

Ali Shilatifard

List of Publications by Year in descending order

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Version: 2024-02-01

175
papers

27,440
citations

6840

81
h-index

7627

156
g-index

183
all docs

183
docs citations

183
times ranked

32821
citing authors

#	ARTICLE	IF	CITATIONS
1	On Healthy Scientific Debates. <i>Science Advances</i> , 2022, 8, eabq1534.	4.7	0
2	Itâ€™s a DoG-eat-DoG worldâ€™ altered transcriptional mechanisms drive downstream-of-gene (DoG) transcript production. <i>Molecular Cell</i> , 2022, 82, 1981-1991.	4.5	12
3	A synthetic lethality screen reveals ING5 as a genetic dependency of catalytically dead Set1A/COMPASS in mouse embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118385119.	3.3	3
4	The dire need for federal support of molecular research, then and now. <i>Science Advances</i> , 2022, 8, .	4.7	0
5	COMPASS and SWI/SNF complexes in development and disease. <i>Nature Reviews Genetics</i> , 2021, 22, 38-58.	7.7	142
6	Acute perturbation strategies in interrogating RNA polymerase II elongation factor function in gene expression. <i>Genes and Development</i> , 2021, 35, 273-285.	2.7	25
7	Therapeutic targeting of transcriptional elongation in diffuse intrinsic pontine glioma. <i>Neuro-Oncology</i> , 2021, 23, 1348-1359.	0.6	12
8	Decoding the protein composition of whole nucleosomes with Nuc-MS. <i>Nature Methods</i> , 2021, 18, 303-308.	9.0	31
9	Crosstalk between nonclassical monocytes and alveolar macrophages mediates transplant ischemia-reperfusion injury through classical monocyte recruitment. <i>JCI Insight</i> , 2021, 6, .	2.3	34
10	The roles of Polycomb repressive complexes in mammalian development and cancer. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 326-345.	16.1	210
11	Building on a strong foundation. <i>Science Advances</i> , 2021, 7, .	4.7	0
12	Epigenetic targeted therapy of stabilized BAP1 in ASXL1 gain-of-function mutated leukemia. <i>Nature Cancer</i> , 2021, 2, 515-526.	5.7	35
13	Epigenetic Reprogramming of Host and Viral Genes by Human Cytomegalovirus Infection in Kasumi-3 Myeloid Progenitor Cells at Early Times Postinfection. <i>Journal of Virology</i> , 2021, 95, .	1.5	5
14	Epigenomic landscape and 3D genome structure in pediatric high-grade glioma. <i>Science Advances</i> , 2021, 7, .	4.7	36
15	A ChIP-exo screen of 887 Protein Capture Reagents Program transcription factor antibodies in human cells. <i>Genome Research</i> , 2021, 31, 1663-1679.	2.4	9
16	TOP2B Enzymatic Activity on Promoters and Introns Modulates Multiple Oncogenes in Human Gliomas. <i>Clinical Cancer Research</i> , 2021, 27, 5669-5680.	3.2	4
17	Expanding the breadth and depth of <i>Science Advances</i> . <i>Science Advances</i> , 2021, 7, .	4.7	0
18	SPT5 stabilization of promoter-proximal RNA polymerase II. <i>Molecular Cell</i> , 2021, 81, 4413-4424.e5.	4.5	46

