Ali Shilatifard

List of Publications by Year
in descending order

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		5876	6630
175 papers	27,440 citations	81 h-index	156 g-index
183 all docs	183 docs citations	183 times ranked	29893 citing authors

#	ARTICLE	IF	CITATIONS
1	An operational definition of epigenetics: Figure 1.. Genes and Development, 2009, 23, 781-783.	2.7	1,457
2	Chromatin Modifications by Methylation and Ubiquitination: Implications in the Regulation of Gene Expression. Annual Review of Biochemistry, 2006, 75, 243-269.	5.0	1,002
3	The COMPASS Family of Histone H3K4 Methylases: Mechanisms of Regulation in Development and Disease Pathogenesis. Annual Review of Biochemistry, 2012, 81, 65-95.	5.0	896
4	Single-Cell Transcriptomic Analysis of Human Lung Provides Insights into the Pathobiology of Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 1517-1536.	2.5	866
5	Monocyte-derived alveolar macrophages drive lung fibrosis and persist in the lung over the life span. Journal of Experimental Medicine, 2017, 214, 2387-2404.	4.2	755
6	The Paf1 Complex Is Required for Histone H3 Methylation by COMPASS and Dot1p: Linking Transcriptional Elongation to Histone Methylation. Molecular Cell, 2003, 11, 721-729.	4.5	642
7	Histone H2B Monoubiquitination Functions Cooperatively with FACT to Regulate Elongation by RNA Polymerase II. Cell, 2006, 125, 703-717.	13.5	636
8	Methylation of Histone H3 by Set2 in Saccharomyces cerevisiae Is Linked to Transcriptional Elongation by RNA Polymerase II. Molecular and Cellular Biology, 2003, 23, 4207-4218.	1.1	600
9	Circuits between infected macrophages and T cells in SARS-CoV-2 pneumonia. Nature, 2021, 590, 635-641.	13.7	524
10	The Language of Histone Crosstalk. Cell, 2010, 142, 682-685.	13.5	505
11	AFF4, a Component of the ELL/P-TEFb Elongation Complex and a Shared Subunit of MLL Chimeras, Can Link Transcription Elongation to Leukemia. Molecular Cell, 2010, 37, 429-437.	4.5	504
12	Bre1, an E3 Ubiquitin Ligase Required for Recruitment and Substrate Selection of Rad6 at a Promoter. Molecular Cell, 2003, 11, 267-274.	4.5	489
13	RNA Polymerase II Elongation Factors of Saccharomyces cerevisiae : a Targeted Proteomics Approach. Molecular and Cellular Biology, 2002, 22, 6979-6992.	1.1	462
14	RAD6-Mediated Transcription-Coupled H2B Ubiquitylation Directly Stimulates H3K4 Methylation in Human Cells. Cell, 2009, 137, 459-471.	13.5	453
15	Integrator, a Multiprotein Mediator of Small Nuclear RNA Processing, Associates with the C-Terminal Repeat of RNA Polymerase II. Cell, 2005, 123, 265-276.	13.5	420
16	Molecular implementation and physiological roles for histone H3 lysine 4 (H3K4) methylation. Current Opinion in Cell Biology, 2008, 20, 341-348.	2.6	418
17	Histone modification: cause or cog?. Trends in Genetics, 2011, 27, 389-396.	2.9	415
18	Epigenetic balance of gene expression by Polycomb and COMPASS families. Science, 2016, 352, aad9780.	6.0	407

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19	Gain-of-function p53 mutants co-opt chromatin pathways to drive cancer growth. Nature, 2015, 525, 206-211.	13.7	386
20	Histone Crosstalk between H2B Monoubiquitination and H3 Methylation Mediated by COMPASS. Cell, 2007, 131, 1084-1096.	13.5	373
21	COMPASS, a Histone H3 (Lysine 4) Methyltransferase Required for Telomeric Silencing of Gene Expression. Journal of Biological Chemistry, 2002, 277, 10753-10755.	1.6	365
22	The histone lysine methyltransferase KMT2D sustains a gene expression program that represses B cell lymphoma development. Nature Medicine, 2015, 21, 1199-1208.	15.2	359
23	The Paf1 Complex Is Essential for Histone Monoubiquitination by the Rad6-Bre1 Complex, Which Signals for Histone Methylation by COMPASS and Dot1p. Journal of Biological Chemistry, 2003, 278, 34739-34742.	1.6	340
