72	Structure of the Chromo Barrel Domain from the MOF Acetyltransferase. Journal of Biological Chemistry, 2005, 280, 32326-32331.	3.4	49

#	Article	IF	CITATIONS
73	hMOF Histone Acetyltransferase Is Required for Histone H4 Lysine 16 Acetylation in Mammalian Cells. Molecular and Cellular Biology, 2005, 25, 6798-6810.	2.3	281
74	NMR Structure of the First PHD Finger of Autoimmune Regulator Protein (AIRE1). Journal of Biological Chemistry, 2005, 280, 11505-11512.	3.4	76
75	Functional integration of the histone acetyltransferase MOF into the dosage compensation complex. EMBO Journal, 2004, 23, 2258-2268.	7.8	108
76	Dosage compensation: an intertwined world of RNA and chromatin remodelling. Current Opinion in Genetics and Development, 2003, 13, 161-169.	3.3	61
77	MOF-Regulated Acetylation of MSL-3 in the Drosophila Dosage Compensation Complex. Molecular Cell, 2003, 11, 1265-1277.	9.7	78
78	The dMi-2 chromodomains are DNA binding modules important for ATP-dependent nucleosome mobilization. EMBO Journal, 2002, 21, 2430-2440.	7.8	132
79	The histone H4 acetyltransferase MOF uses a C2HC zinc finger for substrate recognition. EMBO Reports, 2001, 2, 113-118.	4.5	231
80	Chromodomains are protein–RNA interaction modules. Nature, 2000, 407, 405-409.	27.8	364
81	Activation of Transcription through Histone H4 Acetylation by MOF, an Acetyltransferase Essential for Dosage Compensation in Drosophila. Molecular Cell, 2000, 5, 367-375.	9.7	429