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19	Circuits between infected macrophages and T cells in SARS-CoV-2 pneumonia. <i>Nature</i> , 2021, 590, 635-641.	13.7	524
20	Integrator enforces the fidelity of transcriptional termination at protein-coding genes. <i>Science Advances</i> , 2021, 7, eabe3393.	4.7	23
21	Dietary palmitic acid promotes a prometastatic memory via Schwann cells. <i>Nature</i> , 2021, 599, 485-490.	13.7	126
22	A trivalent nucleosome interaction by PHIP/BRWD2 is disrupted in neurodevelopmental disorders and cancer. <i>Genes and Development</i> , 2021, 35, 1642-1656.	2.7	16
23	UBR7 acts as a histone chaperone for post-nucleosomal histone H3. <i>EMBO Journal</i> , 2021, 40, e108307.	3.5	12
24	EPCO-20. PEDIATRIC HIGH-GRADE GLIOMA EXHIBITS DISTINCT 3D GENOME STRUCTURE THAT IMPACTS TRANSCRIPTION REGULATION. <i>Neuro-Oncology</i> , 2021, 23, vi6-vi6.	0.6	0
25	A non-canonical monovalent zinc finger stabilizes the integration of Cfp1 into the H3K4 methyltransferase complex COMPASS. <i>Nucleic Acids Research</i> , 2020, 48, 421-431.	6.5	6
26	DOT1L-controlled cell-fate determination and transcription elongation are independent of H3K79 methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27365-27373.	3.3	43
27	Reevaluating the roles of histone-modifying enzymes and their associated chromatin modifications in transcriptional regulation. <i>Nature Genetics</i> , 2020, 52, 1271-1281.	9.4	209
28	Lung transplantation for patients with severe COVID-19. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	246
29	Effects of H3.3G34V mutation on genomic H3K36 and H3K27 methylation patterns in isogenic pediatric glioma cells. <i>Acta Neuropathologica Communications</i> , 2020, 8, 219.	2.4	14
30	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. <i>Genes and Development</i> , 2020, 34, 1493-1502.	2.7	14
31	The Human Integrator Complex Facilitates Transcriptional Elongation by Endonucleolytic Cleavage of Nascent Transcripts. <i>Cell Reports</i> , 2020, 32, 107917.	2.9	68
32	NCI-CONNECT: Comprehensive Oncology Network Evaluating Rare CNS Tumors—Histone Mutated Midline Glioma Workshop Proceedings*. <i>Neuro-Oncology Advances</i> , 2020, 2, vdaa007.	0.4	4
33	Targeting DNA Methylation Depletes Uterine Leiomyoma Stem Cell-enriched Population by Stimulating Their Differentiation. <i>Endocrinology</i> , 2020, 161, .	1.4	15
34	Uncoupling histone H3K4 trimethylation from developmental gene expression via an equilibrium of COMPASS, Polycomb and DNA methylation. <i>Nature Genetics</i> , 2020, 52, 615-625.	9.4	76
35	COVID-19: Rescue by transcriptional inhibition. <i>Science Advances</i> , 2020, 6, .	4.7	3
36	NELF Regulates a Promoter-Proximal Step Distinct from RNA Pol II Pause-Release. <i>Molecular Cell</i> , 2020, 78, 261-274.e5.	4.5	110

