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Dnmt1 Rabbit mAb

Catalog # AP75367

Product Information

Application	WB, FC, IP
Primary Accession	P26358
Reactivity	Human
Host	Rabbit
Clonality	Monoclonal Antibody
Isotype	IgG
Conjugate	Unconjugated
Purification	Affinity Purified
Calculated MW	183165

Additional Information

Gene ID	1786
Other Names	DNMT1
Dilution	WB~~1:1000-1:5000 FC~~1:100-1:1000 IP~~1:20
Format	Liquid in 50mM Tris-Glycine(pH 7.4), 0.15M NaCl, 40%Glycerol, 0.01% sodium azide and 0.05% BSA.
Storage	Store at 4°C short term. Aliquot and store at -20°C long term. Avoid freeze/thaw cycles.

Protein Information

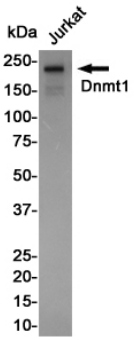
Name	DNMT1 {ECO:0000303|Ref.3, ECO:0000312|HGNC:HGNC:2976}
Function	DNA methyltransferase that methylates CpG residues (PubMed: 17200670, PubMed:18754681, PubMed:21745816, PubMed:26070743). Preferentially methylates hemimethylated DNA (PubMed:21745816, PubMed:26070743). Associates with DNA replication sites in S phase maintaining the methylation pattern in the newly synthesized strand, that is essential for epigenetic inheritance (PubMed:17200670, PubMed:21745816). Associates with chromatin during G2 and M phases to maintain DNA methylation independently of replication (PubMed:21745816). It is responsible for maintaining methylation patterns established in development (PubMed:21745816). DNA methylation is coordinated with methylation of histones (PubMed:16357870). Mediates transcriptional repression by direct binding to HDAC2 (PubMed:10888872). In association with DNMT3B and via the recruitment of CTCFL/BORIS, involved in activation of BAG1 gene expression by modulating dimethylation of promoter histone H3 at H3K4 and H3K9 (PubMed:18413740). 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). Also required to maintain a transcriptionally repressive state of genes in undifferentiated embryonic stem cells (ESCs) (PubMed:24623306). Associates at promoter regions of tumor suppressor genes (TSGs) leading to their gene silencing (PubMed:24623306).
Cellular Location	Nucleus. Chromosome Note=Associates with replication foci during S-phase: recruited to hemimethylated DNA sites via its RFTS domain, which specifically recognizes and binds histone H3 ubiquitinated at 'Lys-14', 'Lys-18' and 'Lys-23' (H3K14ub, H3K18ub and H3K23ub, respectively) (PubMed:29053958). Localized to the perinucleolar region (PubMed:24492612).
Tissue Location	Ubiquitous; highly expressed in fetal tissues, heart, kidney, placenta, peripheral blood mononuclear cells, and expressed at lower levels in spleen, lung, brain, small intestine, colon, liver, and skeletal muscle. Isoform 2 is less expressed than isoform 1.

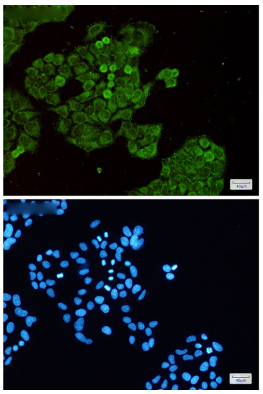
Background

Methylation of DNA at cytosine residues in mammalian cells is a heritable, epigenetic modification that is critical for proper regulation of gene expression, genomic imprinting and development. It is responsible for maintaining methylation patterns established in development. DNA methylation is coordinated with methylation of histones. Mediates transcriptional repression by direct binding to HDAC2.

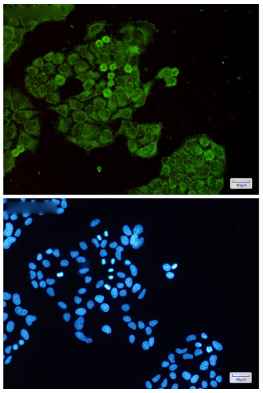
Images

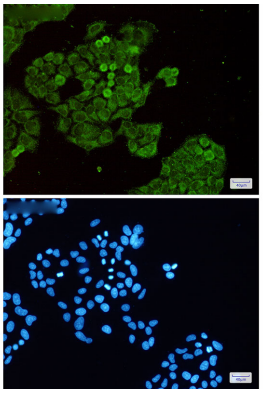


Western blot analysis of Dnmt1 in Jurkat lysates using Dnmt1 antibody.



Immunocytochemistry analysis of Dnmt1(green) in Hela using Dnmt1 antibody,and DAPI(blue)





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