

# Setd1a and NURF mediate chromatin dynamics and gene commitment and differentiation

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Distinct functions of histone H3, lysine 4 methyltransferases in normal and malignant hematopoiesis. Current Opinion in Hematology, 2017, 24, 322-328.	2.5	39
2	SET/MLL family proteins in hematopoiesis and leukemia. International Journal of Hematology, 2017, 105, 7-16.	1.6	42
3	SETD1A protects HSCs from activation-induced functional decline in vivo. Blood, 2018, 131, 1311-1324.	1.4	47
4	A putative RNA binding protein from <i>Plasmodium vivax</i> apicoplast. FEBS Open Bio, 2018, 8, 177-188.	2.3	3
5	Set(d1a)-ing novel links between HSC regulators. Blood, 2018, 131, 1267-1269.	1.4	1
6	CTCF boundary remodels chromatin domain and drives aberrant HOX gene transcription in acute myeloid leukemia. Blood, 2018, 132, 837-848.	1.4	56
7	ATP-Dependent Chromatin Remodeling During Cortical Neurogenesis. Frontiers in Neuroscience, 2018, 12, 226.	2.8	41
8	LncRNA OIP5-AS1 is overexpressed in undifferentiated oral tumors and integrated analysis identifies as a downstream effector of stemness-associated transcription factors. Scientific Reports, 2018, 8, 7018.	3.3	55
9	Cellular dynamics of mammalian red blood cell production in the erythroblastic island niche. Biophysical Reviews, 2019, 11, 873-894.	3.2	28
10	N6-methyladenosine mRNA marking promotes selective translation of regulons required for human erythropoiesis. Nature Communications, 2019, 10, 4596.	12.8	42
11	NPM and NPM-MLF1 interact with chromatin remodeling complexes and influence their recruitment to specific genes. PLoS Genetics, 2019, 15, e1008463.	3.5	9
12	Taurine Promotes Milk Synthesis via the GPR87-PI3K-SETD1A Signaling in BMECs. Journal of Agricultural and Food Chemistry, 2019, 67, 1927-1936.	5.2	33
13	Why are so many MLL lysine methyltransferases required for normal mammalian development?. Cellular and Molecular Life Sciences, 2019, 76, 2885-2898.	5.4	54
14	Circular RNA circ-DONSON facilitates gastric cancer growth and invasion via NURF complex dependent activation of transcription factor SOX4. Molecular Cancer, 2019, 18, 45.	19.2	182
15	Cyclin D1 integrates G9a-mediated histone methylation. Oncogene, 2019, 38, 4232-4249.	5.9	20
16	Deciphering molecular properties of hypermutated gastrointestinal cancer. Journal of Cellular and Molecular Medicine, 2019, 23, 370-379.	3.6	10
17	Understanding the interplay between CpG island-associated gene promoters and H3K4 methylation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194567.	1.9	82
18	The MLL/SET family and haematopoiesis. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194579.	1.9	14

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19	The role of SETD1A and SETD1B in development and disease. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194578.	1.9	12
20	Alteration of CTCF-associated chromatin neighborhood inhibits TAL1-driven oncogenic transcription program and leukemogenesis. <i>Nucleic Acids Research</i> , 2020, 48, 3119-3133.	14.5	19
21	SET1/MLL family of proteins: functions beyond histone methylation. <i>Epigenetics</i> , 2021, 16, 469-487.	2.7	27
22	COMPASS and SWI/SNF complexes in development and disease. <i>Nature Reviews Genetics</i> , 2021, 22, 38-58.	16.3	142
23	Chromatin Modifiers in Transcriptional Regulation: New Findings and Prospects. <i>Acta Naturae</i> , 2021, 13, 16-30.	1.7	2
24	IKAROS is required for the measured response of NOTCH target genes upon external NOTCH signaling. <i>PLoS Genetics</i> , 2021, 17, e1009478.	3.5	4
25	HOXBLINE long non-coding RNA activation promotes leukemogenesis in NPM1-mutant acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 1956.	12.8	28
26	NUCOME: A comprehensive database of nucleosome organization referenced landscapes in mammalian genomes. <i>BMC Bioinformatics</i> , 2021, 22, 321.	2.6	2
27	Epigenetic Reprogramming of CD4+ Helper T Cells as a Strategy to Improve Anticancer Immunotherapy. <i>Frontiers in Immunology</i> , 2021, 12, 669992.	4.8	18
29	RPPA-based proteomics recognizes distinct epigenetic signatures in chronic lymphocytic leukemia with clinical consequences. <i>Leukemia</i> , 2022, 36, 712-722.	7.2	4
36	Single-cell multi-omics of human clonal hematopoiesis reveals that DNMT3A R882 mutations perturb early progenitor states through selective hypomethylation. <i>Nature Genetics</i> , 2022, 54, 1514-1526.	21.4	50
37	Wdr5 is essential for fetal erythropoiesis and hematopoiesis. <i>Experimental Hematology and Oncology</i> , 2023, 12, .	5.0	2
39	Noncoding rules of survival: epigenetic regulation of normal and malignant hematopoiesis. <i>Frontiers in Molecular Biosciences</i> , 0, 10, .	3.5	0