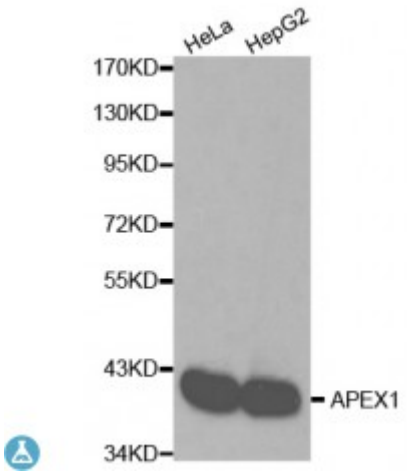
Anti-APEX1 Antibody



Description	Apurinic/apyrimidinic (AP) sites occur frequently in DNA molecules by spontaneous hydrolysis, by DNA damaging agents or by DNA glycosylases that remove specific abnormal bases. AP sites are pre-mutagenic lesions that can prevent normal DNA replication so the cell contains systems to identify and repair such sites. Class II AP endonucleases cleave the phosphodiester backbone 5' to the AP site. This gene encodes the major AP endonuclease in human cells. Splice variants have been found for this gene; all encode the same protein.
Model	STJ116180
Host	Rabbit
Reactivity	Human
Applications	IF, IP, WB
Immunogen	Recombinant fusion protein containing a sequence corresponding to amino acids 1-318 of human APEX1 (NP_542380.1).
Gene ID	328
Gene Symbol	APEX1
Dilution range	WB 1:500 - 1:2000 IF 1:50 - 1:100 IP 1:50 - 1:200
Purification	Affinity purification
Note	For Research Use Only (RUO).
Protein Name	DNA-(apurinic or apyrimidinic site lyase lyase mitochondrial]

Molecular Weight	35.555 kDa
Clonality	Polyclonal
Conjugation	Unconjugated
Isotype	IgG
Formulation	PBS with 0.02% sodium azide, 50% glycerol, pH7.3.
Storage Instruction	Store at -20C. Avoid freeze / thaw cycles.
Database Links	HGNC:587OMIM:107748Reactome:R-HSA-110357
Alternative Names	DNA-(apurinic or apyrimidinic site lyase lyase mitochondrial]
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/apyrimidinic (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,
Cellular Localization	Nucleus, Nucleus, nucleolus, Nucleus speckle, Endoplasmic reticulum, Cytoplasm, DNA-(apurinic or apyrimidinic site) lyase, mitochondrial: Mitochondrion,

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,