Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 6, 2025

Rabbit anti-MED12 Antibody, Affinity Purified

RRID:AB_669756
Type: Antibody

Proper Citation

(Bethyl Cat# A300-774A, RRID:AB_669756)

Antibody Information

URL: http://antibodyregistry.org/AB_669756

Proper Citation: (Bethyl Cat# A300-774A, RRID:AB_669756)

Target Antigen: MED12

Host Organism: rabbit

Clonality: polyclonal

Comments: Applications: WB, IP, IHC
Original Manufacturer
Info: Independent validation by the NYU Lagone was performed for: IHC. This antibody was found to have the following characteristics: Functional in human:FALSE, NonFunctional in human:FALSE, Functional in animal:TRUE, NonFunctional in animal:FALSE

Antibody Name: Rabbit anti-MED12 Antibody, Affinity Purified

Description: This polyclonal targets MED12

Target Organism: mouse, human

Antibody ID: AB_669756

Vendor: Bethyl

Catalog Number: A300-774A

Alternative Catalog Numbers: A300-774A-M, A300-774A-T

Record Creation Time: 20231110T043539+0000

Record Last Update: 20241115T041542+0000

Ratings and Alerts

- Independent validation by the NYU Lagone was performed for: IHC. This antibody was found to have the following characteristics: Functional in human:FALSE, NonFunctional in human:FALSE, Functional in animal:TRUE, NonFunctional in animal:FALSE - NYU Langone's Center for Biospecimen Research and Development https://med.nyu.edu/research/scientific-cores-shared-resources/center-biospecimen-research-development

Warning: Discontinued at Thermo Fisher Scientific
Applications: WB, IP, IHC
Original Manufacturer
Info: Independent validation by the NYU Lagone was performed for: IHC. This antibody was found to have the following characteristics: Functional in human:FALSE, NonFunctional in human:FALSE, Functional in animal:TRUE, NonFunctional in animal:FALSE

Data and Source Information

Source: Antibody Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Sooraj D, et al. (2022) MED12 and BRD4 cooperate to sustain cancer growth upon loss of mediator kinase. Molecular cell, 82(1), 123.

Mukherjee S, et al. (2022) SOX transcription factors direct TCF-independent WNT/?-catenin responsive transcription to govern cell fate in human pluripotent stem cells. Cell reports, 40(8), 111247.

Barral A, et al. (2022) SETDB1/NSD-dependent H3K9me3/H3K36me3 dual heterochromatin maintains gene expression profiles by bookmarking poised enhancers. Molecular cell, 82(4), 816.

Guo R, et al. (2020) MYC Controls the Epstein-Barr Virus Lytic Switch. Molecular cell, 78(4), 653.

Pavlova NN, et al. (2020) Translation in amino-acid-poor environments is limited by tRNAGln

charging. eLife, 9.

Jung YH, et al. (2019) Maintenance of CTCF- and Transcription Factor-Mediated Interactions from the Gametes to the Early Mouse Embryo. Molecular cell, 75(1), 154.

Steinparzer I, et al. (2019) Transcriptional Responses to IFN-? Require Mediator Kinase-Dependent Pause Release and Mechanistically Distinct CDK8 and CDK19 Functions. Molecular cell, 76(3), 485.

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

Pham D, et al. (2019) Batf Pioneers the Reorganization of Chromatin in Developing Effector T Cells via Ets1-Dependent Recruitment of Ctcf. Cell reports, 29(5), 1203.

Agrawal Singh S, et al. (2019) PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells. eLife, 8.

Panigrahi AK, et al. (2018) SRC-3 Coactivator Governs Dynamic Estrogen-Induced Chromatin Looping Interactions during Transcription. Molecular cell, 70(4), 679.

Adachi K, et al. (2018) Esrrb Unlocks Silenced Enhancers for Reprogramming to Naive Pluripotency. Cell stem cell, 23(2), 266.

Gao WW, et al. (2018) JMJD6 Licenses ER?-Dependent Enhancer and Coding Gene Activation by Modulating the Recruitment of the CARM1/MED12 Co-activator Complex. Molecular cell, 70(2), 340.

Bornelöv S, et al. (2018) The Nucleosome Remodeling and Deacetylation Complex Modulates Chromatin Structure at Sites of Active Transcription to Fine-Tune Gene Expression. Molecular cell, 71(1), 56.

Alfonso-Dunn R, et al. (2017) Transcriptional Elongation of HSV Immediate Early Genes by the Super Elongation Complex Drives Lytic Infection and Reactivation from Latency. Cell host & microbe, 21(4), 507.