24	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. Nature Medicine, 2017, 23, 493-500.	15.2	332
25	The MLL3/MLL4 Branches of the COMPASS Family Function as Major Histone H3K4 Monomethylases at Enhancers. Molecular and Cellular Biology, 2013, 33, 4745-4754.	1.1	329
26	Enhancer-associated H3K4 monomethylation by Trithorax-related, the <i>Drosophila</i> homolog of mammalian Mll3/Mll4. Genes and Development, 2012, 26, 2604-2620.	2.7	327
27	Epigenetic modifications of histones in cancer. Genome Biology, 2019, 20, 245.	3.8	322
28	Global Analysis of H3K4 Methylation Defines MLL Family Member Targets and Points to a Role for MLL1-Mediated H3K4 Methylation in the Regulation of Transcriptional Initiation by RNA Polymerase II. Molecular and Cellular Biology, 2009, 29, 6074-6085.	1.1	308
29	Born to run: control of transcription elongation by RNA polymerase II. Nature Reviews Molecular Cell Biology, 2018, 19, 464-478.	16.1	304
30	The super elongation complex (SEC) family in transcriptional control. Nature Reviews Molecular Cell Biology, 2012, 13, 543-547.	16.1	303
31	Human Mediator Subunit MED26 Functions as a Docking Site for Transcription Elongation Factors. Cell, 2011, 146, 92-104.	13.5	293
32	Histone H3 lysine 4 (H3K4) methylation in development and differentiation. Developmental Biology, 2010, 339, 240-249.	0.9	290
33	The super elongation complex (SEC) and MLL in development and disease. Genes and Development, 2011, 25, 661-672.	2.7	289
34	Molecular regulation of H3K4 trimethylation by ASH2L, a shared subunit of MLL complexes. Nature Structural and Molecular Biology, 2006, 13, 852-854.	3.6	288
35	Molecular Regulation of H3K4 Trimethylation by Wdr82, a Component of Human Set1/COMPASS. Molecular and Cellular Biology, 2008, 28, 7337-7344.	1.1	281
36	Linking H3K79 trimethylation to Wnt signaling through a novel Dot1-containing complex (DotCom). Genes and Development, 2010, 24, 574-589.	2.7	272

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37	Molecular Regulation of Histone H3 Trimethylation by COMPASS and the Regulation of Gene Expression. Molecular Cell, 2005, 19, 849-856.	4.5	263
38	Enhancer biology and enhanceropathies. Nature Structural and Molecular Biology, 2014, 21, 210-219.	3.6	259
39	Lung transplantation for patients with severe COVID-19. Science Translational Medicine, 2020, 12, .	5.8	246
40	SET for life: biochemical activities and biological functions of SET domain-containing proteins. Trends in Biochemical Sciences, 2013, 38, 621-639.	3.7	244
41	The RNA Polymerase II Elongation Complex. Annual Review of Biochemistry, 2003, 72, 693-715.	5.0	212
42	The roles of Polycomb repressive complexes in mammalian development and cancer. Nature Reviews Molecular Cell Biology, 2021, 22, 326-345.	16.1	210
43	Reevaluating the roles of histone-modifying enzymes and their associated chromatin modifications in transcriptional regulation. Nature Genetics, 2020, 52, 1271-1281.	9.4	209
44	PAF1, a Molecular Regulator of Promoter-Proximal Pausing by RNA Polymerase II. Cell, 2015, 162, 1003-1015.	13.5	196
45	The COMPASS Family of H3K4 Methylases in Drosophila. Molecular and Cellular Biology, 2011, 31, 4310-4318.	1.1	195
46	A Role for H3K4 Monomethylation in Gene Repression and Partitioning of Chromatin Readers. Molecular Cell, 2014, 53, 979-992.	4.5	191
47	A comprehensive library of histone mutants identifies nucleosomal residues required for H3K4 methylation. Nature Structural and Molecular Biology, 2008, 15, 881-888.	3.6	172
48	Chromatin signatures of cancer. Genes and Development, 2015, 29, 238-249.	2.7	171
49	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. Nature Genetics, 2017, 49, 1647-1653.	9.4	168
