Anti-DNMT1 antibody

Description	Unconjugated Rabbit polyclonal to DNMT1

Model	STJ193054
Host	Rabbit
Reactivity	Human, Mouse, Rat
Applications	ELISA, WB
Gene ID	1786
Gene Symbol	DNMT1
Dilution range	WB 1:500-2000 ELISA 1:5000-20000
Specificity	DNMT1 Polyclonal Antibody detects endogenous levels of protein.
Tissue Specificity	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.
Purification	DNMT1 antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
Note	For Research Use Only (RUO).
Protein Name	DNA cytosine-5-methyltransferase 1 Dnmt1 CXXC-type zinc finger protein 9 DNA methyltransferase HsaI DNA MTase HsaI M.HsaI MCMT
Molecular Weight	177 kDa
Clonality	Polyclonal

Conjugation	Unconjugated
Isotype	IgG
Formulation	Liquid form in PBS containing 50% glycerol,and 0.02% sodium azide.
Concentration	1 mg/ml
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Database Links	HGNC:2976OMIM:126375
Alternative Names	DNA cytosine-5-methyltransferase 1 Dnmt1 CXXC-type zinc finger protein 9 DNA methyltransferase HsaI DNA MTase HsaI M.HsaI MCMT
Function	Methylates CpG residues. Preferentially methylates hemimethylated DNA. Associates with DNA replication sites in S phase maintaining the methylation pattern in the newly synthesized strand, that is essential for epigenetic inheritance. Associates with chromatin during G2 and M phases to maintain DNA methylation independently of replication. 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. 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. 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 . Also required to maintain a transcriptionally repressive state of genes in undifferentiated embryonic stem cells (ESCs) . Associates at promoter regions of tumor suppressor genes (TSGs) leading to their gene silencing . Promotes tumor growth .
Sequence and Domain Family	The N-terminal part is required for homodimerization and acts as a regulatory domain.; The CXXC-type zinc finger specifically binds to unmethylated CpG dinucleotides, positioning the autoinhibitory linker between the DNA and the active site, thus providing a mechanism to ensure that only hemimethylated CpG dinucleotides undergo methylation.
Cellular Localization	Nucleus
Post-translational Modifications	Sumoylated; sumoylation increases activity. Acetylation on multiple lysines, mainly by KAT2B/PCAF, regulates cell cycle G(2)/M transition. Deacetylation of Lys-1349 and Lys-1415 by SIRT1 increases methyltransferase activity. Phosphorylation of Ser-154 by CDKs is important for enzymatic activity and protein stability. Phosphorylation of Ser-143 by AKT1 prevents methylation by SETD7 therebye increasing DNMT1 stability. Methylation at Lys-142 by SETD7 promotes DNMT1 proteasomal degradation. Ubiquitinated by UHRF1; interaction with USP7 counteracts ubiquitination by UHRF1 by promoting deubiquitination and preventing degradation by the proteasome.