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37	Coordinated regulation of cellular identity-associated H3K4me3 breadth by the COMPASS family. <i>Science Advances</i> , 2020, 6, eaaz4764.	4.7	37
38	A genetic analysis reveals novel histone residues required for transcriptional reprogramming upon stress. <i>Nucleic Acids Research</i> , 2020, 48, 3455-3475.	6.5	14
39	The role of histone modifications in leukemogenesis. <i>Journal of Biosciences</i> , 2020, 45, 1.	0.5	4
40	Medicine in the time of corona: Fundamental molecular research is "essential". <i>Science Advances</i> , 2020, 6, eabc2800.	4.7	2
41	HGG-26. H3G34V MUTATION AFFECTS GENOMIC H3K36 METHYLATION IN PEDIATRIC GLIOMA. <i>Neuro-Oncology</i> , 2020, 22, iii348-iii348.	0.6	0
42	The role of histone modifications in leukemogenesis. <i>Journal of Biosciences</i> , 2020, 45, .	0.5	0
43	β-Catenin/Tcf7l2-dependent transcriptional regulation of GLUT1 gene expression by Zic family proteins in colon cancer. <i>Science Advances</i> , 2019, 5, eaax0698.	4.7	28
44	CATACOMB: An endogenous inducible gene that antagonizes H3K27 methylation activity of Polycomb repressive complex 2 via an H3K27M-like mechanism. <i>Science Advances</i> , 2019, 5, eaax2887.	4.7	86
45	LEDGF and HDGF2 relieve the nucleosome-induced barrier to transcription in differentiated cells. <i>Science Advances</i> , 2019, 5, eaay3068.	4.7	61
46	Radiosensitization by Histone H3 Demethylase Inhibition in Diffuse Intrinsic Pontine Glioma. <i>Clinical Cancer Research</i> , 2019, 25, 5572-5583.	3.2	52
47	HGG-10. HISTONE H3G34V MUTATION IS SUFFICIENT TO DRIVE DISTINCT GENOMIC H3K36 METHYLATION PATTERNS IN PEDIATRIC GLIOMA. <i>Neuro-Oncology</i> , 2019, 21, ii88-ii89.	0.6	0
48	The ATPase module of mammalian SWI/SNF family complexes mediates subcomplex identity and catalytic activity-independent genomic targeting. <i>Nature Genetics</i> , 2019, 51, 618-626.	9.4	81
49	UTX Mutations in Human Cancer. <i>Cancer Cell</i> , 2019, 35, 168-176.	7.7	113
50	Epigenetic modifications of histones in cancer. <i>Genome Biology</i> , 2019, 20, 245.	3.8	322
51	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. <i>Clinical Cancer Research</i> , 2019, 25, 222-239.	3.2	66
52	Single-Cell Transcriptomic Analysis of Human Lung Provides Insights into the Pathobiology of Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 1517-1536.	2.5	866
53	Regulation of MLL/COMPASS stability through its proteolytic cleavage by taspase1 as a possible approach for clinical therapy of leukemia. <i>Genes and Development</i> , 2019, 33, 61-74.	2.7	26
54	An Mll4/COMPASS-Lsd1 epigenetic axis governs enhancer function and pluripotency transition in embryonic stem cells. <i>Science Advances</i> , 2018, 4, eaap8747.	4.7	55

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55	A Carcinogen-induced mouse model recapitulates the molecular alterations of human muscle invasive bladder cancer. <i>Oncogene</i> , 2018, 37, 1911-1925.	2.6	102
56	DIPG-63. RADIATION DNA DAMAGE REPAIR INHIBITION BY GSK-J4 INDUCED CHROMATIN COMPACTION IN DIPG. <i>Neuro-Oncology</i> , 2018, 20, i61-i62.	0.6	0
57	PDTM-42. TARGETED INHIBITION OF BET BROMODOMAIN AND JMJD3 PROTEINS FOR THE TREATMENT OF DIFFUSE INTRINSIC PONTINE GLIOMA. <i>Neuro-Oncology</i> , 2018, 20, vi212-vi213.	0.6	0
58	TET2 coactivates gene expression through demethylation of enhancers. <i>Science Advances</i> , 2018, 4, eaau6986.	4.7	86
59	A CHAF1B-Dependent Molecular Switch in Hematopoiesis and Leukemia Pathogenesis. <i>Cancer Cell</i> , 2018, 34, 707-723.e7.	7.7	68
60	Genetic and Epigenetic Dereglulation of Enhancers in Cancer. , 2018, , .		0
61	DDIS-13. UNDERSTANDING GLIOBLASTOMA SUSCEPTIBILITY TO TOP2-TARGETING DRUGS FOR PERSONALIZED THERAPY. <i>Neuro-Oncology</i> , 2018, 20, vi71-vi72.	0.6	0
62	Structural Analysis of the Ash2L/Dpy-30 Complex Reveals a Heterogeneity in H3K4 Methylation. <i>Structure</i> , 2018, 26, 1594-1603.e4.	1.6	26
63	Corepressor SMRT is required to maintain Hox transcriptional memory during somitogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10381-10386.	3.3	10
64	Aberrant activation of non-coding RNA targets of transcriptional elongation complexes contributes to TDP-43 toxicity. <i>Nature Communications</i> , 2018, 9, 4406.	5.8	40
65	Targeting Processive Transcription Elongation via SEC Disruption for MYC-Induced Cancer Therapy. <i>Cell</i> , 2018, 175, 766-779.e17.	13.5	86
66	Promoter bivalency favors an open chromatin architecture in embryonic stem cells. <i>Nature Genetics</i> , 2018, 50, 1452-1462.	9.4	113
67	Metarrestin, a perinucleolar compartment inhibitor, effectively suppresses metastasis. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	55
68	Resetting the epigenetic balance of Polycomb and COMPASS function at enhancers for cancer therapy. <i>Nature Medicine</i> , 2018, 24, 758-769.	15.2	125
69	MLL4 Is Required to Maintain Broad H3K4me3 Peaks and Super-Enhancers at Tumor Suppressor Genes. <i>Molecular Cell</i> , 2018, 70, 825-841.e6.	4.5	123
70	Impactful science as the guiding principle. <i>Science Advances</i> , 2018, 4, eaau1696.	4.7	0
71	Born to run: control of transcription elongation by RNA polymerase II. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 464-478.	16.1	304
72	Enhancer Logic and Mechanics in Development and Disease. <i>Trends in Cell Biology</i> , 2018, 28, 608-630.	3.6	146

