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# Ku70 Antibody

Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP51618

## Product Information

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| **Application** | WB, ICC, IHC-P |
| **Primary Accession** | P12956 |
| **Reactivity** | Human |
| **Host** | Rabbit |
| **Clonality** | Polyclonal |
| **Calculated MW** | 69843 |

## Additional Information

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| **Gene ID** | 2547 |
| **Other Names** | X-ray repair cross-complementing protein 6, 364-, 4299-, 5'-deoxyribose-5-phosphate lyase Ku70, 5'-dRP lyase Ku70, 70 kDa subunit of Ku antigen, ATP-dependent DNA helicase 2 subunit 1, ATP-dependent DNA helicase II 70 kDa subunit, CTC box-binding factor 75 kDa subunit, CTC75, CTCBF, DNA repair protein XRCC6, Lupus Ku autoantigen protein p70, Ku70, Thyroid-lupus autoantigen, TLAA, X-ray repair complementing defective repair in Chinese hamster cells 6, XRCC6, G22P1 |
| **Target/Specificity** | KLH-conjugated synthetic peptide encompassing a sequence within the C-term region of human Ku70. The exact sequence is proprietary. |
| **Dilution** | WB~~1:1000 ICC~~N/A IHC-P~~N/A |
| **Format** | 0.01M PBS, pH 7.2, 0.09% (W/V) Sodium azide, Glycerol 50% |
| **Storage** | Store at -20 °C.Stable for 12 months from date of receipt |

## Protein Information

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| **Name** | XRCC6 ( HGNC:4055) |
| **Synonyms** | G22P1 |
| **Function** | DNA-binding protein critical for the DNA damage response, specifically in repairing double-strand breaks (DSBs) via the classical non-homologous end joining (NHEJ) pathway. It forms a heterodimer with XRCC5 (Ku80), creating the Ku70:Ku80 heterodimer (Ku complex), which serves as a DNA end-binding complex. It primarily binds DSBs and recruits essential repair factors, assembling the core long-range NHEJ complex to facilitate the alignment and ligation of broken DNA ends (PubMed:11493912, PubMed:20493174, PubMed:33854234, PubMed:34352203, PubMed:9742108). This pathway |

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| | ensures the rapid repair of cytotoxic and mutagenic DSBs and contributes to the generation of diversity in T-cell receptors and antibodies through mechanisms such as V(D)J recombination (PubMed:9742108). Likely acts as a 5'-deoxyribose-5-phosphate lyase (5'-dRP lyase), catalyzing the beta-elimination of the 5'-deoxyribose- 5-phosphate at abasic sites near DSBs. This activity cleans the termini of abasic sites, a common form of nucleotide damage, preparing broken ends for ligation (PubMed:20383123). It may also possess 3'-5' DNA helicase activity, although this has not been confirmed in vivo, and its physiological significance remains unclear (PubMed:7957065). Beyond DNA repair, the protein contributes to telomere maintenance (PubMed:29490055). It is also implicated in transcriptional regulation, acting as a cofactor for various transcription factors (PubMed:12145306, PubMed:8621488). It plays a role in the regulation of DNA virus-mediated innate immune response by assembling into the HDP- RNP complex, a complex that serves as a platform for IRF3 phosphorylation and subsequent innate immune response activation through the cGAS-STING pathway (PubMed:28712728). Can also bind RNAs and recruits PRKDC to a wide range of cellular RNAs, including the U3 small nucleolar RNA, playing a role in the biogenesis of ribosomal RNAs (PubMed:32103174). Additionally, it negatively regulates apoptosis by interacting with BAX, sequestering it from the mitochondria, and may possess deubiquitination activity targeting BAX (PubMed:15023334, PubMed:18362350, PubMed:35545041). |
| **Cellular Location** | Nucleus. Chromosome. Cytoplasm. Note=When trimethylated, localizes in the cytoplasm. |

## Background

Single-stranded DNA-dependent ATP-dependent helicase. Has a role in chromosome translocation. The DNA helicase II complex binds preferentially to fork-like ends of double-stranded DNA in a cell cycle-dependent manner. It works in the 3'-5' direction. Binding to DNA may be mediated by XRCC6. Involved in DNA non-homologous end joining (NHEJ) required for double-strand break repair and V(D)J recombination. The XRCC5/6 dimer acts as regulatory subunit of the DNA-dependent protein kinase complex DNA-PK by increasing the affinity of the catalytic subunit PRKDC to DNA by 100-fold. The XRCC5/6 dimer is probably involved in stabilizing broken DNA ends and bringing them together. The assembly of the DNA-PK complex to DNA ends is required for the NHEJ ligation step. Required for osteocalcin gene expression. Probably also acts as a 5'-deoxyribose-5-phosphate lyase (5'-dRP lyase), by catalyzing the beta-elimination of the 5' deoxyribose- 5-phosphate at an abasic site near double-strand breaks. 5'-dRP lyase activity allows to 'clean' the termini of abasic sites, a class of nucleotide damage commonly associated with strand breaks, before such broken ends can be joined. The XRCC5/6 dimer together with APEX1 acts as a negative regulator of transcription.

## References

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Dunham I.,et al.Nature 402:489-495(1999).