

Product datasheet

Recombinant human KMT1A / SUV39H1 protein
ab80289

2 Images

Overview

Product name	Recombinant human KMT1A / SUV39H1 protein
Protein length	Protein fragment

Description

Nature	Recombinant
Source	Escherichia coli

Amino Acid Sequence

Accession	O43463
Species	Human
Molecular weight	64 kDa including tags
Amino acids	82 to 412
Tags	GST tag N-Terminus

Specifications

Our [Abpromise guarantee](#) covers the use of **ab80289** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Biological activity	Specific Activity: 3.5 pmol/min/μg.
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Assay conditions: 50 μl reaction mix (50 mM TRIS pH 8.8, 5mM MgCl₂, 4mM DTT, 0.05% Tween-20, 40 μM S-adenosylmethionine, and 10-100 ng SUV39H1) add to the wells coated with the substrate on a GBioscience Neutraavidin black plate. Incubate for 1 hr. Add antibody against methylated K9 residue of histone H3, incubate 1 hr. Then, add secondary HRP-labeled antibody and incubate 30 min. Finally, add HRP chemiluminescent substrates and read luminescence.

Applications	Functional Studies
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SDS-PAGE

Form

Liquid

Preparation and Storage

Stability and Storage

Shipped on Dry Ice. Upon delivery aliquot. Store at -80°C. Avoid freeze / thaw cycle.

pH: 8.00

Constituents: 0.0462% DTT, 0.395% Tris HCl, 0.05% Tween, 30% Glycerol, 0.58% Sodium chloride

This product is an active protein and may elicit a biological response in vivo, handle with caution.

General Info

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.

Sequence similarities

Belongs to the class V-like SAM-binding methyltransferase superfamily. 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.

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.
In the pre-SET domain, Cys residues bind 3 zinc ions that are arranged in a triangular cluster; some of these Cys residues contribute to the binding of two zinc ions within the cluster.

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.

Cellular localization

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

Images

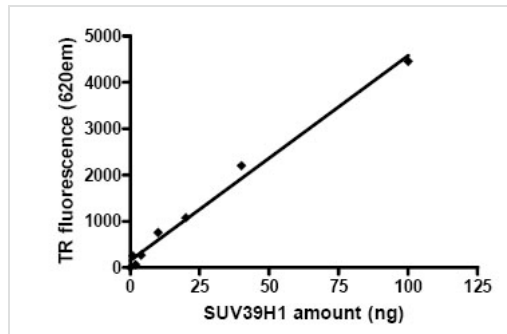
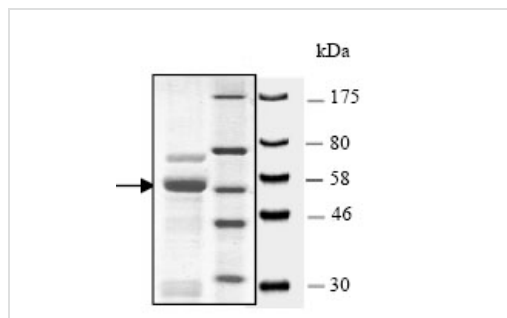


Image showing specific activity of ab80289.

Functional Studies - Recombinant human KMT1A / SUV39H1 protein (ab80289)



10% SDS-PAGE showing ab80289 at approximately 64kDa (3 μ g). 2 μ g of protein loaded.

SDS-PAGE - Recombinant human KMT1A / SUV39H1 protein (ab80289)

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