

CPTC-PCNA-5 (CAB080240)

Uniprot ID: [P12004](#)

Protein name: PCNA_HUMAN

Full name: Proliferating cell nuclear antigen

Function: Auxiliary protein of DNA polymerase delta and is involved in the control of eukaryotic DNA replication by increasing the polymerase's processibility during elongation of the leading strand. Induces a robust stimulatory effect on the 3'-5' exonuclease and 3'- phosphodiesterase, but not apurinic-aprimidinic (AP) endonuclease, APEX2 activities. Has to be loaded onto DNA in order to be able to stimulate APEX2. Plays a key role in DNA damage response (DDR) by being conveniently positioned at the replication fork to coordinate DNA replication with DNA repair and DNA damage tolerance pathways (PubMed:24939902). Acts as a loading platform to recruit DDR proteins that allow completion of DNA replication after DNA damage and promote postreplication repair: Monoubiquitinated PCNA leads to recruitment of translesion (TLS) polymerases, while 'Lys-63'-linked polyubiquitination of PCNA is involved in error-free pathway and employs recombination mechanisms to synthesize across the lesion (PubMed:24695737).

Subcellular location:

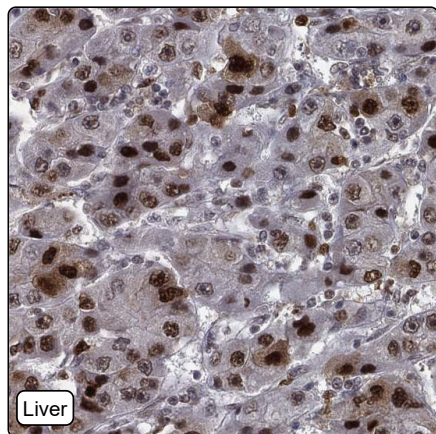
Nucleus (*experimental evidence*)

NOTE: Colocalizes with CREBBP, EP300 and POLD1 to sites of DNA damage (PubMed:24939902). Forms nuclear foci representing sites of ongoing DNA replication and vary in morphology and number during S phase (PubMed:15543136). Co-localizes with SMARCA5/SNF2H and BAZ1B/WSTF at replication foci during S phase (PubMed:15543136). Together with APEX2, is redistributed in discrete nuclear foci in presence of oxidative DNA damaging agents.

Protein existence: Experimental evidence at protein level

Comment:

Immunohistochemistry



IHC protocol:	HIER pH6, Dilution 1:375
IHC test staining:	Nuclear positivity in most tissues.
Literature conformance:	Consistent with extensive gene/protein characterization data
Literature significance:	
RNA similarity:	High consistency between antibody staining and RNA expression data
RNA tissue specificity:	Tissue enhanced (bone marrow)
RNA tissue distribution:	Detected in all
IHC Sibling similarity:	Other antibody shows similar IHC staining pattern
Reliability score:	Supported
APE summary:	Nuclear expression mainly in proliferating cells.
APE explanatory sentences:	High consistency between antibody staining and RNA expression data.
Orthogonal validation:	No
Independent validation:	No
IHC Annotation summary:	Most normal tissues showed moderate to strong nuclear staining. Most cancers showed moderate to strong nuclear staining.