abcam

Product datasheet

Anti-MLH1 antibody [EPR3893] ab108622





★★★★★ 1 Abreviews

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Overview

Product name Anti-MLH1 antibody [EPR3893]

Description Rabbit monoclonal [EPR3893] to MLH1

Host species Rabbit

Tested applications Suitable for: WB

Unsuitable for: Flow Cyt, IHC-P or IP

Species reactivity Reacts with: Mouse, Human

Predicted to work with: Rat

Synthetic peptide. This information is proprietary to Abcam and/or its suppliers. **Immunogen**

Positive control WB: HeLa, HAP1, Jurkat, 293, K562 and SH-SY5Y cell lysates.

General notes To see more of the key markers and tools you need to study the hallmarks of cancer, including

genome instability and mutation, please visit the following page.

This product is a recombinant monoclonal antibody, which offers several advantages including:

- High batch-to-batch consistency and reproducibility

- Improved sensitivity and specificity

- Long-term security of supply

- Animal-free production

For more information see here.

Our RabMAb® technology is a patented hybridoma-based technology for making rabbit monoclonal antibodies. For details on our patents, please refer to **RabMAb**® **patents**.

Properties

Form Liquid

Storage instructions Shipped at 4°C. Store at -20°C. Stable for 12 months at -20°C.

Storage buffer pH: 7.20

Preservative: 0.05% Sodium azide

Constituents: 0.1% BSA, 40% Glycerol (glycerin, glycerine), 9.85% Tris glycine, 50% Tissue

culture supernatant

Purity Tissue culture supernatant

ClonalityMonoclonalClone numberEPR3893

Isotype IgG

Applications

The Abpromise guarantee

Our **Abpromise guarantee** covers the use of ab108622 in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Application	Abreviews	Notes
WB	****(1)	1/1000 - 1/10000. Detects a band of approximately 85 kDa (predicted molecular weight: 85 kDa).

Application notes

Is unsuitable for Flow Cyt,IHC-P or IP.

Target

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-MSH6) 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.

Tissue specificity Involvement in disease

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

Defects in MLH1 are the cause of hereditary non-polyposis colorectal cancer type 2 (HNPCC2) [MIM:609310]. Mutations in more than one gene locus can be involved alone or in combination in the production of the HNPCC phenotype (also called Lynch syndrome). Most families with clinically recognized HNPCC have mutations in either MLH1 or MSH2 genes. HNPCC is an autosomal, dominantly inherited disease associated with marked increase in cancer susceptibility. It is characterized by a familial predisposition to early onset colorectal carcinoma (CRC) and extra-colonic cancers of the gastrointestinal, urological and female reproductive tracts. HNPCC is reported to be the most common form of inherited colorectal cancer in the Western world, and accounts for 15% of all colon cancers. Cancers in HNPCC originate within benign neoplastic polyps termed adenomas. Clinically, HNPCC is often divided into two subgroups. Type I: hereditary predisposition to colorectal cancer, a young age of onset, and carcinoma observed in the proximal colon. Type II: patients have an increased risk for cancers in certain tissues such as the uterus, ovary, breast, stomach, small intestine, skin, and larynx in addition to the colon. Diagnosis of classical HNPCC is based on the Amsterdam criteria: 3 or more relatives affected by colorectal cancer, one a first degree relative of the other two; 2 or more generation affected; 1 or more colorectal cancers presenting before 50 years of age; exclusion of hereditary polyposis syndromes. The term 'suspected HNPCC' or 'incomplete HNPCC' can be used to describe

families who do not or only partially fulfill the Amsterdam criteria, but in whom a genetic basis for colon cancer is strongly suspected.

Defects in MLH1 are a cause of mismatch repair cancer syndrome (MMRCS) [MIM:276300]; also known as Turcot syndrome or brain tumor-polyposis syndrome 1 (BTPS1). MMRCS is an autosomal dominant disorder characterized by malignant tumors of the brain associated with multiple colorectal adenomas. Skin features include sebaceous cysts, hyperpigmented and cafe au lait spots.

Defects in MLH1 are a cause of Muir-Torre syndrome (MuToS) [MIM:158320]; also abbreviated MTS. MuToS is a rare autosomal dominant disorder characterized by sebaceous neoplasms and visceral malignancy.

Note=Defects in MLH1 may contribute to lobular carcinoma in situ (LCIS), a non-invasive neoplastic disease of the breast.

Defects in MLH1 are a cause of susceptibility to endometrial cancer (ENDMC) [MIM:608089]. Note=Some epigenetic changes can be transmitted unchanged through the germline (termed 'epigenetic inheritance'). Evidence that this mechanism occurs in humans is provided by the identification of individuals in whom 1 allele of the MLH1 gene is epigenetically silenced throughout the soma (implying a germline event). These individuals are affected by HNPCC but does not have identifiable mutations in MLH1, even though it is silenced, which demonstrates that an epimutation can phenocopy a genetic disease.

