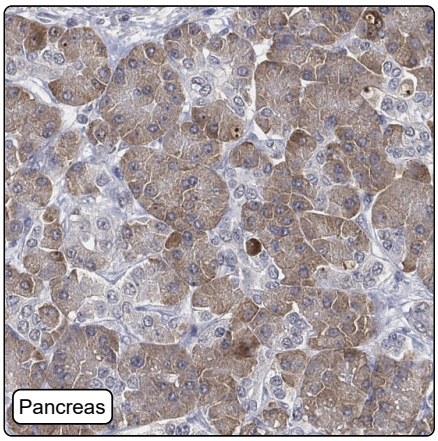
CPTC-POLD1-1 (CAB080372)

Uniprot ID: P28340
Protein name: DPOD1_HUMAN
Full name: DNA polymerase delta catalytic subunit
Tissue specificity: Widely expressed, with high levels of expression in heart and lung.
Function: As the catalytic component of the trimeric (Pol-delta3 complex) and tetrameric DNA polymerase delta complexes (Pol-delta4 complex), plays a crucial role in high fidelity genome replication, including in lagging strand synthesis, and repair. Exhibits both DNA polymerase and 3'- to 5'-exonuclease activities (PubMed:16510448, PubMed:19074196, PubMed:20334433, PubMed:24035200, PubMed:24022480). Requires the presence of accessory proteins POLD2, POLD3 and POLD4 for full activity. Depending upon the absence (Pol-delta3) or the presence of POLD4 (Pol-delta4), displays differences in catalytic activity. Most notably, expresses higher proofreading activity in the context of Pol-delta3 compared with that of Pol-delta4 (PubMed:19074196, PubMed:20334433). Although both Pol-delta3 and Pol-delta4 process Okazaki fragments in vitro, Pol-delta3 may be better suited to fulfill this task, exhibiting near-absence of strand displacement activity compared to Pol-delta4 and stalling on encounter with the 5'-blocking oligonucleotides. Pol-delta3 idling process may avoid the formation of a gap, while maintaining a nick that can be readily ligated (PubMed:24035200). Along with DNA polymerase kappa, DNA polymerase delta carries out approximately half of nucleotide excision repair (NER) synthesis following UV irradiation (PubMed:20227374). Under conditions of DNA replication stress, in the presence of POLD3 and POLD4, may catalyze the repair of broken replication forks through break-induced replication (BIR) (PubMed:24310611). Involved in the translesion synthesis (TLS) of templates carrying O6-methylguanine, 8oxoG or abasic sites (PubMed:19074196, PubMed:24191025).
Subcellular location:
Nucleus (*experimental evidence*)
NOTE: Colocalizes with PCNA and POLD3 at S phase replication sites (PubMed:11595739). After UV irradiation, recruited to DNA damage sites within 2 hours, independently on the cell cycle phase, nor on PCNA ubiquitination. This recruitment requires POLD3, PCNA and RFC1-replication factor C complex (PubMed:20227374, PubMed:22801543).
Protein existence: Experimental evidence at protein level

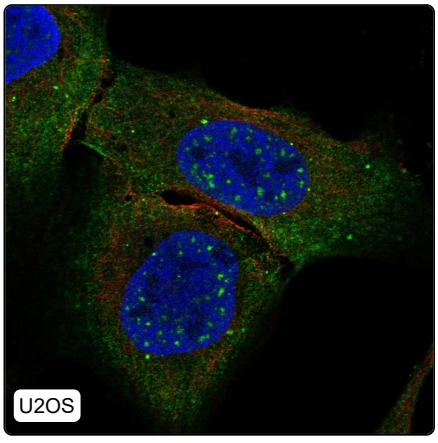
Comment:

Immunohistochemistry



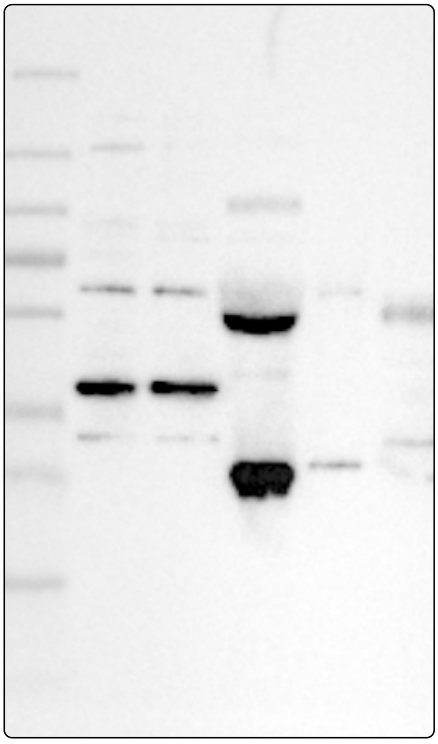
IHC protocol:	HIER pH6, Dilution 1:250
IHC test staining:	Cytoplasmic positivity in gastrointestinal tract, kidney, pancreas and liver. Nucleoli staining in cerebral cortex.
Literature conformance:	Not consistent with gene/protein characterization data
Literature significance:	
RNA similarity:	Very low consistency between antibody staining and RNA expression data
RNA tissue specificity:	Low tissue specificity
RNA tissue distribution:	Detected in many
IHC Sibling similarity:	Other antibody shows dissimilar IHC staining pattern

Immunofluorescence



IF Overlay:	antibody (green), anti-tubulin (red) and DAPI (blue)
IF main location:	Plasma membrane - 12: **Uncertain** (auto)
IF additional location:	Vesicles - 12: **Uncertain** (auto) Nuclear speckles - 3: **Supportive** (auto)
IF approved for publication on HPA:	No
IF in THP-1:	Plasma membrane
IF in U2OS:	Nuc speckles Vesicles Plasma membrane

Western blot



WB Size markers (kDa):	250, 130, 100, 70, 55, 35, 25, 15, 10
WB Lanes:	Marker (1), RT-4 (2), U-251MG (3), Plasma (4), Liver (5), Tonsil (6)
WB Target weight (kDa):	12, 32, 32, 50, 121, 124, 124, 124, 126
WB Validation:	Supported (Band of predicted size in kDa (+/-20%) with additional bands present.)