abcam

ab268072

Anti-APE1 antibody [CPTC-APEX1-2]

Key facts

Isotype	IgG1
Host species	Mouse
Storage buffer	pH: 7.2 - 7.4 Preservative: 0.05% Sodium azide Constituents: PBS, 0.05% BSA
Form	Liquid
Clonality	Monoclonal
Immunogen	Recombinant Full Length Protein corresponding to Human APEX1. Database link P27695
Clone number	CPTC-APEX1-2
Purification technique	Affinity purification Protein A/G
Light chain type	kappa
Concentration	0.2 mg/mL The concentration of this product may be batch-dependent Batch concentration finder →
Purification notes	Purified from Bioreactor concentrate

Reactivity data

Flow Cyt

Tested

Species	Human
Dilution info	1-2 µg for 10^5-10^6 Cells

Notes	-

Not recommended

Species	Recombinant full length protein - Human
Dilution info	-
Notes	-

WB

Tested

Species	Human
Dilution info	1-2 µg/mL
Notes	-

Not recommended

Species	Recombinant full length protein - Human
Dilution info	-
Notes	-

Protein Array

Tested

Species	Recombinant full length protein - Human
Dilution info	-
Notes	-

Expected

Species	Human
Dilution info	Use at an assay dependent concentration.
Notes	-

ICC/IF

Tested

Species	Human
Dilution info	1-2 µg/mL
Notes	-

Not recommended

Species	Recombinant full length protein - Human
Dilution info	-
Notes	-

IHC-P

Tested

Species	Human
Dilution info	1-2 µg/mL
Notes	Perform heat-mediated antigen retrieval with Tris/EDTA buffer pH 9.0 before commencing with IHC staining protocol.

Not recommended

Species	Recombinant full length protein - Human
Dilution info	-
Notes	-

Target data

See full target information APEX1

Function	Multifunctional protein that plays a central role in the cellular response to oxidative stress. The two major activities of APEX1 are DNA repair and redox regulation of transcriptional factors (PubMed:11118054, PubMed:11452037, PubMed:15831793, PubMed:18439621, PubMed:18579163, PubMed:21762700, PubMed:24079850, PubMed:8355688, PubMed:9108029, PubMed:9560228). Functions as an apurinic/apyrimidinic (AP) endodeoxyribonuclease in the base excision repair (BER) pathway of DNA lesions induced by oxidative and alkylating agents. Initiates repair of AP sites in DNA by catalyzing hydrolytic incision of the

phosphodiester backbone immediately adjacent to the damage, generating a single-strand break with 5'-deoxyribose phosphate and 3'-hydroxyl ends. Also incises at AP sites in the DNA strand of DNA/RNA hybrids, single-stranded DNA regions of R-loop structures, and single-stranded RNA molecules (PubMed:15380100, PubMed:16617147, PubMed:18439621, PubMed:19123919, PubMed:19188445, PubMed:19934257, PubMed:20699270, PubMed:21762700, PubMed:24079850, PubMed:8932375, PubMed:8995436, PubMed:9804799). Operates at switch sites of immunoglobulin (Ig) constant regions where it mediates Ig isotype class switch recombination. Processes AP sites induced by successive action of AICDA and UNG. Generates staggered nicks in opposite DNA strands resulting in the formation of double-strand DNA breaks that are finally resolved via non-homologous end joining repair pathway (By similarity). Has 3'-5' exodeoxyribonuclease activity on mismatched deoxyribonucleotides at the 3' termini of nicked or gapped DNA molecules during short-patch BER (PubMed:11832948, PubMed:1719477). Possesses DNA 3' phosphodiesterase activity capable of removing lesions (such as phosphoglycolate and 8-oxoguanine) blocking the 3' side of DNA strand breaks (PubMed:15831793, PubMed:7516064). Also acts as an endoribonuclease involved in the control of single-stranded RNA metabolism. Plays a role in regulating MYC mRNA turnover by preferentially cleaving in between UA and CA dinucleotides of the MYC coding region determinant (CRD). In association with NMD1, plays a role in the rRNA quality control process during cell cycle progression (PubMed:19188445, PubMed:19401441, PubMed:21762700). Acts as a loading factor for POLB onto non-incised AP sites in DNA and stimulates the 5'-terminal deoxyribose 5'-phosphate (dRp) excision activity of POLB (PubMed:9207062). Exerts reversible nuclear redox activity to regulate DNA binding affinity and transcriptional activity of transcriptional factors by controlling the redox status of their DNA-binding domain, such as the FOS/JUN AP-1 complex after exposure to IR (PubMed:10023679, PubMed:11118054, PubMed:11452037, PubMed:18579163, PubMed:8355688, PubMed:9108029). Involved in calcium-dependent down-regulation of parathyroid hormone (PTH) expression by binding to negative calcium response elements (nCaREs). Together with HNRNPL or the dimer XRCC5/XRCC6, associates with nCaRE, acting as an activator of transcriptional repression (PubMed:11809897, PubMed:14633989, PubMed:8621488). May also play a role in the epigenetic regulation of gene expression by participating in DNA demethylation (PubMed:21496894). Stimulates the YBX1-mediated MDR1 promoter activity, when acetylated at Lys-6 and Lys-7, leading to drug resistance (PubMed:18809583). Plays a role in protection from granzyme-mediated cellular repair leading to cell death (PubMed:18179823). Binds DNA and RNA. Associates, together with YBX1, on the MDR1 promoter. Together with NPM1, associates with rRNA (PubMed:19188445, PubMed:19401441, PubMed:20699270).