50	The Mll2 branch of the COMPASS family regulates bivalent promoters in mouse embryonic stem cells. Nature Structural and Molecular Biology, 2013, 20, 1093-1097.	3.6	165
51	Histone H3 lysine-to-methionine mutants as a paradigm to study chromatin signaling. Science, 2014, 345, 1065-1070.	6.0	163
52	Dynamic transcriptional events in embryonic stem cells mediated by the super elongation complex (SEC). Genes and Development, 2011, 25, 1486-1498.	2.7	161
53	Enhancer Malfunction in Cancer. Molecular Cell, 2014, 53, 859-866.	4.5	156
54	Characterization of Human Cyclin-Dependent Kinase 12 (CDK12) and CDK13 Complexes in C-Terminal Domain Phosphorylation, Gene Transcription, and RNA Processing. Molecular and Cellular Biology, 2015, 35, 928-938.	1.1	153

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55	Transcriptional Elongation by RNA Polymerase II and Histone Methylation. Journal of Biological Chemistry, 2003, 278, 26303-26306.	1.6	152
56	Licensed to elongate: a molecular mechanism for MLL-based leukaemogenesis. Nature Reviews Cancer, 2010, 10, 721-728.	12.8	151
57	The Super Elongation Complex Family of RNA Polymerase II Elongation Factors: Gene Target Specificity and Transcriptional Output. Molecular and Cellular Biology, 2012, 32, 2608-2617.	1.1	150
58	Integrator Regulates Transcriptional Initiation and Pause Release following Activation. Molecular Cell, 2014, 56, 128-139.	4.5	147
59	Enhancer Logic and Mechanics in Development and Disease. Trends in Cell Biology, 2018, 28, 608-630.	3.6	146
60	COMPASS and SWI/SNF complexes in development and disease. Nature Reviews Genetics, 2021, 22, 38-58.	7.7	142
61	Detection of Histone H3 mutations in cerebrospinal fluid-derived tumor DNA from children with diffuse midline glioma. Acta Neuropathologica Communications, 2017, 5, 28.	2.4	127
62	Dietary palmitic acid promotes a prometastatic memory via Schwann cells. Nature, 2021, 599, 485-490.	13.7	126
63	Epigenetics of hematopoiesis and hematological malignancies. Genes and Development, 2016, 30, 2021-2041.	2.7	125
64	Resetting the epigenetic balance of Polycomb and COMPASS function at enhancers for cancer therapy. Nature Medicine, 2018, 24, 758-769.	15.2	125
65	Human TFIIH Kinase CDK7 Regulates Transcription-Associated Chromatin Modifications. Cell Reports, 2017, 20, 1173-1186.	2.9	123
66	MLL4 Is Required to Maintain Broad H3K4me3 Peaks and Super-Enhancers at Tumor Suppressor Genes. Molecular Cell, 2018, 70, 825-841.e6.	4.5	123
67	MLL3/MLL4/COMPASS Family on Epigenetic Regulation of Enhancer Function and Cancer. Cold Spring Harbor Perspectives in Medicine, 2016, 6, a026427.	2.9	122
68	<i>Drosophila</i> UTX Is a Histone H3 Lys27 Demethylase That Colocalizes with the Elongating Form of RNA Polymerase II. Molecular and Cellular Biology, 2008, 28, 1041-1046.	1.1	120
69	Structural analysis of the core COMPASS family of histone H3K4 methylases from yeast to human. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20526-20531.	3.3	120
70	Histone H2BK123 monoubiquitination is the critical determinant for H3K4 and H3K79 trimethylation by COMPASS and Dot1. Journal of Cell Biology, 2009, 186, 371-377.	2.3	118
71	Precancer Atlas to Drive Precision Prevention Trials. Cancer Research, 2017, 77, 1510-1541.	0.4	116
72	Promoter bivalency favors an open chromatin architecture in embryonic stem cells. Nature Genetics, 2018, 50, 1452-1462.	9.4	113

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73	UTX Mutations in Human Cancer. Cancer Cell, 2019, 35, 168-176.	7.7	113
74	NELF Regulates a Promoter-Proximal Step Distinct from RNA Pol II Pause-Release. Molecular Cell, 2020, 78, 261-274.e5.	4.5	110
75	Stably paused genes revealed through inhibition of transcription initiation by the TFIIH inhibitor triptolide. Genes and Development, 2015, 29, 39-47.	2.7	109
