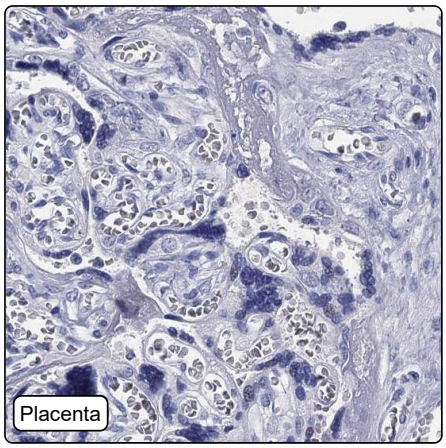
CPTC-MDC1-4 (CAB080120)

Uniprot ID: Q14676
Protein name: MDC1_HUMAN
Full name: Mediator of DNA damage checkpoint protein 1
Tissue specificity: Highly expressed in testis.
Function: Required for checkpoint mediated cell cycle arrest in response to DNA damage within both the S phase and G2/M phases of the cell cycle. May serve as a scaffold for the recruitment of DNA repair and signal transduction proteins to discrete foci of DNA damage marked by 'Ser-139' phosphorylation of histone H2AX. Also required for downstream events subsequent to the recruitment of these proteins. These include phosphorylation and activation of the ATM, CHEK1 and CHEK2 kinases, and stabilization of TP53 and apoptosis. ATM and CHEK2 may also be activated independently by a parallel pathway mediated by TP53BP1.
Subcellular location:
Nucleus (*experimental evidence*)
Chromosome (*by similarity*)
NOTE: Associated with chromatin. Relocalizes to discrete nuclear foci following DNA damage, this requires 'Ser-139' phosphorylation of H2AX. Colocalizes with APTX at sites of DNA double-strand breaks.
Protein existence: Experimental evidence at protein level

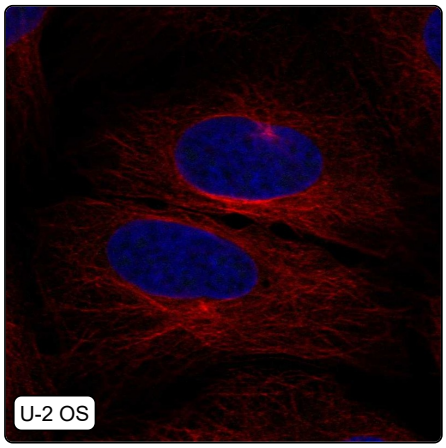
Comment:

Immunohistochemistry



IHC protocol:	HIER pH6, Dilution 1:165
IHC test staining:	Negative in all tissues.
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

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 SiHa:	Negative
IF in SK-MEL-30:	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):	12, 14, 15, 18, 33, 227
WB Validation:	Uncertain (Single band differing more than +/-20% from predicted size in kDa and not supported by experimental and/or bioinformatic data.)