10320 Camino Santa Fe, Suite G
San Diego, CA 92121
Tel: 858.875.1900 Fax: 858.875.1999

SUV39H1 Rabbit pAb

Catalog # AP99949

Product Information

Application	IHC-P, IHC-F, IF
Primary Accession	O43463
Other Accession	O43463
Predicted	Rat, Pig, Human, Mouse, Dog
Host	Rabbit
Clonality	Polyclonal
Calculated MW	47907
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human KMT1A
Epitope Specificity	211-310/412
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Belongs to the histone-lysine methyltransferase family. Suvar3-9 subfamily.Contains 1 chromo domain.Contains 1 post-SET domain.Contains 1 pre-SET domain.Contains 1 SET domain.
SUBUNIT	nteracts with H3 and H4 histones. Interacts with GFI1B, DNMT3B, CBX1, CBX4, KIAA1967/DBC1, MBD1, RUNX1, RUNX3, MYOD1, SMAD5 and RB1. Interacts with SBF1 through the SET domain. Interacts with HDAC1 and HDAC2 through the N-terminus and associates with the core histone deacetylase complex composed of HDAC1, HDAC2, RBBP4 and RBBP7. Component of the eNoSC complex, composed of SIRT1, SUV39H1 and RRP8. In case of infection, interacts with HTLV-1 Tax protein, leading to abrogate Tax transactivation of HTLV-1 LTR. Interacts (via SET domain) with MECOM; enhances MECOM transcriptional repression activity (By similarity).
Post-translational modifications	Phosphorylated on serine residues, and to a lesser degree, on threonine residues. The phosphorylated form is stabilized by SBF1 and is less active in its transcriptional repressor function. Acetylated at Lys-266, leading to inhibition of enzyme activity. SIRT1-mediated deacetylation relieves this inhibition.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	This gene encodes an evolutionarily-conserved protein containing an N-terminal chromodomain and a C-terminal SET domain. The encoded protein is a histone methyltransferase that trimethylates lysine 9 of histone H3, which results in transcriptional gene silencing. Loss of function of this gene disrupts heterochromatin formation and may cause chromosome instability. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Aug 2013]

Additional Information

Gene ID	6839

Other Names	H3-K9-HMTase 1; KMT1A; MG44; SUV39H; DXHXS7466e; mIS6; RGD1565028; Suv39h1l1; SUV91_HUMAN; 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); 2.1.1.355; SUV91_MOUSE; SUV39H1 histone lysine methyltransferase; suppressor of variegation 3-9 (Drosophila) homolog 1; suppressor of variegation 3-9 homolog 1 (Drosophila); suppressor of variegation 3-9 homolog 1
Dilution	IHC-P=1:100-500,IHC-F=1:100-500,IF=1:100-500
Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

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).

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