G-Biosciences Image not found or type unknown

Immunotag™ SUV91 Polyclonal Antibody

Antibody Specification

Catalog No.	ITN2996
Product Description	Immunotag™ SUV91 Polyclonal Antibody
Size	50 µg, 100 µg
Conjugation	HRP, Biotin, FITC, Alexa Fluor® 350, Alexa Fluor® 405, Alexa Fluor® 488, Alexa Fluor® 555, Alexa Fluor® 594, Alexa Fluor® 647
IMPORTANT NOTE	This product is custom manufactured with a lead time of 3-4 weeks. Once in production, this item cannot be cancelled from an order and is not eligible for return.
Target Protein	SUV91
Clonality	Polyclonal
Storage/Stability	-20°C/1 year
Application	WB,ELISA
Recommended Dilution	WB 1:500-2000 ELISA 1:5000-20000
Concentration	1 mg/ml
Reactive Species	Human,Mouse
Host Species	Rabbit
Immunogen	Synthesized peptide derived from part region of human protein
Specificity	SUV91 Polyclonal Antibody detects endogenous levels of protein.
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen
Form	Liquid in PBS containing 50% glycerol, and 0.02% sodium azide.
Gene Name	SUV39H1 KMT1A SUV39H
Accession No.	O43463 O54864
Description	suppressor of variegation 3-9 homolog 1(SUV39H1) Homo sapiens 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],

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Cell Pathway/ Category	Lysine degradation,
Protein Expression	B-cell,Epithelium,Lung,Retina,
Subcellular Localization	chromosome, centromeric region,heterochromatin,condensed nuclear chromosome,nucleus,nuclear lamina,nucleoplasm,chromatin silencing complex,rDNA heterochromatin,
Protein Function	catalytic activity:S-adenosyl-L-methionine + histone L-lysine = S-adenosyl-L-homocysteine + histone N(6)-methyl-L-lysine.,developmental stage:Accumulates during mitosis at centromeres during prometaphase, but dissociates from the centromere at the meta- to anaphase transition.,domain:Although the SET domain contains the active site of enzymatic activity, both pre-SET and post-SET domains are required for methyltransferase activity. The SET domain also participates to stable binding to heterochromatin.,enzyme regulation:Inhibited by S-adenosyl-L-homocysteine.,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 differentiaton, repression by the PML-RARA fusion protein, BMP-induced repression, repression of switch recombination to IgA and regulation of telomere length.,PTM: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.,similarity:Belongs to the histone-lysine methyltransferase family. Suvar3-9 subfamily.,similarity:Contains 1 chromo domain.,similarity:Contains 1 post-SET domain.,similarity:Contains 1 pre-SET domain.,similarity:Contains 1 SET domain.,subcellular location:Associates with centromeric constitutive heterochromatin.,subunit:Interacts with H3 and H4 histones. Interacts with GFI1B, DNMT3B, CBX1, CBX4, 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. In case of infection, interacts with HTLV-1 Tax protein, leading to abrogate Tax transactivation of HTLV-1 LTR.,
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