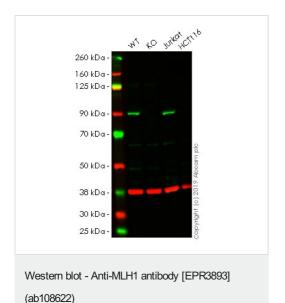
Sequence similarities

Cellular localization

Belongs to the DNA mismatch repair mutL/hexB family.

Nucleus.

Images



All lanes : Anti-MLH1 antibody [EPR3893] (ab108622) at 1/1000 dilution

Lane 1: Wild-type HeLa cell lysate

Lane 2: MLH1 knockout HeLa cell lysate

Lane 3: Jurkat cell lysate

Lane 4: HCT116 cell lysate

Lysates/proteins at 20 µg per lane.

Performed under reducing conditions.

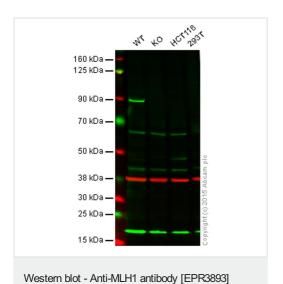
Predicted band size: 85 kDa **Observed band size:** 85 kDa

Observed band size: 85 kDa

Lanes 1-4: Merged signal (red and green). Green - ab108622 observed at 90 kDa. Red - loading control **ab8245** observed at 37 kDa.

ab108622 Anti-MLH1 antibody [EPR3893] was shown to

specifically react with MLH1 in wild-type HeLa cells. Loss of signal was observed when knockout cell line ab267223 (knockout cell lysate ab257172) was used. Wild-type and MLH1 knockout samples were subjected to SDS-PAGE. ab108622 and Anti-GAPDH antibody [6C5] - Loading Control were incubated overnight at 4°C at 1 in 1000 dilution and 1 in 20000 dilution respectively. Blots were developed with Goat anti-Mouse IgG H&L (IRDye® 800CW) preadsorbed (ab216772) and Goat Anti-Rabbit lgG H&L (IRDye® 680RD) preadsorbed (ab216777) secondary antibodies at 1 in 20000 dilution for 1 hour at room temperature before imaging.



(ab108622)

All lanes: Anti-MLH1 antibody [EPR3893] (ab108622) at 1/1000 dilution

Lane 1: Wild-type HAP1 cell lysate

Lane 2: MLH1 knockout HAP1 cell lysate

Lane 3: HCT116 cell lysate

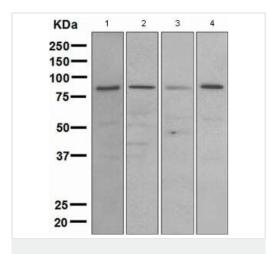
Lane 4: 293T cell lysate

Lysates/proteins at 20 µg per lane.

Predicted band size: 85 kDa

Lanes 1 - 4: Merged signal (red and green). Green - ab108622 observed at 88 kDa. Red - loading control, ab8245, observed at 37 kDa.

ab108622 was shown to recognize MLH1 in wild-type HAP1 cells along with additional cross-reactive bands. No band was observed when MLH1 knockout samples were examined. Wild-type and MLH1 knockout samples were subjected to SDS-PAGE. ab108622 and ab8245 (loading control to GAPDH) were diluted 1/1000 and 1/2000 and incubated overnight at 4°C. Blots were developed with Goat anti-Rabbit IgG H&L (IRDye® 800CW) preadsorbed ab216773 and Goat anti-Mouse IgG H&L (IRDye® 680RD) preadsorbed ab216776 secondary antibodies at 1/10,000 dilution for 1 hour at room temperature before imaging.



Western blot - Anti-MLH1 antibody [EPR3893] (ab108622)

All lanes : Anti-MLH1 antibody [EPR3893] (ab108622) at 1/1000 dilution

Lane 1 : 293 cell lysate

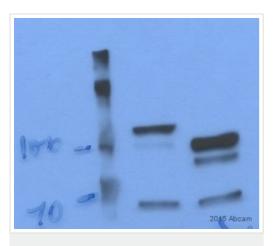
Lane 2 : Jurkat cell lysate

Lane 3 : K562 cell lysate

Lane 4 : SH-SY5Y cell lysate

Lysates/proteins at 10 µg per lane.

Predicted band size: 85 kDa



Western blot - Anti-MLH1 antibody [EPR3893] (ab108622)

This image is courtesy of an anonymous abreview.

All lanes : Anti-MLH1 antibody [EPR3893] (ab108622) at 1/1000 dilution

Lane 1 : Hela Cells Whole Cell Lysates

Lane 2 : HCT116 Whole Cell Lysates

Lysates/proteins at 30 µg per lane.

Secondary

All lanes: Goat Polyclonal to Rabbit IgG (HRP) at 1/2000 dilution

Developed using the ECL technique.

Performed under reducing conditions.

Predicted band size: 85 kDa

Exposure time: 30 seconds



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