

DNA Methyltransferase 1 (Clone 60B1220.1) Antibody
Mouse Monoclonal Antibody
Catalog # ABV11107**Specification**

DNA Methyltransferase 1 (Clone 60B1220.1) Antibody - Product Information

Application	WB
Primary Accession	P26358
Reactivity	Human, Mouse, Zebrafish
Host	Mouse
Clonality	Monoclonal
Isotype	Mouse IgG1κ
Calculated MW	183165

DNA Methyltransferase 1 (Clone 60B1220.1) Antibody - Additional Information**Gene ID** 1786**Application & Usage****Western blot:** 2-4 µg/ml. **IHC** (parffin-embedded sections), **ChIP**, and **IP:** 1-2 µg/ml. However, the optimal conditions should be determined individually.**Other Names**
DNMT1**Target/Specificity**
DNMT1**Antibody Form**
Liquid**Appearance**
Colorless liquid**Formulation**
50 µg of antibody in 100 µl PBS containing 0.05% BSA and 0.05% sodium azide.**Handling**
The antibody solution should be gently mixed before use.**Reconstitution & Storage**
-20 °C**Background Descriptions****Precautions**

DNA Methyltransferase 1 (Clone 60B1220.1) Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

DNA Methyltransferase 1 (Clone 60B1220.1) Antibody - Protein Information

Name DNMT1

Synonyms AIM, CXXC9, DNMT

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 (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). Promotes tumor growth (PubMed:24623306).

Cellular Location

Nucleus. Note=Localized to the perinucleolar region.

Tissue Location

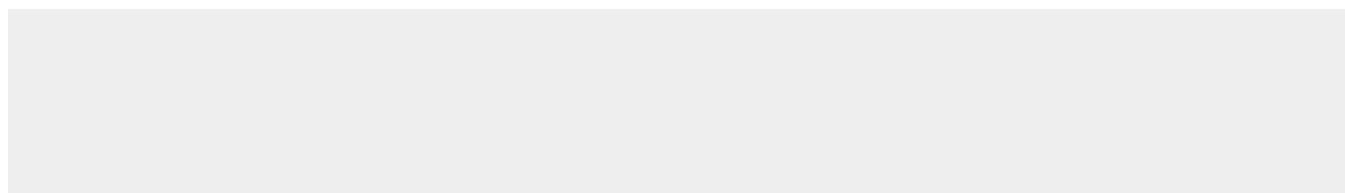
Ubiquitous; highly expressed in fetal tissues, heart, kidney, placenta, peripheral blood mononuclear cells, and expressed at lower levels in spleen, lung, brain, small intestine, colon, liver, and skeletal muscle. Isoform 2 is less expressed than isoform 1.

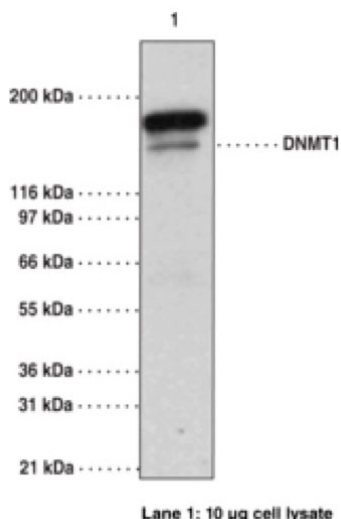
DNA Methyltransferase 1 (Clone 60B1220.1) Antibody - Protocols

Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

DNA Methyltransferase 1 (Clone 60B1220.1) Antibody - Images





Lane 1: 10 µg cell lysate

DNA Methyltransferase 1 (Clone 60B1220.1) Antibody - Background

Methylation of DNA at cytosine residues plays an important role in regulation of gene expression, genomic imprinting, and is essential for mammalian development. Hypermethylation of CpG islands in tumor suppressor genes or hypomethylation of bulk genomic DNA may be linked with development of cancer. To date, three families of mammalian DNA methyltransferase genes have been identified which include DNMT1, DNMT2, and DNMT3. DNMT1 is constitutively expressed in proliferating cells and inactivation of this gene causes global demethylation of genomic DNA and embryonic lethality. DNMT1 co-purifies with the retinoblastoma (Rb) tumour suppressor gene product, E2F1, and HDAC1. DNMT1 also cooperates with Rb to repress transcription from promoters containing E2F-binding sites suggesting a link between DNA methylation, histone deacetylase, and sequence-specific DNA binding activity, as well as a growth-regulatory pathway that is disrupted in nearly all cancer cells.