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73	Structure and Conformational Dynamics of a COMPASS Histone H3K4 Methyltransferase Complex. <i>Cell</i> , 2018, 174, 1117-1126.e12.	13.5	84
74	Epigenetic ConFUSION: SS18-SSX Fusion Rewires BAF Complex to Activate Bivalent Genes in Synovial Sarcoma. <i>Cancer Cell</i> , 2018, 33, 951-953.	7.7	2
75	Detection of histone H3 K27M mutation and post-translational modifications in pediatric diffuse midline glioma via tissue immunohistochemistry informs diagnosis and clinical outcomes. <i>Oncotarget</i> , 2018, 9, 37112-37124.	0.8	44
76	Not All H3K4 Methylations Are Created Equal: Mll2/COMPASS Dependency in Primordial Germ Cell Specification. <i>Molecular Cell</i> , 2017, 65, 460-475.e6.	4.5	81
77	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. <i>Nature Medicine</i> , 2017, 23, 493-500.	15.2	332
78	Inactivation of Ezh2 Upregulates Gfi1 and Drives Aggressive Myc-Driven Group 3 Medulloblastoma. <i>Cell Reports</i> , 2017, 18, 2907-2917.	2.9	61
79	Detection of Histone H3 mutations in cerebrospinal fluid-derived tumor DNA from children with diffuse midline glioma. <i>Acta Neuropathologica Communications</i> , 2017, 5, 28.	2.4	127
80	SET1A/COMPASS and shadow enhancers in the regulation of homeotic gene expression. <i>Genes and Development</i> , 2017, 31, 787-801.	2.7	48
81	Precancer Atlas to Drive Precision Prevention Trials. <i>Cancer Research</i> , 2017, 77, 1510-1541.	0.4	116
82	Multiple Roles for the MLL/COMPASS Family in the Epigenetic Regulation of Gene Expression and in Cancer. <i>Annual Review of Cancer Biology</i> , 2017, 1, 425-446.	2.3	36
83	Therapeutic Targeting of MLL Degradation Pathways in MLL-Rearranged Leukemia. <i>Cell</i> , 2017, 168, 59-72.e13.	13.5	99
84	A cryptic Tudor domain links BRWD2/PHIP to COMPASS-mediated histone H3K4 methylation. <i>Genes and Development</i> , 2017, 31, 2003-2014.	2.7	54
85	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. <i>Nature Genetics</i> , 2017, 49, 1647-1653.	9.4	168
86	Histone H3K4 methylation-dependent and -independent functions of Set1A/COMPASS in embryonic stem cell self-renewal and differentiation. <i>Genes and Development</i> , 2017, 31, 1732-1737.	2.7	68
87	PAF1 regulation of promoter-proximal pause release via enhancer activation. <i>Science</i> , 2017, 357, 1294-1298.	6.0	95
88	Monocyte-derived alveolar macrophages drive lung fibrosis and persist in the lung over the life span. <i>Journal of Experimental Medicine</i> , 2017, 214, 2387-2404.	4.2	755
89	Human TFIIH Kinase CDK7 Regulates Transcription-Associated Chromatin Modifications. <i>Cell Reports</i> , 2017, 20, 1173-1186.	2.9	123
90	A cytoplasmic COMPASS is necessary for cell survival and triple-negative breast cancer pathogenesis by regulating metabolism. <i>Genes and Development</i> , 2017, 31, 2056-2066.	2.7	55

