

## Product datasheet

# Recombinant Human APE1 protein ab103260

[1 Image](#)

### Overview

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<b>Product name</b>	Recombinant Human APE1 protein
<b>Protein length</b>	Full length protein

### Description

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<b>Nature</b>	Recombinant
<b>Source</b>	Escherichia coli

### Amino Acid Sequence

<b>Accession</b>	<a href="#">P27695</a>
<b>Species</b>	Human
<b>Sequence</b>	<b>MASMTGGQQMGRG</b> SMPKRGKKGAVAEDGDELRTPEAKKSKTAAKNDKE AAGEGPALYEDPPDQKTSPSGKPATLKICSWNVDGLRAWIKKKGLDWVKE EAPDILCLQETKCSENKLPALQELPGLSHQYWSAPSDKEGYSGVGLLSR QCPLKVSYGIGEEEHQEGRVMAEFDSFVLVTA YVPNAGRGLVRLEYRQ RWDEAFRKFLLKGLASRKPLVLCGDLNVAHEEIDLRNPKGNKKNAGFTPQE RQGF GELLQAVPLADSFRLYPNTPYAYTFWYMMNARSKNVGWRLDYFL LSHLLPALCDSKIRSKALGSDHCPITLYLAL

<b>Molecular weight</b>	37 kDa including tags
<b>Amino acids</b>	1 to 318
<b>Tags</b>	T7 tag N-Terminus

### Specifications

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Our [Abpromise guarantee](#) covers the use of **ab103260** in the following tested applications.

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

<b>Applications</b>	SDS-PAGE Mass Spectrometry
<b>Mass spectrometry</b>	MALDI-TOF
<b>Purity</b>	> 90 % SDS-PAGE. ab103260 was purified using conventional chromatography techniques.
<b>Form</b>	Liquid

## Preparation and Storage

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### Stability and Storage

Shipped at 4°C. Upon delivery aliquot and store at -20°C or -80°C. Avoid repeated freeze / thaw cycles.

Preservative: None

Constituents: 10% Glycerol, 0.2M Sodium chloride, 20mM Tris HCl, 2mM DTT, pH 8.0

## General Info

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### Function

Multifunctional protein that plays a central role in the cellular response to oxidative stress. The two major activities of APEX1 in DNA repair and redox regulation of transcriptional factors. Functions as a apurinic/aprimidinic (AP) endodeoxyribonuclease in the DNA 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. Does also incise at AP sites in the DNA strand of DNA/RNA hybrids, single-stranded DNA regions of R-loop structures, and single-stranded RNA molecules. Has a 3'-5' exoribonuclease activity on mismatched deoxyribonucleotides at the 3' termini of nicked or gapped DNA molecules during short-patch BER. Possesses a DNA 3' phosphodiesterase activity capable of removing lesions (such as phosphoglycolate) blocking the 3' side of DNA strand breaks. May also play a role in the epigenetic regulation of gene expression by participating in DNA demethylation. 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. Plays a role in the protection from granzymes-mediated cellular repair leading to cell death. Also involved in the DNA cleavage step of class switch recombination (CSR). On the other hand, APEX1 also 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. 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. Stimulates the YBX1-mediated MDR1 promoter activity, when acetylated at Lys-6 and Lys-7, leading to drug resistance. Acts also 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. Associates, together with YBX1, on the MDR1 promoter. Together with NPM1, associates with rRNA. Binds DNA and RNA.

### Sequence similarities

Belongs to the DNA repair enzymes AP/ExoA family.

### Domain

The N-terminus contains the redox activity while the C-terminus exerts the DNA AP-endodeoxyribonuclease activity; both function are independent in their actions. An unconventional mitochondrial targeting sequence (MTS) is harbored within the C-terminus, that appears to be masked by the N-terminal sequence containing the nuclear localization signal (NLS), that probably blocks the interaction between the MTS and Tom proteins.

### Post-translational modifications

Phosphorylated. Phosphorylation by kinase PKC or casein kinase CK2 results in enhanced redox activity that stimulates binding of the FOS/JUN AP-1 complex to its cognate binding site. AP-endodeoxyribonuclease activity is not affected by CK2-mediated phosphorylation. Phosphorylation of Thr-233 by CDK5 reduces AP-endodeoxyribonuclease activity resulting in accumulation of DNA damage and contributing to neuronal death.

Acetylated on Lys-6 and Lys-7. Acetylation is increased by the transcriptional coactivator EP300 acetyltransferase, genotoxic agents like H<sub>2</sub>O<sub>2</sub> and methyl methanesulfonate (MMS).

Acetylation increases its binding affinity to the negative calcium response element (nCaRE) DNA promoter. The acetylated form induces a stronger binding of YBX1 to the Y-box sequence in the MDR1 promoter than the unacetylated form. Deacetylated on lysines. Lys-6 and Lys-7 are deacetylated by SIRT1.

Cleaved at Lys-31 by granzyme A to create the mitochondrial form; leading in reduction of binding to DNA, AP endodeoxynuclease activity, redox activation of transcription factors and to enhanced cell death. Cleaved by granzyme K; leading to intracellular ROS accumulation and enhanced cell death after oxidative stress.

Cys-65 and Cys-93 are nitrosylated in response to nitric oxide (NO) and lead to the exposure of the nuclear export signal (NES).

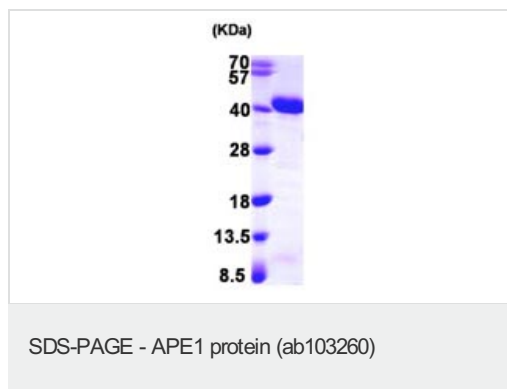
Ubiquitinated by MDM2; leading to translocation to the cytoplasm and proteasomal degradation.

## Cellular localization

Mitochondrion. The cleaved APEX2 is only detected in mitochondria (By similarity).

Translocation from the cytoplasm to the mitochondria is mediated by ROS signaling and cleavage mediated by granzyme A. Tom20-dependent translocated mitochondrial APEX1 level is significantly increased after genotoxic stress and Nucleus. Nucleus, nucleolus. Nucleus speckle. Endoplasmic reticulum. Cytoplasm. Detected in the cytoplasm of B-cells stimulated to switch (By similarity). Colocalized with SIRT1 in the nucleus. Colocalized with YBX1 in nuclear speckles after genotoxic stress. Together with OGG1 is recruited to nuclear speckles in UVA-irradiated cells. Colocalized with nucleolin and NPM1 in the nucleolus. Its nucleolar localization is cell cycle dependent and requires active rRNA transcription. Colocalized with calreticulin in the endoplasmic reticulum. Translocation from the nucleus to the cytoplasm is stimulated in presence of nitric oxide (NO) and function in a CRM1-dependent manner, possibly as a consequence of demasking a nuclear export signal (amino acid position 64-80). S-nitrosylation at Cys-93 and Cys-310 regulates its nuclear-cytosolic shuttling. Ubiquitinated form is localized predominantly in the cytoplasm.

## Images



15% SDS-PAGE analysis of 3µg ab103260.

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