

Setd1a and NURF mediate chromatin dynamics and gene commitment and differentiation

Nucleic Acids Research

44, gkw327

DOI: [10.1093/nar/gkw327](https://doi.org/10.1093/nar/gkw327)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Distinct functions of histone H3, lysine 4 methyltransferases in normal and malignant hematopoiesis. <i>Current Opinion in Hematology</i> , 2017, 24, 322-328.	1.2	39
2	SET/MLL family proteins in hematopoiesis and leukemia. <i>International Journal of Hematology</i> , 2017, 105, 7-16.	0.7	42
3	SETD1A protects HSCs from activation-induced functional decline in vivo. <i>Blood</i> , 2018, 131, 1311-1324.	0.6	47
4	A putative RNA binding protein from <i>Plasmodium vivax</i> apicoplast. <i>FEBS Open Bio</i> , 2018, 8, 177-188.	1.0	3
5	Set(d1a)-ing novel links between HSC regulators. <i>Blood</i> , 2018, 131, 1267-1269.	0.6	1
6	CTCF boundary remodels chromatin domain and drives aberrant HOX gene transcription in acute myeloid leukemia. <i>Blood</i> , 2018, 132, 837-848.	0.6	56
7	ATP-Dependent Chromatin Remodeling During Cortical Neurogenesis. <i>Frontiers in Neuroscience</i> , 2018, 12, 226.	1.4	41
8	LncRNA OIP5-AS1 is overexpressed in undifferentiated oral tumors and integrated analysis identifies as a downstream effector of stemness-associated transcription factors. <i>Scientific Reports</i> , 2018, 8, 7018.	1.6	55
9	Cellular dynamics of mammalian red blood cell production in the erythroblastic island niche. <i>Biophysical Reviews</i> , 2019, 11, 873-894.	1.5	28
10	N6-methyladenosine mRNA marking promotes selective translation of regulons required for human erythropoiesis. <i>Nature Communications</i> , 2019, 10, 4596.	5.8	42
11	NPM and NPM-MLF1 interact with chromatin remodeling complexes and influence their recruitment to specific genes. <i>PLoS Genetics</i> , 2019, 15, e1008463.	1.5	9
12	Taurine Promotes Milk Synthesis via the GPR87-PI3K-SETD1A Signaling in BMECs. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 1927-1936.	2.4	33
13	Why are so many MLL lysine methyltransferases required for normal mammalian development?. <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 2885-2898.	2.4	54
14	Circular RNA circ-DONSON facilitates gastric cancer growth and invasion via NURF complex dependent activation of transcription factor SOX4. <i>Molecular Cancer</i> , 2019, 18, 45.	7.9	182
15	Cyclin D1 integrates G9a-mediated histone methylation. <i>Oncogene</i> , 2019, 38, 4232-4249.	2.6	20
16	Deciphering molecular properties of hypermutated gastrointestinal cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 370-379.	1.6	10
17	Understanding the interplay between CpG island-associated gene promoters and H3K4 methylation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194567.	0.9	82
18	The MLL/SET family and haematopoiesis. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194579.	0.9	14

#	ARTICLE	IF	CITATIONS
19	The role of SETD1A and SETD1B in development and disease. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194578.	0.9	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.	6.5	19
21	SET1/MLL family of proteins: functions beyond histone methylation. <i>Epigenetics</i> , 2021, 16, 469-487.	1.3	27
22	COMPASS and SWI/SNF complexes in development and disease. <i>Nature Reviews Genetics</i> , 2021, 22, 38-58.	7.7	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.	1.5	4
25	HOXBLINE long non-coding RNA activation promotes leukemogenesis in NPM1-mutant acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 1956.	5.8	28
26	NUCOME: A comprehensive database of nucleosome organization referenced landscapes in mammalian genomes. <i>BMC Bioinformatics</i> , 2021, 22, 321.	1.2	2
27	Epigenetic Reprogramming of CD4+ Helper T Cells as a Strategy to Improve Anticancer Immunotherapy. <i>Frontiers in Immunology</i> , 2021, 12, 669992.	2.2	18
29	RPPA-based proteomics recognizes distinct epigenetic signatures in chronic lymphocytic leukemia with clinical consequences. <i>Leukemia</i> , 2022, 36, 712-722.	3.3	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.	9.4	50