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91	PDTM-28. TARGETED INHIBITION OF EZH2 AND BET BROMODOMAIN PROTEINS FOR THE TREATMENT OF DIFFUSE INTRINSIC PONTINE GLIOMAS. <i>Neuro-Oncology</i> , 2017, 19, vi196-vi196.	0.6	2
92	Editorial overview: Cancer genomics: Darwin meets Waddington: the interplay between cancer genomes and epigenomes. <i>Current Opinion in Genetics and Development</i> , 2016, 36, iv-vi.	1.5	1
93	Epigenetics of hematopoiesis and hematological malignancies. <i>Genes and Development</i> , 2016, 30, 2021-2041.	2.7	125
94	MLL3/MLL4/COMPASS Family on Epigenetic Regulation of Enhancer Function and Cancer. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2016, 6, a026427.	2.9	122
95	An Evolutionary Conserved Epigenetic Mark of Polycomb Response Elements Implemented by Trx/MLL/COMPASS. <i>Molecular Cell</i> , 2016, 63, 318-328.	4.5	60
96	Epigenetic balance of gene expression by Polycomb and COMPASS families. <i>Science</i> , 2016, 352, aad9780.	6.0	407
97	Regulation of the imprinted <i>Dlk1-Dio3</i> locus by allele-specific enhancer activity. <i>Genes and Development</i> , 2016, 30, 92-101.	2.7	55
98	Drosophila TDP-43 RNA-Binding Protein Facilitates Association of Sister Chromatid Cohesion Proteins with Genes, Enhancers and Polycomb Response Elements. <i>PLoS Genetics</i> , 2016, 12, e1006331.	1.5	27
99	Set1/COMPASS and Mediator are repurposed to promote epigenetic transcriptional memory. <i>ELife</i> , 2016, 5, .	2.8	107
100	Mitotic Transcriptional Activation: Clearance of Actively Engaged Pol II via Transcriptional Elongation Control in Mitosis. <i>Molecular Cell</i> , 2015, 60, 435-445.	4.5	102
101	Stably paused genes revealed through inhibition of transcription initiation by the TFIID inhibitor triptolide. <i>Genes and Development</i> , 2015, 29, 39-47.	2.7	109
102	Characterization of Human Cyclin-Dependent Kinase 12 (CDK12) and CDK13 Complexes in C-Terminal Domain Phosphorylation, Gene Transcription, and RNA Processing. <i>Molecular and Cellular Biology</i> , 2015, 35, 928-938.	1.1	153
103	Zic2 Is an Enhancer-Binding Factor Required for Embryonic Stem Cell Specification. <i>Molecular Cell</i> , 2015, 57, 685-694.	4.5	92
104	Chromatin signatures of cancer. <i>Genes and Development</i> , 2015, 29, 238-249.	2.7	171
105	A phosphorylation switch on RbBP5 regulates histone H3 Lys4 methylation. <i>Genes and Development</i> , 2015, 29, 123-128.	2.7	42
106	PAF1, a Molecular Regulator of Promoter-Proximal Pausing by RNA Polymerase II. <i>Cell</i> , 2015, 162, 1003-1015.	13.5	196
107	Analysis of dynamic changes in retinoid-induced transcription and epigenetic profiles of murine <i>Hox</i> clusters in ES cells. <i>Genome Research</i> , 2015, 25, 1229-1243.	2.4	64
108	The histone lysine methyltransferase KMT2D sustains a gene expression program that represses B cell lymphoma development. <i>Nature Medicine</i> , 2015, 21, 1199-1208.	15.2	359

