CPTC-PCNA-3 (CAB080241)

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-apyrimidinic (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

Stomach
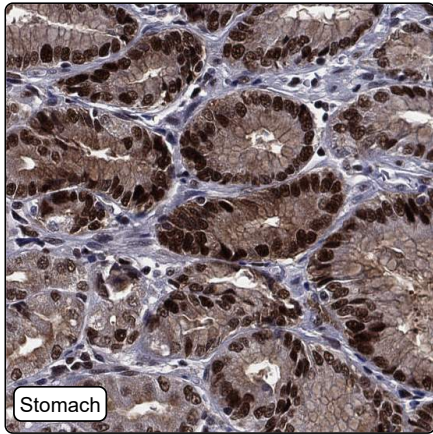
IHC protocol:	HIER pH6, Dilution 1:10000
IHC test staining:	Nuclear positivity in most tissues.
Literature conformance:	Consistent with extensive gene/protein characterization data
Literature significance:	
RNA similarity:	High consistency between antibody staining and RNA expression data
RNA tissue 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:	Strong nuclear positivity was observed in most normal tissues. All cancers showed strong nuclear positivity.