

SUV39H1 Antibody Blocking Peptide
Synthetic peptide
Catalog # BP1190a**Specification**

SUV39H1 Antibody Blocking Peptide - Product Information

Primary Accession [O43463](#)
Other Accession [NP_003164](#)

SUV39H1 Antibody Blocking Peptide - 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

The synthetic peptide sequence used to generate the antibody [AP1190a](/product/products/AP1190a) was selected from the region of human SUV39H1. A 10 to 100 fold molar excess to antibody is recommended. Precise conditions should be optimized for a particular assay.

Format

Peptides are lyophilized in a solid powder format. Peptides can be reconstituted in solution using the appropriate buffer as needed.

Storage

Maintain refrigerated at 2-8°C for up to 6 months. For long term storage store at -20°C.

Precautions

This product is for research use only. Not for use in diagnostic or therapeutic procedures.

SUV39H1 Antibody Blocking Peptide - Protein Information

Name SUV39H1

Synonyms KMT1A, SUV39H

Function

Histone methyltransferase that specifically trimethylates 'Lys-9' of histone H3 using monomethylated H3 'Lys-9' as substrate. Also weakly methylates histone H1 (in vitro). H3 'Lys-9' trimethylation represents a specific tag for epigenetic transcriptional repression by recruiting HP1 (CBX1, CBX3 and/or CBX5) proteins to methylated histones. Mainly functions in heterochromatin regions, thereby playing a central role in the establishment of constitutive heterochromatin at pericentric and telomere regions. H3 'Lys-9' trimethylation is also required to direct DNA methylation at pericentric repeats. 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. 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. 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. 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.

Cellular Location

Nucleus. Nucleus lamina. Nucleus, nucleoplasm Chromosome, centromere. Note=Associates with centromeric constitutive heterochromatin

SUV39H1 Antibody Blocking Peptide - Protocols

Provided below are standard protocols that you may find useful for product applications.

- [Blocking Peptides](#)

SUV39H1 Antibody Blocking Peptide - Images

SUV39H1 Antibody Blocking Peptide - 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 gene RIZ1 is a tumor suppressor gene and a FOUNGING 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.

SUV39H1 Antibody Blocking Peptide - 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).