

CPTC-TP53BP1-1 (CAB079980)

Uniprot ID: [Q12888](#)

Protein name: TP53B_HUMAN

Full name: TP53-binding protein 1

Function: Double-strand break (DSB) repair protein involved in response to DNA damage, telomere dynamics and class-switch recombination (CSR) during antibody genesis (PubMed:12364621, PubMed:22553214, PubMed:23333306, PubMed:17190600, PubMed:21144835, PubMed:28241136). Plays a key role in the repair of double-strand DNA breaks (DSBs) in response to DNA damage by promoting non-homologous end joining (NHEJ)- mediated repair of DSBs and specifically counteracting the function of the homologous recombination (HR) repair protein BRCA1 (PubMed:22553214, PubMed:23727112, PubMed:23333306). In response to DSBs, phosphorylation by ATM promotes interaction with RIF1 and dissociation from NUDT16L1/TIRR, leading to recruitment to DSBs sites (PubMed:28241136). Recruited to DSBs sites by recognizing and binding histone H2A monoubiquitinated at 'Lys-15' (H2AK15Ub) and histone H4 dimethylated at 'Lys-20' (H4K20me2), two histone marks that are present at DSBs sites (PubMed:23760478, PubMed:28241136, PubMed:17190600). Required for immunoglobulin class-switch recombination (CSR) during antibody genesis, a process that involves the generation of DNA DSBs (PubMed:23345425). Participates in the repair and the orientation of the broken DNA ends during CSR (By similarity). In contrast, it is not required for classic NHEJ and V(D)J recombination (By similarity). Promotes NHEJ of dysfunctional telomeres via interaction with PAXIP1 (PubMed:23727112).

Subcellular location:

Nucleus (*experimental evidence*)

Chromosome (*experimental evidence*)

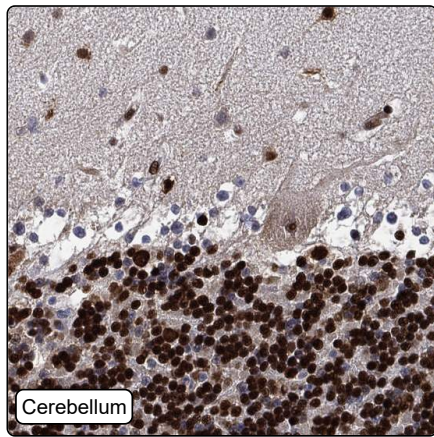
Chromosome > Centromere > Kinetochore (*by similarity*)

NOTE: Localizes to the nucleus in absence of DNA damage (PubMed:28241136). Following DNA damage, recruited to sites of DNA damage, such as double strand breaks (DSBs): recognizes and binds histone H2A monoubiquitinated at 'Lys-15' (H2AK15Ub) and histone H4 dimethylated at 'Lys-20' (H4K20me2), two histone marks that are present at DSBs sites (PubMed:23333306, PubMed:23760478, PubMed:24703952, PubMed:28241136, PubMed:17190600). Associated with kinetochores during mitosis (By similarity).

Protein existence: Experimental evidence at protein level

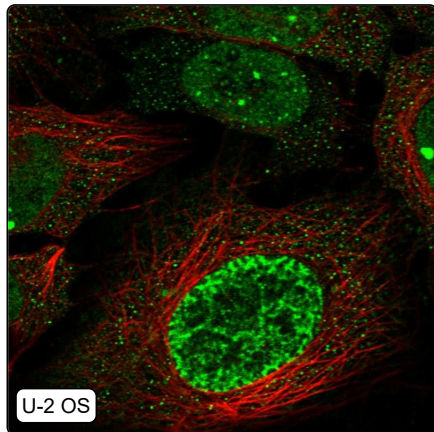
Comment: ICC-IF: We will try to get a good staining of this antibody in two more cell lines, before publication on the HPA. /Ulrika Axelsson

Immunohistochemistry



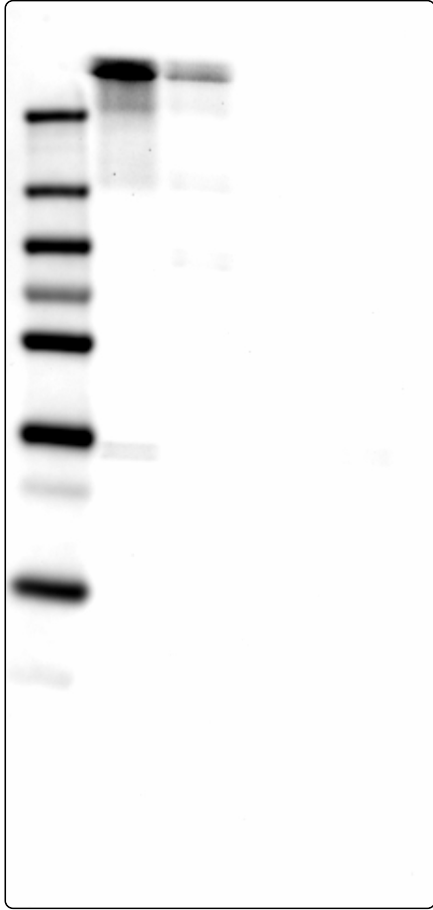
IHC protocol:	HIER pH6, Dilution 1:7000
IHC test staining:	Moderate to strong nuclear positivity in essentially all tissues.
Literature conformance:	Consistent with extensive gene/protein characterization data
Literature significance:	
RNA consistency:	Consistent with RNA expression data
IHC Sibling similarity:	Other antibody shows similar IHC staining pattern

Immunofluorescence



IF Overlay:	antibody (green), anti-tubuline (red) and DAPI (blue)
IF main location:	Nuclear bodies - 3: Supportive (auto) Nucleoplasm - 3: Supportive (auto)
IF additional location:	Vesicles - 12: Uncertain (auto) Mitotic chromosome - 3: Supportive (manual)
IF Antibody score:	Supportive
IF in A549:	Negative
IF in HEK 293:	Negative
IF in U-2 OS:	Nucleoplasm Nuclear bodies Mitotic chromosome Vesicles

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):	15, 16, 112, 209, 214, 214, 214
WB Validation:	Uncertain (Weak band of predicted size but with additional bands of higher intensity also present.)