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109	Gain-of-function p53 mutants co-opt chromatin pathways to drive cancer growth. <i>Nature</i> , 2015, 525, 206-211.	13.7	386
110	Molecular Basis for DPY-30 Association to COMPASS-like and NURF Complexes. <i>Structure</i> , 2014, 22, 1821-1830.	1.6	40
111	Enhancer Malfunction in Cancer. <i>Molecular Cell</i> , 2014, 53, 859-866.	4.5	156
112	Enhancer biology and enhanceropathies. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 210-219.	3.6	259
113	A Role for H3K4 Monomethylation in Gene Repression and Partitioning of Chromatin Readers. <i>Molecular Cell</i> , 2014, 53, 979-992.	4.5	191
114	Context dependency of Set1/COMPASS-mediated histone H3 Lys4 trimethylation. <i>Genes and Development</i> , 2014, 28, 115-120.	2.7	46
115	Histone H3 lysine-to-methionine mutants as a paradigm to study chromatin signaling. <i>Science</i> , 2014, 345, 1065-1070.	6.0	163
116	Inhibit Globally, Act Locally: CDK7 Inhibitors in Cancer Therapy. <i>Cancer Cell</i> , 2014, 26, 158-159.	7.7	29
117	Integrator Regulates Transcriptional Initiation and Pause Release following Activation. <i>Molecular Cell</i> , 2014, 56, 128-139.	4.5	147
118	Regulation of MYC Expression and Differential JQ1 Sensitivity in Cancer Cells. <i>PLoS ONE</i> , 2014, 9, e87003.	1.1	51
119	The Mll2 branch of the COMPASS family regulates bivalent promoters in mouse embryonic stem cells. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1093-1097.	3.6	165
120	The Little Elongation Complex Functions at Initiation and Elongation Phases of snRNA Gene Transcription. <i>Molecular Cell</i> , 2013, 51, 493-505.	4.5	54
121	The MLL3/MLL4 Branches of the COMPASS Family Function as Major Histone H3K4 Monomethylases at Enhancers. <i>Molecular and Cellular Biology</i> , 2013, 33, 4745-4754.	1.1	329
122	SET for life: biochemical activities and biological functions of SET domain-containing proteins. <i>Trends in Biochemical Sciences</i> , 2013, 38, 621-639.	3.7	244
123	The RNA Pol II Elongation Factor Ell3 Marks Enhancers in ES Cells and Primes Future Gene Activation. <i>Cell</i> , 2013, 152, 144-156.	13.5	83
124	Drosophila SETs Its Sights on Cancer: Trr/MLL3/4 COMPASS-Like Complexes in Development and Disease. <i>Molecular and Cellular Biology</i> , 2013, 33, 1698-1701.	1.1	20
125	Transcriptional elongation checkpoint control in development and disease. <i>Genes and Development</i> , 2013, 27, 1079-1088.	2.7	63
126	(Poly)Combing the Pediatric Cancer Genome for Answers. <i>Science</i> , 2013, 340, 823-824.	6.0	11