76	Set1/COMPASS and Mediator are repurposed to promote epigenetic transcriptional memory. ELife, 2016, 5, .	2.8	107
77	The H3K27me3 Demethylase dUTX Is a Suppressor of Notch- and Rb-Dependent Tumors in <i>Drosophila</i>. Molecular and Cellular Biology, 2010, 30, 2485-2497.	1.1	106
78	The trithorax-group gene in Drosophila little imaginal discs encodes a trimethylated histone H3 Lys4 demethylase. Nature Structural and Molecular Biology, 2007, 14, 344-346.	3.6	104
79	Mitotic Transcriptional Activation: Clearance of Actively Engaged Pol II via Transcriptional Elongation Control in Mitosis. Molecular Cell, 2015, 60, 435-445.	4.5	102
80	A Carcinogen-induced mouse model recapitulates the molecular alterations of human muscle invasive bladder cancer. Oncogene, 2018, 37, 1911-1925.	2.6	102
81	Therapeutic Targeting of MLL Degradation Pathways in MLL-Rearranged Leukemia. Cell, 2017, 168, 59-72.e13.	13.5	99
82	PAF1 regulation of promoter-proximal pause release via enhancer activation. Science, 2017, 357, 1294-1298.	6.0	95
83	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. Molecular Cell, 2015, 57, 685-694.	4.5	92
84	TET2 coactivates gene expression through demethylation of enhancers. Science Advances, 2018, 4, eaau6986.	4.7	86
85	Targeting Processive Transcription Elongation via SEC Disruption for MYC-Induced Cancer Therapy. Cell, 2018, 175, 766-779.e17.	13.5	86
86	CATACOMB: An endogenous inducible gene that antagonizes H3K27 methylation activity of Polycomb repressive complex 2 via an H3K27M-like mechanism. Science Advances, 2019, 5, eaax2887.	4.7	86
87	Structure and Conformational Dynamics of a COMPASS Histone H3K4 Methyltransferase Complex. Cell, 2018, 174, 1117-1126.e12.	13.5	84
88	The RNA Pol II Elongation Factor Ell3 Marks Enhancers in ES Cells and Primes Future Gene Activation. Cell, 2013, 152, 144-156.	13.5	83
89	Not All H3K4 Methylations Are Created Equal: Mll2/COMPASS Dependency in Primordial Germ Cell Specification. Molecular Cell, 2017, 65, 460-475.e6.	4.5	81
90	The ATPase module of mammalian SWI/SNF family complexes mediates subcomplex identity and catalytic activityâ€"independent genomic targeting. Nature Genetics, 2019, 51, 618-626.	9.4	81

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91	Uncoupling histone H3K4 trimethylation from developmental gene expression via an equilibrium of COMPASS, Polycomb and DNA methylation. Nature Genetics, 2020, 52, 615-625.	9.4	76
92	The Little Elongation Complex Regulates Small Nuclear RNA Transcription. Molecular Cell, 2011, 44, 954-965.	4.5	75
93	Structure and Function of RNA Polymerase II Elongation Factor ELL. Journal of Biological Chemistry, 1997, 272, 22355-22363.	1.6	71
94	Histone H3K4 methylation-dependent and -independent functions of Set1A/COMPASS in embryonic stem cell self-renewal and differentiation. Genes and Development, 2017, 31, 1732-1737.	2.7	68
95	A CHAF1B-Dependent Molecular Switch in Hematopoiesis and Leukemia Pathogenesis. Cancer Cell, 2018, 34, 707-723.e7.	7.7	68
96	The Human Integrator Complex Facilitates Transcriptional Elongation by Endonucleolytic Cleavage of Nascent Transcripts. Cell Reports, 2020, 32, 107917.	2.9	68
97	Identification, Cloning, Expression, and Biochemical Characterization of the Testis-specific RNA Polymerase II Elongation Factor ELL3. Journal of Biological Chemistry, 2000, 275, 32052-32056.	1.6	66
98	Polycomb Repressive Complex 2-Dependent and -Independent Functions of Jarid2 in Transcriptional Regulation in <i>Drosophila</i>. Molecular and Cellular Biology, 2012, 32, 1683-1693.	1.1	66
99	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. Clinical Cancer Research, 2019, 25, 222-239.	3.2	66
