Asifa Akhtar

List of Publications by Year
in descending order

81 papers	7,998 citations	57758 44 h-index	62596 80 g-index
86 all docs	86 docs citations	86 times ranked	9111 citing authors

#	Article	IF	Citations
1	High-resolution TADs reveal DNA sequences underlying genome organization in flies. Nature Communications, 2018, 9, 189.	12.8	652
2	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
3	DHX9 suppresses RNA processing defects originating from the Alu invasion of the human genome. Nature, 2017, 544, 115-119.	27.8	415
4	The nuclear envelope and transcriptional control. Nature Reviews Genetics, 2007, 8, 507-517.	16.3	396
5	Nuclear Pore Components Are Involved in the Transcriptional Regulation of Dosage Compensation in Drosophila. Molecular Cell, 2006, 21, 811-823.	9.7	368
6	Chromodomains are proteinâ€"RNA interaction modules. Nature, 2000, 407, 405-409.	27.8	364
7	Considerations when investigating lncRNA function in vivo. ELife, 2014, 3, e03058.	6.0	309
8	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
9	Modulation of cellular processes by histone and non-histone protein acetylation. Nature Reviews Molecular Cell Biology, 2022, 23, 329-349.	37.0	239
10	Dosage compensation in Drosophila melanogaster: epigenetic fine-tuning of chromosome-wide transcription. Nature Reviews Genetics, 2012, 13, 123-134.	16.3	232
11	The histone H4 acetyltransferase MOF uses a C2HC zinc finger for substrate recognition. EMBO Reports, 2001, 2, 113-118.	4.5	231
12	Nuclear Pore Proteins Nup153 and Megator Define Transcriptionally Active Regions in the Drosophila Genome. PLoS Genetics, 2010, 6, e1000846.	3.5	218
13	Revealing long noncoding RNA architecture and functions using domain-specific chromatin isolation by RNA purification. Nature Biotechnology, 2014, 32, 933-940.	17.5	161
14	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
15	Rapid evolutionary turnover underlies conserved lncRNAâ€"genome interactions. Genes and Development, 2016, 30, 191-207.	5.9	152
16	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
17	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
18	The dMi-2 chromodomains are DNA binding modules important for ATP-dependent nucleosome mobilization. EMBO Journal, 2002, 21, 2430-2440.	7.8	132

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19	The Nonspecific Lethal Complex Is a Transcriptional Regulator in Drosophila. Molecular Cell, 2010, 38, 827-841.	9.7	131
20	MOF Acetyl Transferase Regulates Transcription and Respiration in Mitochondria. Cell, 2016, 167, 722-738.e23.	28.9	130
21	The many lives of KATs â€" detectors, integrators and modulators of the cellular environment. Nature Reviews Genetics, 2019, 20, 7-23.	16.3	129
22	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
23	Functional integration of the histone acetyltransferase MOF into the dosage compensation complex. EMBO Journal, 2004, 23, 2258-2268.	7.8	108
24	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
25	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
26	X-chromosome-wide profiling of MSL-1 distribution and dosage compensation in Drosophila. Genes and Development, 2006, 20, 871-883.	5.9	88
27	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
28	The NSL Complex Regulates Housekeeping Genes in Drosophila. PLoS Genetics, 2012, 8, e1002736.	3.5	80
29	MOF-Regulated Acetylation of MSL-3 in the Drosophila Dosage Compensation Complex. Molecular Cell, 2003, 11, 1265-1277.	9.7	78
30	NMR Structure of the First PHD Finger of Autoimmune Regulator Protein (AIRE1). Journal of Biological Chemistry, 2005, 280, 11505-11512.	3.4	76
31	MOF-associated complexes ensure stem cell identity and Xist repression. ELife, 2014, 3, e02024.	6.0	76
32	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
33	<i>Drosophila</i> Dosage Compensation Involves Enhanced Pol II Recruitment to Male X-Linked Promoters. Science, 2012, 337, 742-746.	12.6	69
34	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
35	The MOF Chromobarrel Domain Controls Genome-wide H4K16 Acetylation and Spreading of the MSL Complex. Developmental Cell, 2012, 22, 610-624.	7.0	63
36	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

