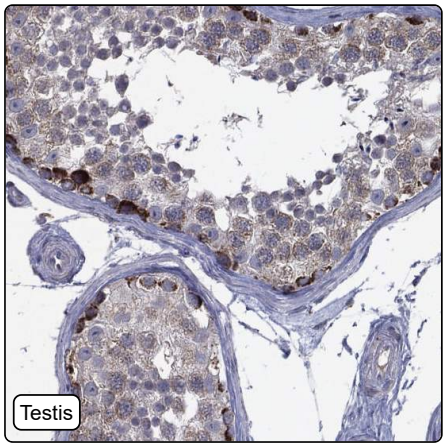
CPTC-RNF168-1 (CAB080254)

Uniprot ID: Q8IYW5
Protein name: RN168_HUMAN
Full name: E3 ubiquitin-protein ligase RNF168
Function: E3 ubiquitin-protein ligase required for accumulation of repair proteins to sites of DNA damage. Acts with UBE2N/UBC13 to amplify the RNF8-dependent histone ubiquitination. Recruited to sites of DNA damage at double-strand breaks (DSBs) by binding to ubiquitinated histone H2A and H2AX and amplifies the RNF8-dependent H2A ubiquitination, promoting the formation of 'Lys-63'-linked ubiquitin conjugates. This leads to concentrate ubiquitinated histones H2A and H2AX at DNA lesions to the threshold required for recruitment of TP53BP1 and BRCA1. Also recruited at DNA interstrand cross-links (ICLs) sites and promotes accumulation of 'Lys-63'-linked ubiquitination of histones H2A and H2AX, leading to recruitment of FAAP20/C1orf86 and Fanconi anemia (FA) complex, followed by interstrand cross-link repair. H2A ubiquitination also mediates the ATM-dependent transcriptional silencing at regions flanking DSBs in cis, a mechanism to avoid collision between transcription and repair intermediates. Also involved in class switch recombination in immune system, via its role in regulation of DSBs repair. Following DNA damage, promotes the ubiquitination and degradation of JMJD2A/KDM4A in collaboration with RNF8, leading to unmask H4K20me2 mark and promote the recruitment of TP53BP1 at DNA damage sites. Not able to initiate 'Lys-63'-linked ubiquitination in vitro; possibly due to partial occlusion of the UBE2N/UBC13-binding region. Catalyzes monoubiquitination of 'Lys-13' and 'Lys-15' of nucleosomal histone H2A (H2AK13Ub and H2AK15Ub, respectively).
Subcellular location:
Nucleus (*match to sequence model, experimental evidence*)
NOTE: Localizes to double-strand breaks (DSBs) sites of DNA damage.
Protein existence: Experimental evidence at protein level

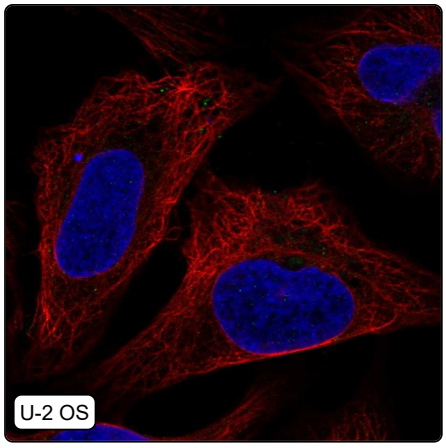
Comment:

Immunohistochemistry



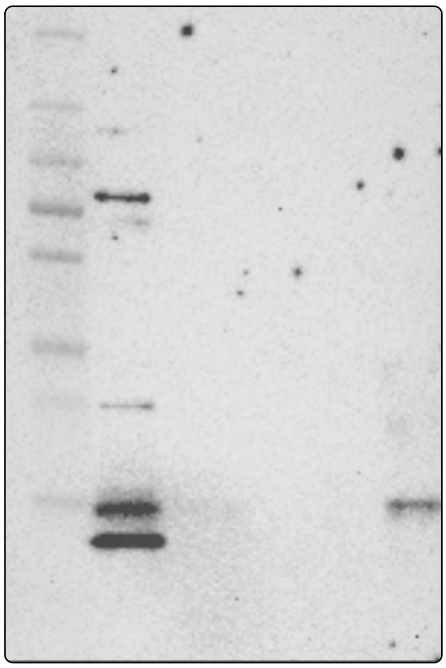
IHC protocol:	HIER pH6, Dilution 1:200
IHC test staining:	Cytoplasmic positivity in testis.
Literature conformance:	Not consistent with gene/protein characterization data
Literature significance:	
RNA similarity:	Very low consistency between antibody staining and RNA expression data
RNA tissue specificity:	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:	
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):	65
WB Validation:	Uncertain (Weak band of predicted size but with additional bands of higher intensity also present.)