100	Codependency of H2B monoubiquitination and nucleosome reassembly on Chd1. Genes and Development, 2012, 26, 914-919.	2.7	64
101	Analysis of dynamic changes in retinoid-induced transcription and epigenetic profiles of murine <i>Hox</i> clusters in ES cells. Genome Research, 2015, 25, 1229-1243.	2.4	64
102	Transcriptional elongation checkpoint control in development and disease. Genes and Development, 2013, 27, 1079-1088.	2.7	63
103	Bur1/Bur2 and the Ctk Complex in Yeast: The Split Personality of Mammalian P-TEFb. Cell Cycle, 2006, 5, 1066-1068.	1.3	62
104	Inactivation of Ezh2 Upregulates Gfi1 and Drives Aggressive Myc-Driven Group 3 Medulloblastoma. Cell Reports, 2017, 18, 2907-2917.	2.9	61
105	LEDGF and HDGF2 relieve the nucleosome-induced barrier to transcription in differentiated cells. Science Advances, 2019, 5, eaay3068.	4.7	61
106	An Evolutionary Conserved Epigenetic Mark of Polycomb Response Elements Implemented by Trx/MLL/COMPASS. Molecular Cell, 2016, 63, 318-328.	4.5	60
107	Ctk Complex-Mediated Regulation of Histone Methylation by COMPASS. Molecular and Cellular Biology, 2007, 27, 709-720.	1.1	59
108	Regulation of the imprinted <i>Dlk1-Dio3</i> locus by allele-specific enhancer activity. Genes and Development, 2016, 30, 92-101.	2.7	55

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109	A cytoplasmic COMPASS is necessary for cell survival and triple-negative breast cancer pathogenesis by regulating metabolism. Genes and Development, 2017, 31, 2056-2066.	2.7	55
110	An Mll4/COMPASS-Lsd1 epigenetic axis governs enhancer function and pluripotency transition in embryonic stem cells. Science Advances, 2018, 4, eaap8747.	4.7	55
111	Metarrestin, a perinucleolar compartment inhibitor, effectively suppresses metastasis. Science Translational Medicine, 2018, 10, .	5.8	55
112	Regulation of H3K4 Trimethylation via Cps40 (Spp1) of COMPASS Is Monoubiquitination Independent: Implication for a Phe/Tyr Switch by the Catalytic Domain of Set1. Molecular and Cellular Biology, 2009, 29, 3478-3486.	1.1	54
113	The Little Elongation Complex Functions at Initiation and Elongation Phases of snRNA Gene Transcription. Molecular Cell, 2013, 51, 493-505.	4.5	54
114	A cryptic Tudor domain links BRWD2/PHIP to COMPASS-mediated histone H3K4 methylation. Genes and Development, 2017, 31, 2003-2014.	2.7	54
115	Radiosensitization by Histone H3 Demethylase Inhibition in Diffuse Intrinsic Pontine Glioma. Clinical Cancer Research, 2019, 25, 5572-5583.	3.2	52
116	Regulation of MYC Expression and Differential JQ1 Sensitivity in Cancer Cells. PLoS ONE, 2014, 9, e87003.	1.1	51
117	SET1A/COMPASS and shadow enhancers in the regulation of homeotic gene expression. Genes and Development, 2017, 31, 787-801.	2.7	48
118	Context dependency of Set1/COMPASS-mediated histone H3 Lys4 trimethylation. Genes and Development, 2014, 28, 115-120.	2.7	46
119	SPT5 stabilization of promoter-proximal RNA polymerase II. Molecular Cell, 2021, 81, 4413-4424.e5.	4.5	46
120	Detection of histone H3 K27M mutation and post-translational modifications in pediatric diffuse midline glioma via tissue immunohistochemistry informs diagnosis and clinical outcomes. Oncotarget, 2018, 9, 37112-37124.	0.8	44
121	DOT1L-controlled cell-fate determination and transcription elongation are independent of H3K79 methylation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27365-27373.	3.3	43
122	A phosphorylation switch on RbBP5 regulates histone H3 Lys4 methylation. Genes and Development, 2015, 29, 123-128.	2.7	42
123	Molecular Basis for DPY-30 Association to COMPASS-like and NURF Complexes. Structure, 2014, 22, 1821-1830.	1.6	40
124	Aberrant activation of non-coding RNA targets of transcriptional elongation complexes contributes to TDP-43 toxicity. Nature Communications, 2018, 9, 4406.	5.8	40
