Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 27, 2025

ENCODE Project Antibody validation H3K36me3

RRID:AB_306966
Type: Antibody

Proper Citation

(Abcam Cat# ab9050, RRID:AB_306966)

Antibody Information

URL: http://antibodyregistry.org/AB_306966

Proper Citation: (Abcam Cat# ab9050, RRID:AB_306966)

Target Antigen: H3K36me3

Host Organism: rabbit

Clonality: polyclonal

Comments: Rabbit polyclonal. Antibody Target: H3K36me3
Validation: ENCODE PROJECT validation information available
Info: Independent validation by the NYU Lagone was performed for: IHC. This antibody was found to have the following characteristics: Functional in human:TRUE, NonFunctional in human:FALSE, Functional in animal:FALSE, NonFunctional in animal:FALSE

Antibody Name: ENCODE Project Antibody validation H3K36me3

Description: This polyclonal targets H3K36me3

Target Organism: mouse

Antibody ID: AB_306966

Vendor: Abcam

Catalog Number: ab9050

Record Creation Time: 20241016T233723+0000

Record Last Update: 20241017T005952+0000

Ratings and Alerts

- ENCODE PROJECT External validation for lot: 927884 is available under ENCODE ID: ENCAB570ZTO - ENCODE https://www.encodeproject.org/antibodies/ENCAB570ZTO

No alerts have been found for ENCODE Project Antibody validation H3K36me3.

Data and Source Information

Source: Antibody Registry

Usage and Citation Metrics

We found 113 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Köhler AR, et al. (2024) Modular dual-color BiAD sensors for locus-specific readout of epigenome modifications in single cells. Cell reports methods, 4(4), 100739.

Dror I, et al. (2024) XIST directly regulates X-linked and autosomal genes in naive human pluripotent cells. Cell, 187(1), 110.

Ko EK, et al. (2024) Disruption of H3K36 methylation provokes cellular plasticity to drive aberrant glandular formation and squamous carcinogenesis. Developmental cell, 59(2), 187.

Mateo-Bonmatí E, et al. (2024) A CPF-like phosphatase module links transcription termination to chromatin silencing. Molecular cell, 84(12), 2272.

Francette AM, et al. (2024) Multiple direct and indirect roles of the Paf1 complex in transcription elongation, splicing, and histone modifications. Cell reports, 43(9), 114730.

Hong Y, et al. (2024) SAFB restricts contact domain boundaries associated with L1 chimeric transcription. Molecular cell, 84(9), 1637.

Crespo R, et al. (2024) PCID2 dysregulates transcription and viral RNA processing to promote HIV-1 latency. iScience, 27(3), 109152.

Abu-Zaid A, et al. (2024) Histone lysine demethylase 4 family proteins maintain the transcriptional program and adrenergic cellular state of MYCN-amplified neuroblastoma. Cell reports. Medicine, 5(3), 101468.

Lu P, et al. (2024) Spatiotemporal role of SETD2-H3K36me3 in murine pancreatic organogenesis. Cell reports, 43(2), 113703.

Bi S, et al. (2024) The sirtuin-associated human senescence program converges on the activation of placenta-specific gene PAPPA. Developmental cell.

Zhou N, et al. (2024) Histone methylation readers MRG1/2 interact with PIF4 to promote thermomorphogenesis in Arabidopsis. Cell reports, 43(2), 113726.

Taglini F, et al. (2024) DNMT3B PWWP mutations cause hypermethylation of heterochromatin. EMBO reports, 25(3), 1130.

Niu N, et al. (2024) Tumor cell-intrinsic epigenetic dysregulation shapes cancer-associated fibroblasts heterogeneity to metabolically support pancreatic cancer. Cancer cell, 42(5), 869.

Jamge B, et al. (2023) Histone variants shape chromatin states in Arabidopsis. eLife, 12.

Manjón AG, et al. (2023) Perturbations in 3D genome organization can promote acquired drug resistance. Cell reports, 42(10), 113124.

Hu Y, et al. (2023) Lineage-specific 3D genome organization is assembled at multiple scales by IKAROS. Cell, 186(24), 5269.

Wang L, et al. (2023) TONSOKU is required for the maintenance of repressive chromatin modifications in Arabidopsis. Cell reports, 42(7), 112738.

Modur V, et al. (2023) Mechanism of inert inflammation in an immune checkpoint blockade-resistant tumor subtype bearing transcription elongation defects. Cell reports, 42(4), 112364.

Vad-Nielsen J, et al. (2023) Genome-wide epigenetic and mRNA-expression profiling followed by CRISPR/Cas9-mediated gene-disruptions corroborate the MIR141/MIR200C-ZEB1/ZEB2-FGFR1 axis in acquired EMT-associated EGFR TKI-resistance in NSCLC cells. Translational lung cancer research, 12(1), 42.

Dar MS, et al. (2023) Dnmt3bas coordinates transcriptional induction and alternative exon inclusion to promote catalytically active Dnmt3b expression. Cell reports, 42(6), 112587.