SANTA CRUZ BIOTECHNOLOGY, INC.

PMS2 (E-19): sc-617

SANTA CRUZ BIOTECHNOLOGY

The Power to Question

BACKGROUND

The finding that mutations in DNA mismatch repair genes are associated with hereditary nonpolyposis colorectal cancer (HNPCC) has resulted in considerable interest in the understanding of the mechanism of DNA mismatch repair. Initially, inherited mutations in the MSH2 and MLH1 homologs of the bacterial DNA mismatch repair genes MutS and MutL were demonstrated at high frequency in HNPCC and were shown to be associated with microsatellite instability. The demonstration that 10 to 45% of pancreatic, gastric, breast, ovarian and small cell lung cancers also display microsatellite instability has been interpreted to suggest that DNA mismatch repair is not restricted to HNPCC tumors but is a common feature in tumor initiation or progression. Two additional homologs of the prokaryotic MutL gene, designated PMS1 and PMS2, have been identified and shown to be mutated in the germline of HNPCC patients.

REFERENCES

1. Peltomäki, P., et al. 1993. Genetic mapping of a locus predisposing to human colorectal cancer. Science 260: 810-812.
2. Ionov, Y., et al. 1993. Ubiquitous somatic mutations in simple repeated sequences reveal a new mechanism for colonic carcinogenesis. Nature 363: 558-561.
3. Nicolaides, N.C., et al. 1994. Mutations of two PMS homologues in hereditary nonpolyposis colon cancer. Nature 371: 75-80.

SOURCE

PMS2 (E-19) is an affinity purified rabbit polyclonal antibody raised against a peptide mapping at the N-terminus of PMS2 of human origin.

PRODUCT

Each vial contains 200 µg IgG in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

Blocking peptide available for competition studies, sc-617 P, (100 µg peptide in 0.5 ml PBS containing < 0.1% sodium azide and 0.2% BSA).

APPLICATIONS

PMS2 (E-19) is recommended for detection of a broad range of PMS isoforms of human and, to a lesser extent, mouse and rat origin by Western Blotting (starting dilution 1:200, 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), immunohistochemistry (including paraffin-embedded sections) (starting dilution 1:50, dilution range 1:50-1:500) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

Molecular Weight of PMS2: 110 kDa.

Positive Controls: HeLa nuclear extract: sc-2120, Jurkat nuclear extract: sc-2132 or A-431 nuclear extract: sc-2122.

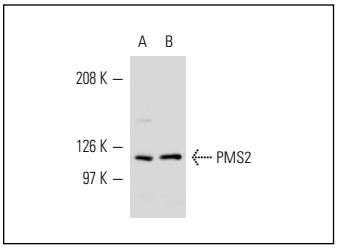
RESEARCH USE

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

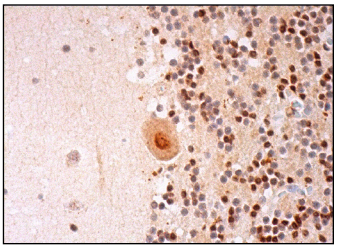
STORAGE

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

DATA



PMS2 (E-19): sc-617. Western blot analysis of PMS2 expression in Jurkat (**A**) and NIH/3T3 (**B**) nuclear extracts.



PMS2 (E-19): sc-617. Immunoperoxidase staining of formalin fixed, paraffin-embedded human cerebellum tissue showing nuclear and cytoplasmic staining of Purkinje cells and nuclear staining of cells in granular layer and cells in molecular layer.

SELECT PRODUCT CITATIONS

1. Nicolaides, N.C., et al. 1998. A naturally occurring hPMS2 mutation can confer a dominant negative mutator phenotype. Mol. Cell. Biol. 18: 1635-1641.
2. Zhu, B., et al. 2002. Intrathecal Fas ligand infusion strengthens immunoprivilege of central nervous system and suppresses experimental autoimmune encephalomyelitis. J. Immunol. 169: 1561-1569.
3. Tomer, G., et al. 2002. Contribution of human MLH1 and PMS2 ATPase activities to DNA mismatch repair. J. Biol. Chem. 277: 21801-21809.
4. Francia, G., et al. 2004. Gene expression analysis of tumor spheroids reveals a role for suppressed DNA mismatch repair in multicellular resistance to alkylating agents. Mol. Cell. Biol. 24: 6837-6849.
5. Mohd, A.B., et al. 2006. Truncation of the C-terminus of human MLH1 blocks intracellular stabilization of PMS2 and disrupts DNA mismatch repair. DNA Repair 5: 347-361.
6. Borràs, E., et al. 2012. Comprehensive functional assessment of MLH1 variants of unknown significance. Hum. Mutat. 33: 1576-1588.

PROTOCOLS

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