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37	Dosage compensation: an intertwined world of RNA and chromatin remodelling. Current Opinion in Genetics and Development, 2003, 13, 161-169.	3.3	61
38	The NSL complex maintains nuclear architecture stability via lamin A/C acetylation. Nature Cell Biology, 2019, 21, 1248-1260.	10.3	61
39	Intergenerationally Maintained Histone H4 Lysine 16 Acetylation Is Instructive for Future Gene Activation. Cell, 2020, 182, 127-144.e23.	28.9	57
40	The MSL complex: juggling RNAâ€"protein interactions for dosage compensation and beyond. Current Opinion in Genetics and Development, 2015, 31, 1-11.	3.3	55
41	Cotranscriptional recruitment of the dosage compensation complex to X-linked target genes. Genes and Development, 2007, 21, 2030-2040.	5.9	52
42	Functional mechanisms and abnormalities of the nuclear lamina. Nature Cell Biology, 2021, 23, 116-126.	10.3	52
43	Multiple facets of nuclear periphery in gene expression control. Current Opinion in Cell Biology, 2011, 23, 346-353.	5.4	51
44	Structure of the Chromo Barrel Domain from the MOF Acetyltransferase. Journal of Biological Chemistry, 2005, 280, 32326-32331.	3.4	49
45	An epigenetic regulator emerges as microtubule minus-end binding and stabilizing factor in mitosis. Nature Communications, 2015, 6, 7889.	12.8	48
46	roX RNAs: Non-coding regulators of the male X chromosome in flies. RNA Biology, 2009, 6, 113-121.	3.1	45
47	The right dose for every sex. Chromosoma, 2007, 116, 95-106.	2.2	44
48	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
49	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
50	Epigenetic Regulators as the Gatekeepers of Hematopoiesis. Trends in Genetics, 2021, 37, 125-142.	6.7	40
51	Chemotherapy-induced transposable elements activate MDA5 to enhance haematopoietic regeneration. Nature Cell Biology, 2021, 23, 704-717.	10.3	40
52	CAPRI enables comparison of evolutionarily conserved RNA interacting regions. Nature Communications, 2019, 10, 2682.	12.8	39
53	Systematic Identification of Cell-Cell Communication Networks in the Developing Brain. IScience, 2019, 21, 273-287.	4.1	37
54	RNA nucleation by MSL2 induces selective X chromosome compartmentalization. Nature, 2021, 589, 137-142.	27.8	34

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55	A general precursor ion-like scanning mode on quadrupole-TOF instruments compatible with chromatographic separation. Proteomics, 2006, 6, 41-53.	2.2	32
56	Xâ€•chromosome targeting and dosage compensation are mediated by distinct domains in MSLâ€•3. EMBO Reports, 2006, 7, 531-538.	4.5	29
57	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
58	Neural metabolic imbalance induced by MOF dysfunction triggers pericyte activation and breakdown of vasculature. Nature Cell Biology, 2020, 22, 828-841.	10.3	27
59	The MSL complex: X chromosome and beyond. Current Opinion in Genetics and Development, 2010, 20, 171-178.	3.3	26
60	Drosophila dosage compensation. Fly, 2011, 5, 147-154.	1.7	26
61	A mutually exclusive stemâ€“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
62	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
63	Facultative dosage compensation of developmental genes on autosomes in Drosophila and mouse embryonic stem cells. Nature Communications, 2018, 9, 3626.	12.8	21
64	FLASH: ultra-fast protocol to identify RNAâ€“protein interactions in cells. Nucleic Acids Research, 2020, 48, e15-e15.	14.5	21
65	Evolutionary conserved NSL complex/BRD4 axis controls transcription activation via histone acetylation. Nature Communications, 2020, 11, 2243.	12.8	21
66	<i>Drosophila</i> MCRS2 Associates with RNA Polymerase II Complexes To Regulate Transcription. Molecular and Cellular Biology, 2010, 30, 4744-4755.	2.3	20
67	A decade of molecular cell biology: achievements and challenges. Nature Reviews Molecular Cell Biology, 2011, 12, 669-674.	37.0	20
68	X chromosomal regulation in flies: when less is more. Chromosome Research, 2009, 17, 603-19.	2.2	19
69	Functional interplay between MSL1 and CDK7 controls RNA polymerase II Ser5 phosphorylation. Nature Structural and Molecular Biology, 2016, 23, 580-589.	8.2	19
70	The Epigenome Network of Excellence. PLoS Biology, 2005, 3, e177.	5.6	18
71	Temporal expression of MOF acetyltransferase primes transcription factor networks for erythroid fate. Science Advances, 2020, 6, eaaz4815.	10.3	17
72	MAPCap allows high-resolution detection and differential expression analysis of transcription start sites. Nature Communications, 2019, 10, 3219.	12.8	16

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73	Histone H4 lysine 16 acetylation controls central carbon metabolism and diet-induced obesity in mice. Nature Communications, 2021, 12, 6212.	12.8	16
74	Nephronophthisis gene products display RNA-binding properties and are recruited to stress granules. Scientific Reports, 2020, 10, 15954.	3.3	13
75	Distinct mechanisms mediate X chromosome dosage compensation in <i>Anopheles</i> and <i>Drosophila</i>. Life Science Alliance, 2021, 4, e202000996.	2.8	13
76	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
77	Differential H4K16ac levels ensure a balance between quiescence and activation in hematopoietic stem cells. Science Advances, 2021, 7, .	10.3	11
78	Cofactor Analogues as Active Site Probes in Lysine Acetyltransferases. Journal of Medicinal Chemistry, 2019, 62, 2582-2597.	6.4	8
79	The nucleus and gene expression: the center of the cyclone. Current Opinion in Cell Biology, 2012, 24, 293-295.	5.4	1
80	Finding your way through the science maze. Nature Cell Biology, 2018, 20, 1000-1000.	10.3	0
81	Repetitive Elements Enhance Hematopoietic Regeneration Via Activation of the Innate Immune Receptor MDA5. Blood, 2019, 134, 818-818.	1.4	0