

Resource Summary Report

Generated by [RRID](#) on Jul 29, 2026

Anti-acetyl-Histone H3 (Lys27)

RRID:AB_310550

Type: Antibody

Proper Citation

Millipore Cat# 07-360, RRID:AB_310550

Antibody Information

URL: http://antibodyregistry.org/AB_310550

Proper Citation: Millipore Cat# 07-360, RRID:AB_310550

Target Antigen: acetyl-Histone H3 (Lys27)

Host Organism: rabbit

Clonality: polyclonal

Comments: seller recommendations: IgG; IgG ChIP, WB; ChIP; Western Blot

Antibody Name: Anti-acetyl-Histone H3 (Lys27)

Description: This polyclonal targets acetyl-Histone H3 (Lys27)

Target Organism: h, yeastfungi, vrt

Antibody ID: AB_310550

Vendor: Millipore

Catalog Number: 07-360

Record Creation Time: 20250819T211122+0000

Record Last Update: 20250819T220832+0000

Ratings and Alerts

No rating or validation information has been found for Anti-acetyl-Histone H3 (Lys27).

No alerts have been found for Anti-acetyl-Histone H3 (Lys27).

Data and Source Information

Source: [Antibody Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Dang D, et al. (2025) Isocitrate dehydrogenase 1 primes group-3 medulloblastomas for cuproptosis. *Cancer cell*, 43(6), 1159.

Dong L, et al. (2025) RACK7 senses and fine-tunes enhancer activity. *iScience*, 28(8), 113083.

Do BT, et al. (2024) Nucleotide depletion promotes cell fate transitions by inducing DNA replication stress. *Developmental cell*, 59(16), 2203.

Nguyen CDK, et al. (2024) PRMT1 promotes epigenetic reprogramming associated with acquired chemoresistance in pancreatic cancer. *Cell reports*, 43(5), 114176.

Liu N, et al. (2023) Histone H3 lysine 27 crotonylation mediates gene transcriptional repression in chromatin. *Molecular cell*, 83(13), 2206.

Swaffer MP, et al. (2023) RNA polymerase II dynamics and mRNA stability feedback scale mRNA amounts with cell size. *Cell*, 186(24), 5254.

Xu W, et al. (2022) Dynamic control of chromatin-associated m6A methylation regulates nascent RNA synthesis. *Molecular cell*, 82(6), 1156.

García-Eguren G, et al. (2022) Glucocorticoid-induced Fingerprints on Visceral Adipose Tissue Transcriptome and Epigenome. *The Journal of clinical endocrinology and metabolism*, 107(1), 150.

Hsieh WC, et al. (2022) Glucose starvation induces a switch in the histone acetylome for activation of gluconeogenic and fat metabolism genes. *Molecular cell*, 82(1), 60.

Liang Q, et al. (2022) Essential role of MESP1-RING1A complex in cardiac differentiation. *Developmental cell*, 57(22), 2533.

Wu LY, et al. (2022) Dynamic chromatin state profiling reveals regulatory roles of auxin and cytokinin in shoot regeneration. *Developmental cell*, 57(4), 526.

Jung HS, et al. (2021) SOX17 integrates HOXA and arterial programs in hemogenic endothelium to drive definitive lympho-myeloid hematopoiesis. *Cell reports*, 34(7), 108758.

Lei I, et al. (2021) Acetyl-CoA production by specific metabolites promotes cardiac repair after myocardial infarction via histone acetylation. *eLife*, 10.

Lin X, et al. (2020) Enhancer-Driven lncRNA BDNF-AS Induces Endocrine Resistance and Malignant Progression of Breast Cancer through the RNH1/TRIM21/mTOR Cascade. *Cell reports*, 31(10), 107753.

Hu R, et al. (2020) Myt Transcription Factors Prevent Stress-Response Gene Overactivation to Enable Postnatal Pancreatic ? Cell Proliferation, Function, and Survival. *Developmental cell*, 53(4), 390.

Luo X, et al. (2020) Epigenetic Mechanisms Contribute to Evolutionary Adaptation of Gene Network Activity under Environmental Selection. *Cell reports*, 33(4), 108306.

Pattschull G, et al. (2019) The Myb-MuvB Complex Is Required for YAP-Dependent Transcription of Mitotic Genes. *Cell reports*, 27(12), 3533.

Benabdallah NS, et al. (2019) Decreased Enhancer-Promoter Proximity Accompanying Enhancer Activation. *Molecular cell*, 76(3), 473.

Liu Z, et al. (2019) Nucleoporin Seh1 Interacts with Olig2/Brd7 to Promote Oligodendrocyte Differentiation and Myelination. *Neuron*, 102(3), 587.

Yamagishi M, et al. (2019) Targeting Excessive EZH1 and EZH2 Activities for Abnormal Histone Methylation and Transcription Network in Malignant Lymphomas. *Cell reports*, 29(8), 2321.