

SUV39H1 (44.1): sc-23961

BACKGROUND

Distinct modifications of histone tails, such as acetylation, phosphorylation and methylation, regulate nuclear processes by organizing the chromatin into higher order structures. Higher-order chromatin influences chromosome function and epigenetic gene regulation. Human and murine SUV39H1 are mammalian homologues of *Drosophila* Su(var)3-9 and of *Schizosaccharomyces pombe* clr4, which encode Histone H3-specific methyltransferases. SUV39H1, suppressor of variegation 3-9, selectively methylates lysine 9 of the amino terminus of Histone H3 to generate a binding site for HP1 proteins. These HP1 proteins belong to a family of heterochromatic adaptor molecules that are implicated in both gene silencing and supra-nucleosomal chromatin structure. SUV39H1 contains both SET and chromo domains and is ubiquitously expressed. The enrichment of SUV39H1 at heterochromatic foci during interphase and centromere-specific localization during metaphase depends on the C-terminal SET domain. SUV39H1 is phosphorylated specifically at the G₁/S cell cycle transition and, when forcibly expressed, suppresses cell growth. SUV39H1 acts as a long-range repressor that is capable of acting over several kilobases to silence basal promoters.

REFERENCES

1. Agaard, L., et al. 1999. Functional mammalian homologues of the *Drosophila* PEV-modifier Su(var)3-9 encode centromere-associated proteins which complex with the heterochromatin component M31. *EMBO J.* 18: 1923-1938.
2. Rea, S., et al. 2000. Regulation of chromatin structure by site-specific Histone H3 methyltransferases. *Nature* 406: 593-599.
3. Melcher, M., et al. 2000. Structure-function analysis of SUV39H1 reveals a dominant role in heterochromatin organization, chromosome segregation, and mitotic progression. *Mol. Cell. Biol.* 20: 3728-3741.

CHROMOSOMAL LOCATION

Genetic locus: SUV39H1 (human) mapping to Xp11.23; Suv39h1 (mouse) mapping to X A1.1.

SOURCE

SUV39H1 (44.1) is a mouse monoclonal antibody raised against purified SUV39H1 protein.

PRODUCT

Each vial contains 200 µg IgG₁ kappa light chain in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

SUV39H1 (44.1) is available conjugated to agarose (sc-23961 AC), 500 µg/0.25 ml agarose in 1 ml, for IP; to HRP (sc-23961 HRP), 200 µg/ml, for WB, IHC(P) and ELISA; to either phycoerythrin (sc-23961 PE), fluorescein (sc-23961 FITC), Alexa Fluor® 488 (sc-23961 AF488), Alexa Fluor® 546 (sc-23961 AF546), Alexa Fluor® 594 (sc-23961 AF594) or Alexa Fluor® 647 (sc-23961 AF647), 200 µg/ml, for WB (RGB), IF, IHC(P) and FCM; and to either Alexa Fluor® 680 (sc-23961 AF680) or Alexa Fluor® 790 (sc-23961 AF790), 200 µg/ml, for Near-Infrared (NIR) WB, IF and FCM.

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APPLICATIONS

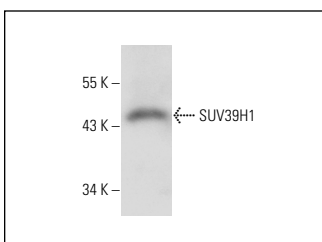
SUV39H1 (44.1) is recommended for detection of N-terminal (195 aa) SUV39H1 of mouse, rat and human origin by Western Blotting (starting dilution 1:200, dilution range 1:100-1:1000), immunoprecipitation [1-2 µg per 100-500 µg of total protein (1 ml of cell lysate)], immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500) and immunohistochemistry (including paraffin-embedded sections) (starting dilution 1:50, dilution range 1:50-1:500).

Suitable for use as control antibody for SUV39H1 siRNA (h): sc-38463, SUV39H1 siRNA (m): sc-38464, SUV39H1 shRNA Plasmid (h): sc-38463-SH, SUV39H1 shRNA Plasmid (m): sc-38464-SH, SUV39H1 shRNA (h) Lentiviral Particles: sc-38463-V and SUV39H1 shRNA (m) Lentiviral Particles: sc-38464-V.

Molecular Weight of SUV39H1: 45 kDa.

Positive Controls: HeLa nuclear extract: sc-2120 or HeLa whole cell lysate: sc-2200.

DATA



SUV39H1 (44.1): sc-23961. Western blot analysis of SUV39H1 expression in HeLa whole cell lysate.

SELECT PRODUCT CITATIONS

1. Li, Y., et al. 2010. Synergistic epigenetic reactivation of estrogen receptor- α (ER α) by combined green tea polyphenol and histone deacetylase inhibitor in ER α -negative breast cancer cells. *Mol. Cancer* 9: 274.
2. Zhao, F., et al. 2010. Triptolide alters histone H3K9 and H3K27 methylation state and induces G₀/G₁ arrest and caspase-dependent apoptosis in multiple myeloma *in vitro*. *Toxicology* 267: 70-79.
3. Iwase, S., et al. 2011. ATRX ADD domain links an atypical histone methylation recognition mechanism to human mental-retardation syndrome. *Nat. Struct. Mol. Biol.* 18: 769-776.
4. Tsuboi, M., et al. 2020. Chromate exposure induces DNA hypermethylation of the mismatch repair gene MLH1 in lung cancer. *Mol. Carcinog.* 59: 24-31.
5. Tanaka, M., et al. 2022. The role of H3K9me3 in oral squamous cell carcinoma. *Biochem. Biophys. Res. Commun.* 640: 56-63.

STORAGE

Store at 4° C, **DO NOT FREEZE**. Stable for one year from the date of shipment. Non-hazardous. No MSDS required.

RESEARCH USE

For research use only, not for use in diagnostic procedures.