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127	Polycomb Repressive Complex 2-Dependent and -Independent Functions of Jarid2 in Transcriptional Regulation in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2012, 32, 1683-1693.	1.1	66
128	The Super Elongation Complex Family of RNA Polymerase II Elongation Factors: Gene Target Specificity and Transcriptional Output. <i>Molecular and Cellular Biology</i> , 2012, 32, 2608-2617.	1.1	150
129	Enhancer-associated H3K4 monomethylation by Trithorax-related, the <i>Drosophila</i> homolog of mammalian Mll3/Mll4. <i>Genes and Development</i> , 2012, 26, 2604-2620.	2.7	327
130	Codependency of H2B monoubiquitination and nucleosome reassembly on Chd1. <i>Genes and Development</i> , 2012, 26, 914-919.	2.7	64
131	SnapShot: Histone Lysine Methylase Complexes. <i>Cell</i> , 2012, 149, 498-498.e1.	13.5	38
132	The super elongation complex (SEC) family in transcriptional control. <i>Nature Reviews Molecular Cell Biology</i> , 2012, 13, 543-547.	16.1	303
133	The COMPASS Family of Histone H3K4 Methylases: Mechanisms of Regulation in Development and Disease Pathogenesis. <i>Annual Review of Biochemistry</i> , 2012, 81, 65-95.	5.0	896
134	Human Mediator Subunit MED26 Functions as a Docking Site for Transcription Elongation Factors. <i>Cell</i> , 2011, 146, 92-104.	13.5	293
135	The Little Elongation Complex Regulates Small Nuclear RNA Transcription. <i>Molecular Cell</i> , 2011, 44, 954-965.	4.5	75
136	Histone modification: cause or cog?. <i>Trends in Genetics</i> , 2011, 27, 389-396.	2.9	415
137	The COMPASS Family of H3K4 Methylases in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4310-4318.	1.1	195
138	Dynamic transcriptional events in embryonic stem cells mediated by the super elongation complex (SEC). <i>Genes and Development</i> , 2011, 25, 1486-1498.	2.7	161
139	The super elongation complex (SEC) and MLL in development and disease. <i>Genes and Development</i> , 2011, 25, 661-672.	2.7	289
140	Structural analysis of the core COMPASS family of histone H3K4 methylases from yeast to human. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20526-20531.	3.3	120
141	Licensed to elongate: a molecular mechanism for MLL-based leukaemogenesis. <i>Nature Reviews Cancer</i> , 2010, 10, 721-728.	12.8	151
142	The H3K27me3 Demethylase dUTX Is a Suppressor of Notch- and Rb-Dependent Tumors in <i>Drosophila</i> . <i>Molecular and Cellular Biology</i> , 2010, 30, 2485-2497.	1.1	106
143	Linking H3K79 trimethylation to Wnt signaling through a novel Dot1-containing complex (DotCom). <i>Genes and Development</i> , 2010, 24, 574-589.	2.7	272
144	AFF4, a Component of the ELL/P-TEFb Elongation Complex and a Shared Subunit of MLL Chimeras, Can Link Transcription Elongation to Leukemia. <i>Molecular Cell</i> , 2010, 37, 429-437.	4.5	504

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145	The Language of Histone Crosstalk. <i>Cell</i> , 2010, 142, 682-685.	13.5	505
146	Histone H3 lysine 4 (H3K4) methylation in development and differentiation. <i>Developmental Biology</i> , 2010, 339, 240-249.	0.9	290
147	Lessons learned from yeast about human leukemia. <i>FASEB Journal</i> , 2010, 24, 78.2.	0.2	0
148	Histone H2BK123 monoubiquitination is the critical determinant for H3K4 and H3K79 trimethylation by COMPASS and Dot1. <i>Journal of Cell Biology</i> , 2009, 186, 371-377.	2.3	118
149	Regulation of H3K4 Trimethylation via Cps40 (Spp1) of COMPASS Is Monoubiquitination Independent: Implication for a Phe/Tyr Switch by the Catalytic Domain of Set1. <i>Molecular and Cellular Biology</i> , 2009, 29, 3478-3486.	1.1	54
150	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. <i>Molecular and Cellular Biology</i> , 2009, 29, 6074-6085.	1.1	308
151	An operational definition of epigenetics: Figure 1.. <i>Genes and Development</i> , 2009, 23, 781-783.	2.7	1,457
152	RAD6-Mediated Transcription-Coupled H2B Ubiquitylation Directly Stimulates H3K4 Methylation in Human Cells. <i>Cell</i> , 2009, 137, 459-471.	13.5	453
153	A comprehensive library of histone mutants identifies nucleosomal residues required for H3K4 methylation. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 881-888.	3.6	172
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