Revision 1

Store at -20C

#93140

DNMT3A Antibody Sampler Kit

1 Kit (3 x 20 microliters)

Cell Signaling TECHNOLOGY®

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For Research Use Only. Not for Use in Diagnostic Procedures.

Product Includes	Product #	Quantity	Mol. Wt	Isotype/Source
DNMT3A (E9P2F) Rabbit mAb	49768	20 µl	85, 95, 130 kDa	Rabbit IgG
DNMT3A (D23G1) Rabbit mAb	3598	20 µl	130 kDa	Rabbit IgG
DNMT3A Isoform 2 (E1Y5O) Rabbit mAb	44807	20 µl	95 kDa	Rabbit IgG
Anti-rabbit IgG, HRP-linked Antibody	7074	100 µl		Goat

Please visit cellsignal.com for individual component applications, species cross-reactivity, dilutions, protocols, and additional product information.

Description

The DNMT3A Antibody Sampler Kit provides an economical means of detecting various isoforms of DNMT3A, including isoform 1 (DNMT3A1) and isoform 2 (DNMT3A2). The kit includes enough antibodies to perform two western blot experiments with each primary antibody.

Storage

Supplied in 10 mM sodium HEPES (pH 7.5), 150 mM NaCl, 100 µg/ml BSA, 50% glycerol and less than 0.02% sodium azide. Store at –20°C. *Do not aliquot the antibodies.*

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 (1,2). Three families of mammalian DNA methyltransferases have been identified: DNMT1, DNMT2, and DNMT3 (1,2). DNMT1 is constitutively expressed in proliferating cells and functions as a maintenance methyltransferase, transferring proper methylation patterns to newly synthesized DNA during replication. DNMT3A and DNMT3B are strongly expressed in embryonic stem cells with reduced expression in adult somatic tissues. DNMT3A and DNMT3B function as *de novo* methyltransferases that methylate previously unmethylated regions of DNA. DNMT2 is expressed at low levels in adult somatic tissues and its inactivation affects neither *de novo* nor maintenance DNA methylation. DNMT1, DNMT3A, and DNMT3B together form a protein complex that interacts with histone deacetylases (HDAC1, HDAC2, Sin3A), transcriptional repressor proteins (RB, TAZ-1), and heterochromatin proteins (HP1, SUV39H1) to maintain proper levels of DNA methylation and facilitate gene silencing (3-8). Improper DNA methylation contributes to diseased states such as cancer (1,2). Hypermethylation of promoter CpG islands within tumor suppressor genes correlates with gene silencing and the development of cancer. In addition, hypomethylation of bulk genomic DNA correlates with and may contribute to the onset of cancer. DNMT1, DNMT3A, and DNMT3B are overexpressed in many cancers, including acute and chronic myelogenous leukemias, in addition to colon, breast, and stomach carcinomas (9-12).~There are at least two protein isoforms expressed from the DNMT3A locus, DNMT3A isoform 1 (DNMT3A1) and DNMT3A isoform 2 (DNMT3A2). DNMT3A2 is expressed from an intronic promoter that is downstream from the DNMT3A1 promoter (13,14). As a result, the N-terminal 223 amino acids found in DNMT3A1 are replaced by a different 24 amino acid found in DNMT3A2. Although they have distinct N-termini, both isoforms contain the PWWP domain required for binding to tri-methylated histone H3 lysine 36 (H3K36me3) and the ADD domain required for histone binding and transcriptional regulation. DNMT3A1 is lowly expressed in most cell and tissue types and is localized to heterochromatic regions. DNMT3A2 expression appears to be developmentally regulated and limited to embryonic stem cells, where it is localized to euchromatic regions of the genome, suggesting distinct functions for DNMT3A1 and DNMT3A2. DNMT3A2 is the predominant isoform responsible for *de novo* DNA methylation in embryonic stem cells. In addition, DNMT3A2 is mutated and/or highly expressed in a number of different cancers, including acute myeloid leukemia (AML), teratocarcinoma, neuroblastoma, and lung, testicular, gastric, and breast cancer (13-17).

Background References

1. Hermann, A. et al. (2004) *Cell. Mol. Life Sci.* 61, 2571-87.
2. Turek-Plewa, J. and Jagodziński, P.P. (2005) *Cell. Mol. Biol. Lett.* 10, 631-47.
3. Kim, G.D. et al. (2002) *EMBO J.* 21, 4183-95.
4. Fuks, F. et al. (2001) *EMBO J.* 20, 2536-44.
5. Geiman, T.M. et al. (2004) *Biochem. Biophys. Res. Commun.* 318, 544-55.
6. Rountree, M.R. et al. (2000) *Nat. Genet.* 25, 269-77.
7. Pradhan, S. and Kim, G.D. (2002) *EMBO J.* 21, 779-88.
8. Fuks, F. et al. (2003) *Nucleic Acids Res.* 31, 2305-12.
9. Mizuno, S. et al. (2001) *Blood* 97, 1172-9.

10. Robertson, K.D. et al. (1999) *Nucleic Acids Res.* 27, 2291-8.
11. Xie, S. et al. (1999) *Gene* 236, 87-95.
12. Kanai, Y. et al. (2001) *Int. J. Cancer* 91, 205-12.
13. Gujar, H. et al. (2019) *Genes (Basel)* 10, pii: E172. doi: 10.3390/genes10020172.
14. Chen, B.F. and Chan, W.Y. (2014) *Epigenetics* 9, 669-77.
15. Chen, B.F. et al. (2014) *Epigenetics* 9, 119-28.
16. Gao, J. et al. (2013) *J Exp Clin Cancer Res* 32, 86.
17. Yu, Z. et al. (2015) *Mol Carcinog* 54, 707-19.

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Limited Uses