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SUV39H1 Antibody

Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP1190a

Product Information

Application	WB, E
Primary Accession	O43463
Other Accession	NP_003164
Reactivity	Human, Rat, Mouse
Host	Rabbit
Clonality	Polyclonal
Isotype	Rabbit IgG
Calculated MW	47907

Additional Information

Gene ID	6839
Other Names	Histone-lysine N-methyltransferase SUV39H1, Histone H3-K9 methyltransferase 1, H3-K9-HMTase 1, Lysine N-methyltransferase 1A, Position-effect variegation 3-9 homolog, Suppressor of variegation 3-9 homolog 1, Su(var)3-9 homolog 1, SUV39H1, KMT1A, SUV39H
Target/Specificity	Purified recombinant GST fusion protein encoding N-terminal of human SUV39H1.
Dilution	WB~~1:1000 E~~Use at an assay dependent concentration.
Format	Purified polyclonal antibody supplied in PBS with 0.09% (W/V) sodium azide. This antibody is prepared by Saturated Ammonium Sulfate (SAS) precipitation followed by dialysis against PBS.
Storage	Maintain refrigerated at 2-8°C for up to 2 weeks. For long term storage store at -20°C in small aliquots to prevent freeze-thaw cycles.
Precautions	SUV39H1 Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

Protein Information

Name	SUV39H1
Synonyms	KMT1A, SUV39H
Function	Histone methyltransferase that specifically mediates trimethylation of 'Lys-9' of histone H3 (H3K9me3) using monomethylated H3 'Lys-9' (H3K9me1)

	as substrate (PubMed:10949293, PubMed:11242053, PubMed:18004385, PubMed:40440427). Also weakly methylates histone H1 (in vitro) (PubMed:10949293). H3 'Lys-9' trimethylation represents a specific tag for epigenetic transcriptional repression by recruiting HP1 (CBX1, CBX3 and/or CBX5) proteins to methylated histones (PubMed:10949293, PubMed:11242053, PubMed:18004385). Mainly functions in heterochromatin regions, thereby playing a central role in the establishment of constitutive heterochromatin at pericentric and telomere regions (By similarity). H3 'Lys-9' trimethylation is also required to direct DNA methylation at pericentric repeats (PubMed:41094145). SUV39H1 is targeted to histone H3 via its interaction with RB1 and is involved in many processes, such as repression of MYOD1-stimulated differentiation, regulation of the control switch for exiting the cell cycle and entering differentiation, repression by the PML-RARA fusion protein, BMP-induced repression, repression of switch recombination to IgA and regulation of telomere length (PubMed:11484059, PubMed:14765126, PubMed:16449642, PubMed:16818776, PubMed:16858404, PubMed:30111536). Involved in the maintenance of H3K9me3 mark following DNA replication, when histone marks are diluted: HP1 recognizes the preexisting H3K9me3 mark and serves as a platform to recruit SUV39H1 to modify the adjacent newly incorporated histones (PubMed:10949293, PubMed:11242053, PubMed:40440427). Component of the eNoSC (energy-dependent nucleolar silencing) complex, a complex that mediates silencing of rDNA in response to intracellular energy status and acts by recruiting histone- modifying enzymes (PubMed:18485871). The eNoSC complex is able to sense the energy status of cell: upon glucose starvation, elevation of NAD(+)/NADP(+) ratio activates SIRT1, leading to histone H3 deacetylation followed by dimethylation of H3 at 'Lys-9' (H3K9me2) by SUV39H1 and the formation of silent chromatin in the rDNA locus (PubMed:18485871). Recruited by the large PER complex to the E-box elements of the circadian target genes such as PER2 itself or PER1, contributes to the conversion of local chromatin to a heterochromatin- like repressive state through H3 'Lys-9' trimethylation (By similarity).
Cellular Location	Nucleus. Chromosome. Nucleus lamina. Nucleus, nucleoplasm. Chromosome, centromere. Note=Associates with centromeric constitutive heterochromatin (PubMed:10671371). Recruited to pericentromeric heterochromatin via its chromo domain, which specifically recognizes and binds histone H3 monoubiquitinated at 'Lys- 14' (H3K14ub) (PubMed:41094145).

Background

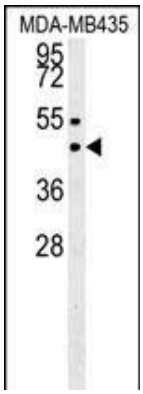
Similar to acetylation and phosphorylation, histone methylation at the N-terminal tail has emerged as an important role in regulating chromatin dynamics and gene activity. Histone methylation occurs on arginine and lysine residues and is catalyzed by two families of proteins, the protein arginine methyltransferase family and the SET-domain-containing methyltransferase family. Five members have been identified in the arginine methyltransferase family. About 27 are grouped into the SET-domain family, and another 17 make up the PR domain family that is related to the SET domain family. The retinoblastoma protein-interacting zinc finger geneRIZ1 is a tumor suppressor gene and a FOUNDING member of the PR domain family. RIZ1 inactivation is commonly found in many types of human cancers and occurs through loss of mRNA expression, frame shift mutation, chromosomal deletion, and missense mutation. RIZ1 is also a tumor susceptibility gene in mice. The loss of RIZ1 mRNA in human cancers was shown to associate with DNA methylation of its promoter CpG island. Methylation of the RIZ1 promoter strongly correlated with lost or decreased RIZ1 mRNA expression in breast, liver, colon, and lung cancer cell lines as well as in liver cancer tissues.

References

Fujita, N., et al., J. Biol. Chem. 278(26):24132-24138 (2003). Macaluso, M., et al., Oncogene 22(23):3511-3517

(2003). Schotta, G., et al., EMBO J. 21(5):1121-1131 (2002). Vaute, O., et al., Nucleic Acids Res. 30(2):475-481 (2002). Rea, S., et al., Nature 406(6796):593-599 (2000).

Images



SUV39H1 (Cat. #AP1190a) western blot analysis in MDA-MB435 cell line lysates (35ug/lane). This demonstrates the SUV39H1 antibody detected the SUV39H1 protein (arrow).

Citations

- Epigenetic regulation of surfactant protein A gene (SP-A) expression in fetal lung reveals a critical role for Suv39h methyltransferases during development and hypoxia.
- High expressions of histone methylation- and phosphorylation-related proteins are associated with prognosis of oral squamous cell carcinoma in male population of Taiwan.

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