

Anti-MLH1 Picoband Antibody
Catalog # ABO12410

Specification

Anti-MLH1 Picoband Antibody - Product Information

Application	WB
Primary Accession	P40692
Host	Rabbit
Reactivity	Human, Mouse, Rat
Clonality	Polyclonal
Format	Lyophilized

Description

Rabbit IgG polyclonal antibody for DNA mismatch repair protein Mlh1(MLH1) detection. Tested with WB in Human;Mouse;Rat.

Reconstitution

Add 0.2ml of distilled water will yield a concentration of 500ug/ml.

Anti-MLH1 Picoband Antibody - Additional Information

Gene ID 4292

Other Names

DNA mismatch repair protein Mlh1, MutL protein homolog 1, MLH1, COCA2

Calculated MW

84601 MW KDa

Application Details

Western blot, 0.1-0.5 µg/ml, Human, Mouse, Rat

Subcellular Localization

Nucleus .

Tissue Specificity

Colon, lymphocytes, breast, lung, spleen, testis, prostate, thyroid, gall bladder and heart.

Protein Name

DNA mismatch repair protein Mlh1

Contents

Each vial contains 5mg BSA, 0.9mg NaCl, 0.2mg Na₂HPO₄, 0.05mg Na₃.

Immunogen

A synthetic peptide corresponding to a sequence at the C-terminus of human MLH1 (722-756aa KALRSHILPPKHFTEDGNILQLANLPDLYKVFERC), different from the related mouse sequence by three amino acids, and from the related rat sequence by four amino acids.

Purification

Immunogen affinity purified.

Cross Reactivity

No cross reactivity with other proteins.

Storage

At -20°C for one year. After r°Constitution, at 4°C for one month. It°Can also be aliquotted and stored frozen at -20°C for a longer time.Avoid repeated freezing and thawing.

Anti-MLH1 Picoband Antibody - Protein Information

Name MLH1

Synonyms COCA2

Function

Heterodimerizes with PMS2 to form MutL alpha, a component of the post-replicative DNA mismatch repair system (MMR). DNA repair is initiated by MutS alpha (MSH2-MSH6) or MutS beta (MSH2-MSH3) binding to a dsDNA mismatch, then MutL alpha is recruited to the heteroduplex. Assembly of the MutL-MutS-heteroduplex ternary complex in presence of RFC and PCNA is sufficient to activate endonuclease activity of PMS2. It introduces single-strand breaks near the mismatch and thus generates new entry points for the exonuclease EXO1 to degrade the strand containing the mismatch. DNA methylation would prevent cleavage and therefore assure that only the newly mutated DNA strand is going to be corrected. MutL alpha (MLH1-PMS2) interacts physically with the clamp loader subunits of DNA polymerase III, suggesting that it may play a role to recruit the DNA polymerase III to the site of the MMR. Also implicated in DNA damage signaling, a process which induces cell cycle arrest and can lead to apoptosis in case of major DNA damages. Heterodimerizes with MLH3 to form MutL gamma which plays a role in meiosis.

Cellular Location

Nucleus. Chromosome Note=Recruited to chromatin in a MCM9-dependent manner

Tissue Location

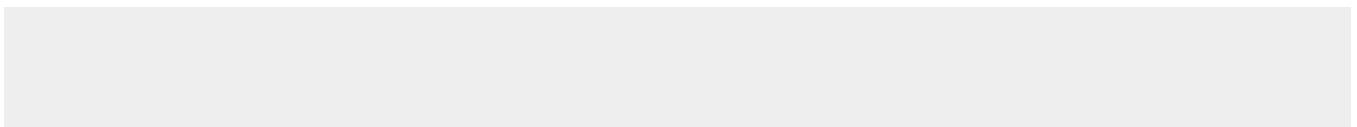
Colon, lymphocytes, breast, lung, spleen, testis, prostate, thyroid, gall bladder and heart

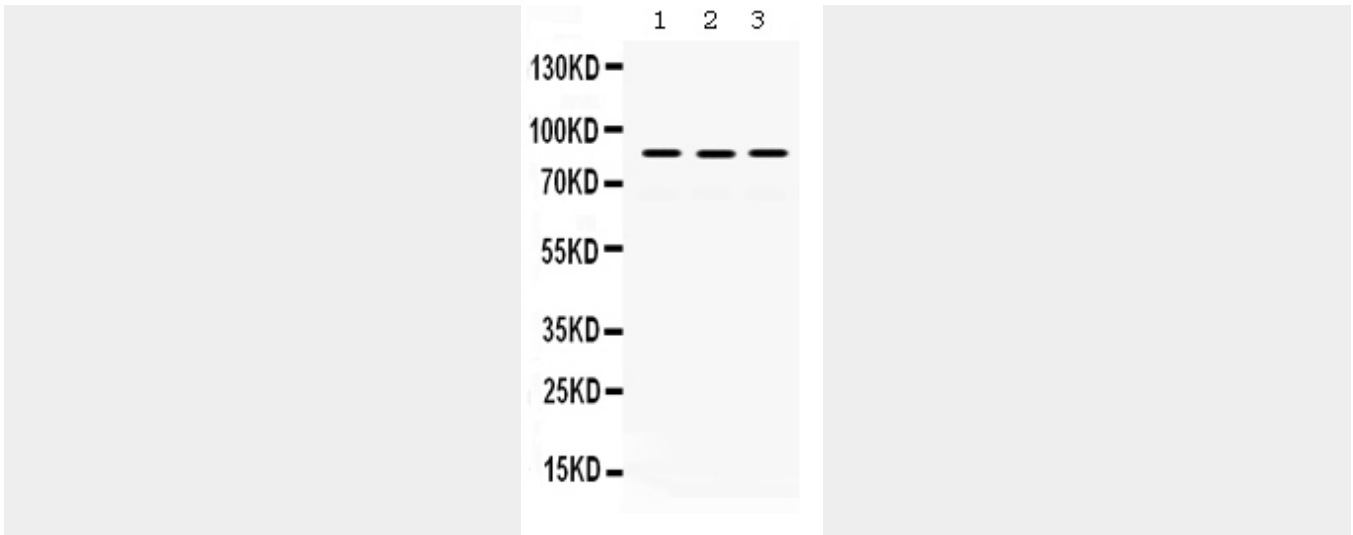
Anti-MLH1 Picoband Antibody - Protocols

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](#)

Anti-MLH1 Picoband Antibody - Images





Anti- MLH1 Picoband antibody, ABO12410, Western blotting All lanes: Anti MLH1 (ABO12410) at 0.5ug/ml Lane 1: Rat Lung Tissue Lysate at 50ug Lane 2: Mouse Testis Tissue Lysate at 50ug Lane 3: COLO320 Whole Cell Lysate at 40ug Predicted bind size: 84KD Observed bind size: 84KD

Anti-MLH1 Picoband Antibody - Background

MutL homolog 1, colon cancer, nonpolyposis type 2 (*E. coli*) is a protein that in humans is encoded by the *MLH1* gene located on Chromosome 3. This gene was identified as a locus frequently mutated in hereditary nonpolyposis colon cancer (HNPCC). It is a human homolog of the *E. coli* DNA mismatch repair gene *mutL*, consistent with the characteristic alterations in microsatellite sequences (RER+ phenotype) found in HNPCC. Alternative splicing results in multiple transcript variants encoding distinct isoforms. Additional transcript variants have been described, but their full-length natures have not been determined.