

NSUN5 (H-10): sc-376147

BACKGROUND

NSUN5 (NOL1/NOP2/Sun domain family, member 5), also known as NOL1, p120 or NOL1R, is a 429 amino acid protein that belongs to the methyltransferase superfamily and exists as multiple alternatively spliced isoforms. Expressed ubiquitously with higher expression in heart, placenta and skeletal muscle, NSUN5 is thought to function as an S-adenosyl-L-methionine-dependent methyl-transferase whose absence may be associated with the pathogenesis of Williams syndrome. NSUN5 is subject to post-translational phosphorylation, probably by ATM or ATR. The gene encoding NSUN5 maps to human chromosome 7, which houses over 1,000 genes and comprises nearly 5% of the human genome. Defects in some of the genes localized to chromosome 7 have been linked to osteogenesis imperfecta, Williams syndrome, Pendred syndrome, Lissencephaly, Citrullinemia and Shwachman-Diamond syndrome.

CHROMOSOMAL LOCATION

Genetic locus: NSUN5 (human) mapping to 7q11.23.

SOURCE

NSUN5 (H-10) is a mouse monoclonal antibody raised against amino acids 227-365 mapping near the C-terminus of NSUN5 of human origin.

PRODUCT

Each vial contains 200 µg IgG₁ kappa light chain in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

NSUN5 (H-10) is available conjugated to agarose (sc-376147 AC), 500 µg/0.25 ml agarose in 1 ml, for IP; to HRP (sc-376147 HRP), 200 µg/ml, for WB, IHC(P) and ELISA; to either phycoerythrin (sc-376147 PE), fluorescein (sc-376147 FITC), Alexa Fluor[®] 488 (sc-376147 AF488), Alexa Fluor[®] 546 (sc-376147 AF546), Alexa Fluor[®] 594 (sc-376147 AF594) or Alexa Fluor[®] 647 (sc-376147 AF647), 200 µg/ml, for WB (RGB), IF, IHC(P) and FCM; and to either Alexa Fluor[®] 680 (sc-376147 AF680) or Alexa Fluor[®] 790 (sc-376147 AF790), 200 µg/ml, for Near-Infrared (NIR) WB, IF and FCM.

APPLICATIONS

NSUN5 (H-10) is recommended for detection of NSUN5 of human origin by Western Blotting (starting dilution 1:100, dilution range 1:100-1:1000), immunoprecipitation [1-2 µg per 100-500 µg of total protein (1 ml of cell lysate)], immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

Suitable for use as control antibody for NSUN5 siRNA (h): sc-89751, NSUN5 shRNA Plasmid (h): sc-89751-SH and NSUN5 shRNA (h) Lentiviral Particles: sc-89751-V.

Molecular Weight of NSUN5: 47 kDa.

Positive Controls: COLO 320DM cell lysate: sc-2226 or K-562 whole cell lysate: sc-2203.

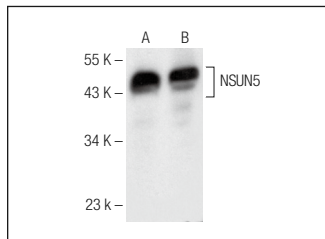
RESEARCH USE

For research use only, not for use in diagnostic procedures.

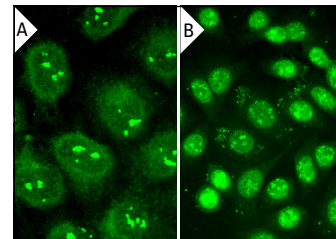
STORAGE

Store at 4° C, ****DO NOT FREEZE****. Stable for one year from the date of shipment. Non-hazardous. No MSDS required.

DATA



NSUN5 (H-10): sc-376147. Western blot analysis of NSUN5 expression in COLO 320DM (A) and K-562 (B) whole cell lysates.



NSUN5 (H-10): sc-376147. Immunofluorescence staining of methanol-fixed HeLa cells showing nucleolar and nuclear localization (A). Immunofluorescence staining of formalin-fixed SW480 cells showing nucleolar and nuclear localization (B).

SELECT PRODUCT CITATIONS

- Warda, A.S., et al. 2016. Effects of the Bowen-Conradi syndrome mutation in EMG1 on its nuclear import, stability and nucleolar recruitment. *Hum. Mol. Genet.* 25: 5353-5364.
- Serikawa, T., et al. 2018. Comprehensive identification of proteins binding to RNA G-quadruplex motifs in the 5' UTR of tumor-associated mRNAs. *Biochimie* 144: 169-184.
- Heissenberger, C., et al. 2019. Loss of the ribosomal RNA methyltransferase NSUN5 impairs global protein synthesis and normal growth. *Nucleic Acids Res.* 47: 11807-11825.
- Wang, Y., et al. 2021. Mutations in RNA methyltransferase gene NSUN5 confer high risk of outflow tract malformation. *Front. Cell Dev. Biol.* 9: 623394.
- Zhou, J., et al. 2023. RNA cytosine methyltransferase NSUN5 promotes protein synthesis and tumorigenic phenotypes in glioblastoma. *Mol. Oncol.* 17: 1763-1783.
- Gu, X., et al. 2024. RNA 5-methylcytosine writer NSUN5 promotes hepatocellular carcinoma cell proliferation via a ZBED3-dependent mechanism. *Oncogene* 43: 624-635.
- Cai, Z., et al. 2024. RNA modification Regulators' Co-Expression Score (RMRCoeS) predicts biochemical recurrence and therapy response in prostate cancer: a multi-omics and experimental validation study. *Int. Immunopharmacol.* 139: 112723.

PROTOCOLS

See our web site at www.scbt.com for detailed protocols and support products.

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