## CPTC-NUDT16L1-1 (CAB080237)

## Uniprot ID: Q9BRJ7

Protein name: TIRR_HUMAN
Full name: Tudor-interacting repair regulator protein
Function: Key regulator of TP53BP1 required to stabilize TP53BP1 and regulate its recruitment to chromatin (PubMed:28241136). In absence of DNA damage, interacts with the tandem Tudor-like domain of TP53BP1, masking the region that binds histone H4 dimethylated at 'Lys-20' (H4K20me2), thereby preventing TP53BP1 recruitment to chromatin and maintaining TP53BP1 localization to the nucleus (PubMed:28241136). Following DNA damage, ATM-induced phosphorylation of TP53BP1 and subsequent recruitment of RIF1 leads to dissociate NUDT16L1/TIRR from TP53BP1, unmasking the tandem Tudor-like domain and allowing recruitment of TP53BP1 to DNA double strand breaks (DSBs) (PubMed:28241136). Binds U8 snoRNA (PubMed:18820299).

## Subcellular location

Nucleus (experimental evidence)
Protein existence: Experimental evidence at protein level

## Comment:

## Immunohistochemistry



| IHC protocol: | HIER pH6, Dilution 1:600 |
| :--- | :--- |
| IHC test staining: | Cytoplasmic positivity in smooth muscle. |
| 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): | $19,21,22,23,26$ |
| WB Validation: | Uncertain (Weak band of predicted size but with additional bands of higher intensity <br> also present.) |

