



## Rabbit Anti-KMT1A antibody

SL5708R

<b>Product Name:</b>	KMT1A
<b>Chinese Name:</b>	组蛋白H3 K9甲基转移酶抗体
<b>Alias:</b>	H3 K9 HMTase; H3 K9 HMTase1; H3-K9-HMTase 1; Histone H3 K9 methylation; Histone H3 Lys 9 methylation; Histone H3-K9 methyltransferase 1; Histone H3-K9 methyltransferase1; Histone lysine N methyltransferase H3 lysine 9 specific 1; Histone lysine N methyltransferase, H3 lysine 9 specific 1; Histone-lysine N-methyltransferase SUV39H1; KMT1 A; Lysine N methyltransferase 1A; Lysine N-methyltransferase 1A; MG44; mIS6; Position-effect variegation 3-9 homolog; Su(var)3 9 homolog 1; Su(var)3-9 homolog 1; Suppressor of variegation 3 9 homolog 1 (Drosophila); Suppressor of variegation 3-9 homolog 1; SUV39 H1; SUV39H; SUV39H1; SUV91 HUMAN.
<b>Organism Species:</b>	Rabbit
<b>Clonality:</b>	Polyclonal
<b>React Species:</b>	Human,Mouse,Rat,Dog,Pig,Cow,
<b>Applications:</b>	ELISA=1:500-1000IHC-P=1:400-800IHC-F=1:400-800IF=1:100-500 (Paraffin sections need antigen repair) not yet tested in other applications. optimal dilutions/concentrations should be determined by the end user.
<b>Molecular weight:</b>	48kDa
<b>Cellular localization:</b>	The nucleus
<b>Form:</b>	Lyophilized or Liquid
<b>Concentration:</b>	1mg/ml
<b>immunogen:</b>	KLH conjugated synthetic peptide derived from human Histone H3 Lys 9 methylation/SUV39H1:211-310/412
<b>Lsotype:</b>	IgG
<b>Purification:</b>	affinity purified by Protein A
<b>Storage Buffer:</b>	0.01M TBS(pH7.4) with 1% BSA, 0.03% Proclin300 and 50% Glycerol.
<b>Storage:</b>	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. The lyophilized antibody is stable at room temperature for at least one month and for greater than a year when kept at -20°C. 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.
<b>PubMed:</b>	<a href="#">PubMed</a>
<b>Product Detail:</b>	<p>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.</p> <p><b>Function:</b>  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.</p> <p><b>Subunit:</b>  nteracts with H3 and H4 histones. Interacts with GF11B, 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).</p> <p><b>Subcellular Location:</b></p>

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

**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.

**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.

**SWISS:**

O43463

**Gene ID:**

6839

**Database links:**

[Entrez Gene: 6839](#)Human

[Entrez Gene: 20937](#)Mouse

[Entrez Gene: 302553](#)Rat

[Omim: 300254](#)Human

[SwissProt: O43463](#)Human

[SwissProt: O54864](#)Mouse

[Unigene: 522639](#)Human

[Unigene: 479743](#)Mouse

[Unigene: 9244](#)Mouse

**Important Note:**

This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.