125	SnapShot: Histone Lysine Methylase Complexes. Cell, 2012, 149, 498-498.e1.	13.5	38
126	Coordinated regulation of cellular identityâ€"associated H3K4me3 breadth by the COMPASS family. Science Advances, 2020, 6, eaaz4764.	4.7	37

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127	Multiple Roles for the MLL/COMPASS Family in the Epigenetic Regulation of Gene Expression and in Cancer. Annual Review of Cancer Biology, 2017, 1, 425-446.	2.3	36
128	Epigenomic landscape and 3D genome structure in pediatric high-grade glioma. Science Advances, 2021, 7, .	4.7	36
129	Epigenetic targeted therapy of stabilized BAP1 in ASXL1 gain-of-function mutated leukemia. Nature Cancer, 2021, 2, 515-526.	5.7	35
130	Crosstalk between nonclassical monocytes and alveolar macrophages mediates transplant ischemia-reperfusion injury through classical monocyte recruitment. JCI Insight, 2021, 6, .	2.3	34
131	Decoding the protein composition of whole nucleosomes with Nuc-MS. Nature Methods, 2021, 18, 303-308.	9.0	31
132	Inhibit Globally, Act Locally: CDK7 Inhibitors in Cancer Therapy. Cancer Cell, 2014, 26, 158-159.	7.7	29
133	Î²-Catenin/Tcf7l2â€"dependent transcriptional regulation of GLUT1 gene expression by Zic family proteins in colon cancer. Science Advances, 2019, 5, eaax0698.	4.7	28
134	Drosophila TDP-43 RNA-Binding Protein Facilitates Association of Sister Chromatid Cohesion Proteins with Genes, Enhancers and Polycomb Response Elements. PLoS Genetics, 2016, 12, e1006331.	1.5	27
135	Structural Analysis of the Ash2L/Dpy-30 Complex Reveals a Heterogeneity in H3K4 Methylation. Structure, 2018, 26, 1594-1603.e4.	1.6	26
136	Regulation of MLL/COMPASS stability through its proteolytic cleavage by taspase1 as a possible approach for clinical therapy of leukemia. Genes and Development, 2019, 33, 61-74.	2.7	26
137	Acute perturbation strategies in interrogating RNA polymerase II elongation factor function in gene expression. Genes and Development, 2021, 35, 273-285.	2.7	25
138	Integrator enforces the fidelity of transcriptional termination at protein-coding genes. Science Advances, 2021, 7, eabe3393.	4.7	23
139	Drosophila SETs Its Sights on Cancer: Trr/MLL3/4 COMPASS-Like Complexes in Development and Disease. Molecular and Cellular Biology, 2013, 33, 1698-1701.	1.1	20
140	A trivalent nucleosome interaction by PHIP/BRWD2 is disrupted in neurodevelopmental disorders and cancer. Genes and Development, 2021, 35, 1642-1656.	2.7	16
141	Targeting DNA Methylation Depletes Uterine Leiomyoma Stem Cellâ€"enriched Population by Stimulating Their Differentiation. Endocrinology, 2020, 161, .	1.4	15
142	Effects of H3.3G34V mutation on genomic H3K36 and H3K27 methylation patterns in isogenic pediatric glioma cells. Acta Neuropathologica Communications, 2020, 8, 219.	2.4	14
143	A small UTX stabilization domain of Trr is conserved within mammalian MLL3-4/COMPASS and is sufficient to rescue loss of viability in null animals. Genes and Development, 2020, 34, 1493-1502.	2.7	14
144	A genetic analysis reveals novel histone residues required for transcriptional reprogramming upon stress. Nucleic Acids Research, 2020, 48, 3455-3475.	6.5	14

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145	Therapeutic targeting of transcriptional elongation in diffuse intrinsic pontine glioma. Neuro-Oncology, 2021, 23, 1348-1359.	0.6	12
146	UBR7 acts as a histone chaperone for postâ€•nucleosomal histone H3. EMBO Journal, 2021, 40, e108307.	3.5	12
147	Itâ€™s a DoG-eat-DoG worldâ€”altered transcriptional mechanisms drive downstream-of-gene (DoG) transcript production. Molecular Cell, 2022, 82, 1981-1991.	4.5	12
148	(Poly)Combing the Pediatric Cancer Genome for Answers. Science, 2013, 340, 823-824.	6.0	11