Storage

Shipped at conditions	Blue Ice
Appropriate short-term storage duration	1-2 weeks
Appropriate short-term storage conditions	+4°C

Appropriate long-term storage conditions	-20°C
Aliquoting information	Upon delivery aliquot
Storage information	Avoid freeze / thaw cycle

Supplementary info

This supplementary information is collated from multiple sources and compiled automatically.

Activity summary	APE1 also known as APEX1 or apurinic/apyrimidinic endonuclease 1 functions as an important DNA repair enzyme. It plays a pivotal role in the base excision repair (BER) pathway where it recognizes and processes apurinic/apyrimidinic sites in DNA. APE1 has a molecular mass of about 37 kDa. It is expressed primarily in the nucleus with detectable levels in the cytoplasm. The expression of APE1 spans across various tissue types indicating its essential role in maintaining genomic stability.
Biological function summary	APE1 enzymatically cleaves the phosphodiester bond at abasic sites creating a nick in the DNA backbone for further repair steps. This action prevents mutations and maintains DNA integrity. APE1 also functions as a redox factor regulating the transcriptional activity of several transcription factors. It is not part of a larger complex but interacts with various BER pathway proteins such as DNA polymerase beta and XRCC1. This interaction is important for the effective repair of damaged DNA and cellular response to oxidative stress.
Pathways	APE1 is integrated within the base excision repair and redox signaling pathways. These pathways are fundamental for repairing single-strand breaks and modulating the cellular oxidative stress response. APE1 coordinates closely with other proteins like PNKP and OGG1 in the BER pathway ensuring precise and effective DNA repair. Through its redox activity APE1 influences pathways involving NF-kB and AP-1 demonstrating its multifaceted roles in cellular processes.
Associated diseases and disorders	Alterations in APE1 function associate with cancer progression and neurodegenerative diseases. Overexpression or mutations in APE1 correlate with increased tumor resistance to chemotherapy in several cancers including lung and ovarian cancer. APE1's interaction with proteins like p53 and HMGB1 connects it to the etiology and progression of these malignancies. Furthermore impaired APE1 activity links to neurodegenerative disorders such as Alzheimer's disease where DNA repair deficiency contributes to neuronal damage and cognitive decline.

Product promise

Tested

We have tested this species and application combination and it works. It is covered by our product promise.

Expected

We have not tested this specific species and application combination in-house, but expect it will work. It is covered by our product promise.

Predicted

This species and application combination has not been tested, but we predict it will work based on strong homology. However, this combination is not covered by our product promise.

