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SETDB1/KMT1E Rabbit pAb

Catalog # AP97470

Product Information

Application	IHC-P, IHC-F, IF
Primary Accession	Q15047
Other Accession	Q15047
Reactivity	Rat
Predicted	Pig, Human, Mouse, Rabbit, Dog, Horse, Sheep
Host	Rabbit
Clonality	Polyclonal
Calculated MW	143157
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human KMT1E
Epitope Specificity	201-300/1291
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 MBD (methyl-CpG-binding) domain. Contains 1 post-SET domain. Contains 1 pre-SET domain. Contains 1 SET domain. Contains 2 Tudor domains.
SUBUNIT	Interacts with MBD1; interaction is abolished when MBD1 is sumoylated. Interacts with ATF7IP and ATF7IP2; the interaction with ATF7IP is required to stimulate histone methyltransferase activity and facilitate the conversion of dimethylated to trimethylated H3 'Lys-9'. During DNA replication, it is recruited by SETDB1 to form a S phase-specific complex that facilitates methylation of H3 'Lys-9' during replication-coupled chromatin assembly and is at least composed of the CAF-1 subunit CHAF1A, MBD1 and SETDB1. Interacts with ERG, TRIM28/TIF1B, CBX1, CBX5, CHD7, DNMT3A, HDAC1, HDAC2, NLK, PPARG, SIN3A, SIN3B, DNMT3B and SUMO2. Interacts with MPHOSPH8.
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 a histone methyltransferase which regulates histone methylation, gene silencing, and transcriptional repression. This gene has been identified as a target for treatment in Huntington Disease, given that gene silencing and transcription dysfunction likely play a role in the disease pathogenesis. Alternatively spliced transcript variants of this gene have been described.[provided by RefSeq, Jun 2011]

Additional Information

Gene ID	9869
Other Names	ESET; H3-K9-HMTase4; KG1T; KMT1E; TDRD21; mKIAA0067; SETB1_HUMAN; SETDB1; ERG-associated protein with SET domain (ESET); Histone H3-K9

	methyltransferase 4 (H3-K9-HMTase 4); Lysine N-methyltransferase 1E; SET domain bifurcated 1; 2.1.1.366; KIAA0067; SETB1_MOUSE; SET domain bifurcated histone lysine methyltransferase 1; SET domain, bifurcated 1; tudor domain containing 21
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	SETDB1 {ECO:0000303|PubMed:11959841, ECO:0000312|HGNC:HGNC:10761}
Function	Histone methyltransferase that specifically trimethylates 'Lys-9' of histone H3 (H3K9me3) (PubMed:11959841, PubMed:12869583, PubMed:14536086, PubMed:27237050, PubMed:39096901). 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:11959841, PubMed:12869583, PubMed:14536086, PubMed:27237050, PubMed:39096901). Mainly functions in euchromatin regions, thereby playing a central role in the silencing of euchromatic genes (PubMed:12869583, PubMed:14536086, PubMed:27237050, PubMed:39096901). H3 'Lys-9' trimethylation is coordinated with DNA methylation (PubMed:12869583, PubMed:14536086, PubMed:27237050, PubMed:39096901). Forms a complex with MBD1 and ATF7IP that represses transcription and couples DNA methylation and histone 'Lys-9' trimethylation (PubMed:14536086). Its activity is dependent on MBD1 and is heritably maintained through DNA replication by being recruited by CAF-1 (PubMed:14536086). SETDB1 is targeted to histone H3 by TRIM28/TIF1B, a factor recruited by KRAB zinc-finger proteins (PubMed:24623306). Required for HUSH-mediated heterochromatin formation and gene silencing (PubMed:27732843). Probably forms a corepressor complex required for activated KRAS-mediated promoter hypermethylation and transcriptional silencing of tumor suppressor genes (TSGs) or other tumor-related genes in colorectal cancer (CRC) cells (PubMed:24623306). Required to maintain a transcriptionally repressive state of genes in undifferentiated embryonic stem cells (ESCs) (PubMed:24623306). In ESCs, in collaboration with TRIM28, is also required for H3K9me3 and silencing of endogenous and introduced retroviruses in a DNA- methylation independent-pathway (PubMed:37938770). Associates at promoter regions of tumor suppressor genes (TSGs) leading to their gene silencing (PubMed:24623306). The SETDB1-TRIM28-ZNF274 complex may play a role in recruiting ATRX to the 3'-exons of zinc-finger coding genes with atypical chromatin signatures to establish or maintain/protect H3K9me3 at these transcriptionally active regions (PubMed:27029610). Also catalyzes mono- and dimethylation of 'Lys-9' of free histone H3 (H3K9me1 and H3K9me2) during translation in the cytoplasm, which is then transported to the nucleus and incorporated into nucleosomes (PubMed:26405197).
Cellular Location	Nucleus. Cytoplasm. Chromosome Note=Associated with non-pericentromeric regions of chromatin (PubMed:27029610). Recruited to H3K9me and H3K19ac marks on chromatin (PubMed:29234025). Excluded from nucleoli and islands of condensed chromatin (PubMed:27732843).
Tissue Location	Widely expressed. High expression in testis.

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