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SETDB1 Antibody

Purified Mouse Monoclonal Antibody
Catalog # AO1483a

Product Information

Application	WB, E
Primary Accession	Q15047
Reactivity	Human, Mouse, Monkey
Host	Mouse
Clonality	Monoclonal
Clone Names	5H6D4
Isotype	IgG1
Calculated MW	143157
Description	This gene encodes a histone methyltransferase. The encoded enzyme catalyzes the reaction of S-adenosyl-L-methionine and histone L-lysine to produce S-adenosyl-L-homocysteine and histone N(6)-methyl-L-lysine. The encoded protein likely functions in transcriptional repression.Tissue specificity: Widely expressed. High expression in testis.
Immunogen	Purified recombinant fragment of human SETDB1 expressed in E. Coli.
Formulation	Ascitic fluid containing 0.03% sodium azide.

Additional Information

Gene ID	9869
Other Names	Histone-lysine N-methyltransferase SETDB1, 2.1.1.43, ERG-associated protein with SET domain, ESET, Histone H3-K9 methyltransferase 4, H3-K9-HMTase 4, Lysine N-methyltransferase 1E, SET domain bifurcated 1, SETDB1, KIAA0067, KMT1E
Dilution	WB~~1/500 - 1/2000 E~~N/A
Storage	Maintain refrigerated at 2-8°C for up to 6 months. For long term storage store at -20°C in small aliquots to prevent freeze-thaw cycles.
Precautions	SETDB1 Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

Protein Information

Name	SETDB1 (HGNC:10761)

Function	Histone methyltransferase that specifically trimethylates 'Lys-9' of histone H3. 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 euchromatin regions, thereby playing a central role in the silencing of euchromatic genes. H3 'Lys-9' trimethylation is coordinated with DNA methylation (PubMed:12869583, PubMed:27237050, PubMed:39096901). Required for HUSH-mediated heterochromatin formation and gene silencing. Forms a complex with MBD1 and ATF7IP that represses transcription and couples DNA methylation and histone 'Lys-9' trimethylation (PubMed:14536086, PubMed:27732843). 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. 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 (By similarity). 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).
Cellular Location	Nucleus. Cytoplasm. Chromosome. Note=Associated with non-pericentromeric regions of chromatin. Excluded from nucleoli and islands of condensed chromatin.
Tissue Location	Widely expressed. High expression in testis.

References

1. Proteomics. 2005 Sep;5(14):3589-99. 2. Proc Natl Acad Sci U S A. 2006 Apr 4;103(14):5308-13. 3. Mol Cell Biochem. 2007 Nov;305(1-2):35-44.

Images

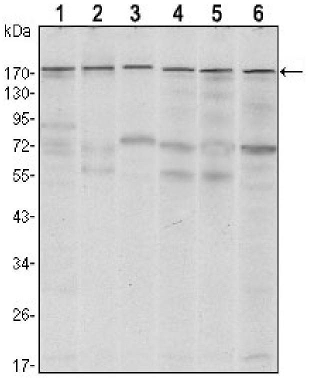

Figure 1: Western blot analysis using SETDB1 mouse mAb against MCF-7 (1),T47D (2), HEK293 (3), JURKAT (4), NIH/3T3 (5) and F9 (6) cell lysate.

Please note: All products are 'FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES'.