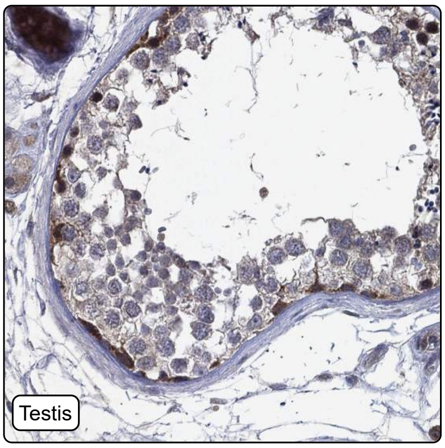
CPTC-TERF2-1 (CAB080269)

Uniprot ID: Q15554
Protein name: TERF2_HUMAN
Full name: Telomeric repeat-binding factor 2
Tissue specificity: Ubiquitous. Highly expressed in spleen, thymus, prostate, uterus, testis, small intestine, colon and peripheral blood leukocytes.
Function: Binds the telomeric double-stranded 5'-TTAGGG-3' repeat and plays a central role in telomere maintenance and protection against end-to-end fusion of chromosomes. In addition to its telomeric DNA-binding role, required to recruit a number of factors and enzymes required for telomere protection, including the shelterin complex, TERF2IP/RAP1 and DCLRE1B/Apollo. Component of the shelterin complex (telosome) that is involved in the regulation of telomere length and protection. Shelterin associates with arrays of double-stranded 5'- TTAGGG-3' repeats added by telomerase and protects chromosome ends; without its protective activity, telomeres are no longer hidden from the DNA damage surveillance and chromosome ends are inappropriately processed by DNA repair pathways. Together with DCLRE1B/Apollo, plays a key role in telomeric loop (T loop) formation by generating 3' single-stranded overhang at the leading end telomeres: T loops have been proposed to protect chromosome ends from degradation and repair. Required both to recruit DCLRE1B/Apollo to telomeres and activate the exonuclease activity of DCLRE1B/Apollo. Preferentially binds to positive supercoiled DNA. Together with DCLRE1B/Apollo, required to control the amount of DNA topoisomerase (TOP1, TOP2A and TOP2B) needed for telomere replication during fork passage and prevent aberrant telomere topology. Recruits TERF2IP/RAP1 to telomeres, thereby participating in to repressing homology-directed repair (HDR), which can affect telomere length.
Subcellular location:
Nucleus (*match to sequence model, experimental evidence*)
Chromosome > Telomere (*experimental evidence*)
NOTE: Colocalizes with telomeric DNA in interphase cells and is located at chromosome ends during metaphase.
Protein existence: Experimental evidence at protein level

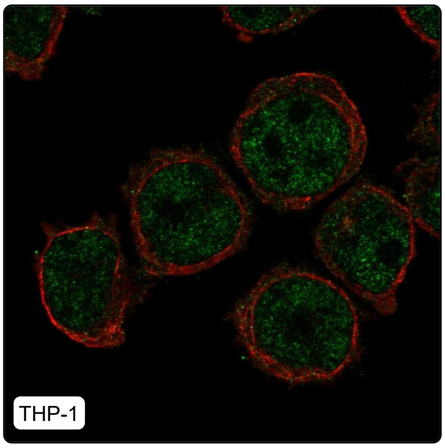
Comment:

Immunohistochemistry



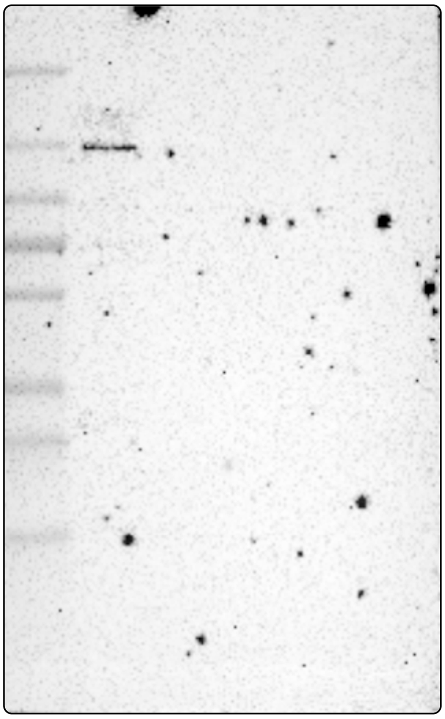
IHC protocol:	HIER pH6, Dilution 1:600
IHC test staining:	Cytoplasmic positivity in testis.
Literature conformance:	Not consistent with gene/protein characterization data
Literature significance:	
RNA similarity:	Very low consistency between antibody staining and RNA expression data
RNA tissue specificity:	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:	Cytosol - 12: **Uncertain** (auto)
IF additional location:	Nucleoplasm - 3: **Supportive** (auto)
IF approved for publication on HPA:	No
IF in THP-1:	Nucleoplasm Cytosol
IF in U-2 OS:	Cytosol

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):	6, 10, 15, 23, 27, 32, 32, 60
WB Validation:	Uncertain (Single band differing more than +/-20% from predicted size in kDa and not supported by experimental and/or bioinformatic data.)