149	Corepressor SMRT is required to maintain Hox transcriptional memory during somitogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10381-10386.	3.3	10
150	A ChIP-exo screen of 887 Protein Capture Reagents Program transcription factor antibodies in human cells. Genome Research, 2021, 31, 1663-1679.	2.4	9
151	A non-canonical monovalent zinc finger stabilizes the integration of Cfp1 into the H3K4 methyltransferase complex COMPASS. Nucleic Acids Research, 2020, 48, 421-431.	6.5	6
152	Epigenetic Reprogramming of Host and Viral Genes by Human Cytomegalovirus Infection in Kasumi-3 Myeloid Progenitor Cells at Early Times Postinfection. Journal of Virology, 2021, 95, .	1.5	5
153	NCI-CONNECT: Comprehensive Oncology Network Evaluating Rare CNS Tumorsâ€”Histone Mutated Midline Glioma Workshop Proceedings*. Neuro-Oncology Advances, 2020, 2, vdaa007.	0.4	4
154	The role of histone modifications in leukemogenesis. Journal of Biosciences, 2020, 45, 1.	0.5	4
155	TOP2B Enzymatic Activity on Promoters and Introns Modulates Multiple Oncogenes in Human Gliomas. Clinical Cancer Research, 2021, 27, 5669-5680.	3.2	4
156	COVID-19: Rescue by transcriptional inhibition. Science Advances, 2020, 6, .	4.7	3
157	A synthetic lethality screen reveals ING5 as a genetic dependency of catalytically dead Set1A/COMPASS in mouse embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2118385119.	3.3	3
158	PDTM-28. TARGETED INHIBITION OF EZH2 AND BET BROMODOMAIN PROTEINS FOR THE TREATMENT OF DIFFUSE INTRINSIC PONTINE GLIOMAS. Neuro-Oncology, 2017, 19, vi196-vi196.	0.6	2
159	Epigenetic ConFUSION: SS18-SSX Fusion Rewires BAF Complex to Activate Bivalent Genes in Synovial Sarcoma. Cancer Cell, 2018, 33, 951-953.	7.7	2
160	Medicine in the time of corona: Fundamental molecular research is â€œessentialâ€• Science Advances, 2020, 6, eabc2800.	4.7	2
161	Editorial overview: Cancer genomics: Darwin meets Waddington: the interplay between cancer genomes and epigenomes. Current Opinion in Genetics and Development, 2016, 36, iv-vi.	1.5	1
162	DIPG-63. RADIATION DNA DAMAGE REPAIR INHIBITION BY GSK-J4 INDUCED CHROMATIN COMPACTION IN DIPG. Neuro-Oncology, 2018, 20, i61-i62.	0.6	0

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163	PDTM-42. TARGETED INHIBITION OF BET BROMODOMAIN AND JMJD3 PROTEINS FOR THE TREATMENT OF DIFFUSE INTRINSIC PONTINE GLIOMA. Neuro-Oncology, 2018, 20, vi212-vi213.	0.6	0
164	Genetic and Epigenetic Deregulation of Enhancers in Cancer. , 2018, , .		0
165	DDIS-13. UNDERSTANDING GLIOBLASTOMA SUSCEPTIBILITY TO TOP2-TARGETING DRUGS FOR PERSONALIZED THERAPY. Neuro-Oncology, 2018, 20, vi71-vi72.	0.6	0
166	Impactful science as the guiding principle. Science Advances, 2018, 4, eaau1696.	4.7	0
167	HGG-10. HISTONE H3G34V MUTATION IS SUFFICIENT TO DRIVE DISTINCT GENOMIC H3K36 METHYLATION PATTERNS IN PEDIATRIC GLIOMA. Neuro-Oncology, 2019, 21, ii88-ii89.	0.6	0
168	Building on a strong foundation. Science Advances, 2021, 7, .	4.7	0
169	Expanding the breadth and depth of <i>Science Advances</i>. Science Advances, 2021, 7, .	4.7	0
170	Lessons learned from yeast about human leukemia. FASEB Journal, 2010, 24, 78.2.	0.2	0
171	HGG-26. H3G34V MUTATION AFFECTS GENOMIC H3K36 METHYLATION IN PEDIATRIC GLIOMA. Neuro-Oncology, 2020, 22, iii348-iii348.	0.6	0
172	The role of histone modifications in leukemogenesis. Journal of Biosciences, 2020, 45, .	0.5	0
173	On Healthy Scientific Debates. Science Advances, 2022, 8, eabq1534.	4.7	0
174	EPCO-20. PEDIATRIC HIGH-GRADE GLIOMA EXHIBITS DISTINCT 3D GENOME STRUCTURE THAT IMPACTS TRANSCRIPTION REGULATION. Neuro-Oncology, 2021, 23, vi6-vi6.	0.6	0
175	The dire need for federal support of molecular research, then and now. Science Advances, 2022, 8, .	4.7	0