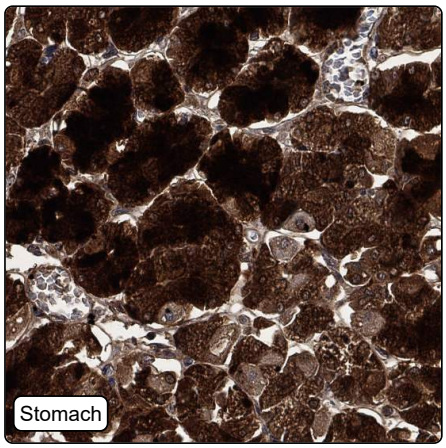
CPTC-RPA1-1 (CAB080255)

Uniprot ID: P27694
Protein name: RFA1_HUMAN
Full name: Replication protein A 70 kDa DNA-binding subunit
Function: As part of the heterotrimeric replication protein A complex (RPA/RP-A), binds and stabilizes single-stranded DNA intermediates, that form during DNA replication or upon DNA stress. It prevents their reannealing and in parallel, recruits and activates different proteins and complexes involved in DNA metabolism (PubMed:27723720, PubMed:27723717). Thereby, it plays an essential role both in DNA replication and the cellular response to DNA damage (PubMed:9430682). In the cellular response to DNA damage, the RPA complex controls DNA repair and DNA damage checkpoint activation. Through recruitment of ATRIP activates the ATR kinase a master regulator of the DNA damage response (PubMed:24332808). It is required for the recruitment of the DNA double-strand break repair factors RAD51 and RAD52 to chromatin in response to DNA damage (PubMed:17765923). Also recruits to sites of DNA damage proteins like XPA and XPG that are involved in nucleotide excision repair and is required for this mechanism of DNA repair (PubMed:7697716). Plays also a role in base excision repair (BER) probably through interaction with UNG (PubMed:9765279). Also recruits SMARCAL1/HARP, which is involved in replication fork restart, to sites of DNA damage. May also play a role in telomere maintenance (PubMed:17959650). As part of the alternative replication protein A complex, aRPA, binds single-stranded DNA and probably plays a role in DNA repair. Compared to the RPA2-containing, canonical RPA complex, may not support chromosomal DNA replication and cell cycle progression through S-phase. The aRPA may not promote efficient priming by DNA polymerase alpha but could support DNA synthesis by polymerase delta in presence of PCNA and replication factor C (RFC), the dual incision/excision reaction of nucleotide excision repair and RAD51-dependent strand exchange (PubMed:19996105).
Subcellular location:
Nucleus (*experimental evidence*)
Nucleus > PML body (*experimental evidence*)
NOTE: Enriched in PML bodies in cells displaying alternative lengthening of their telomeres.
Protein existence: Experimental evidence at protein level

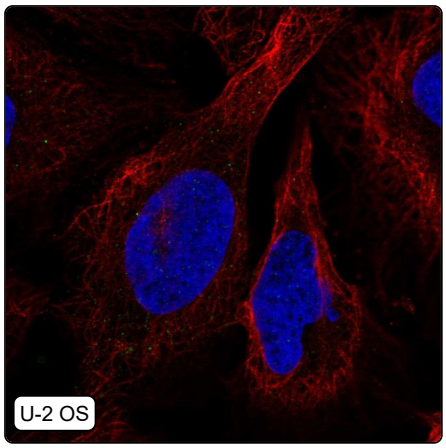
Comment:

Immunohistochemistry



IHC protocol:	HIER pH6, Dilution 1:150
IHC test staining:	Nuclear positivity in few tissues with additional strong cytoplasmic positivity in stomach.
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 all
IHC Sibling similarity:	Other antibody shows dissimilar IHC staining pattern
IHC fail comment:	ANTIBODY FAILED: Not consistent with RNA

Immunofluorescence



IF Overlay:	antibody (green), anti-tubulin (red) and DAPI (blue)
IF main location:	
IF additional location:	
IF approved for publication on HPA:	No
IF in THP-1:	Negative
IF in U-2 OS:	Negative

Western blot

WB Size markers (kDa):	250, 130, 100, 70, 55, 35, 25, 15, 10
WB Lanes:	Marker (1), RT4 (2), U-251 MG (3), Plasma (4), Liver (5), Tonsil (6)
WB Target weight (kDa):	13, 16, 35, 68
WB Validation:	Uncertain (Single band differing more than +/-20% from predicted size in kDa and not supported by experimental and/or bioinformatic data.)