Not recommended

We do not recommend this combination. It is not covered by our product promise.

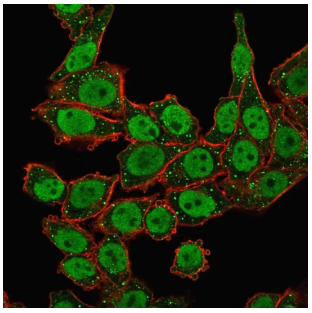
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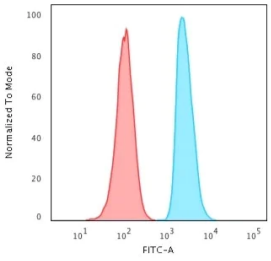
5 product images



Immunocytochemistry/ Immunofluorescence - Anti-APE1 antibody [CPTC-APEX1-2] (ab268072)

APE1 Immunocytochemistry/ Immunofluorescence staining using mouse Anti-APE1 antibody

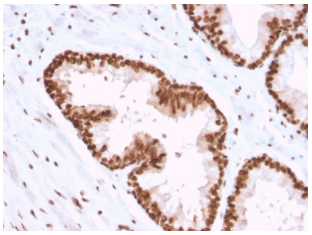
Immunofluorescence staining of human HeLa cells labeling APE1 with ab268072 followed by Goat anti-Mouse IgG-CF488 (Green). Phalloidin CF640 stains the membrane red.



Flow Cytometry - Anti-APE1 antibody [CPTC-APEX1-2] (ab268072)

APE1 Flow Cytometry staining using mouse Anti-APE1 antibody

Flow Cytometryetric analysis of HeLa cells stained for APE1 using ab268072. Goat anti-Mouse IgG-CF488 (Blue); Isotype Control (Red).

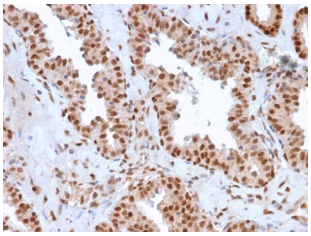


Immunohistochemistry (Formalin/PFA-fixed paraffin-embedded sections) - Anti-APE1 antibody [CPTC-APEX1-2] (ab268072)

APE1 Immunohistochemistry (Formalin/PFA-fixed paraffin-embedded sections) staining using mouse Anti-APE1 antibody

Formalin-fixed, paraffin-embedded human Prostate Carcinoma tissue stained for APE1 using ab268072 at 2 µg/ml in immunohistochemical analysis

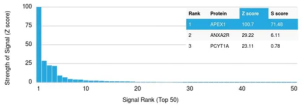
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Immunohistochemistry (Formalin/PFA-fixed paraffin-embedded sections) - Anti-APE1 antibody [CPTC-APEX1-2] (ab268072)

APE1 Immunohistochemistry (Formalin/PFA-fixed paraffin-embedded sections) staining using mouse Anti-APE1 antibody

Formalin-fixed, paraffin-embedded human Prostate Carcinoma tissue stained for APE1 using ab268072 at 2 µg/ml in immunohistochemical analysis.



Protein Array - Anti-APE1 antibody [CPTC-APEX1-2] (ab268072)

Protein Array containing more than 19,000 full-length human proteins using ab268072. Z- and S-Score: The Z-score represents the strength of a signal that a monoclonal antibody (MAb) (in combination with a fluorescently-tagged anti-IgG secondary antibody) produces when binding to a particular protein on the HuProtTM array. Z-scores are described in units of standard deviations (SD's) above the mean value of all signals generated on that array. If targets on HuProtTM are arranged in descending order of the Z-score, the S-score is the difference (also in units of SD's) between the Z-score. S-score therefore represents the relative target specificity of a MAb to its intended target. A MAb is considered to specific to its intended target, if the MAb has an S-score of at least 2.5. For example, if a MAb binds to protein X with a Z-score of 43 and to protein Y with a Z-score of 14, then the S-score for the binding of that MAb to protein X is equal to 29.

Please note: All products are 'FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC OR THERAPEUTIC PROCEDURES'.