

Uniprot ID: [P49427](#)

# CDC34-2

**Protein name:** UB2R1\_HUMAN

**Full name:** Ubiquitin-conjugating enzyme E2 R1

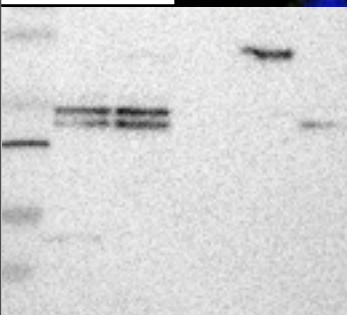
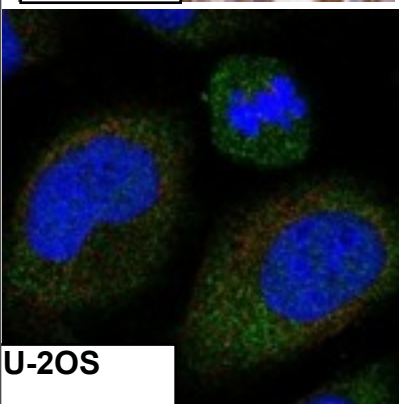
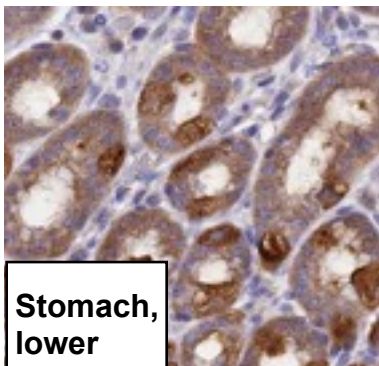
**Protein existence:** evidence at protein level

**Function:** Accepts ubiquitin from the E1 complex and catalyzes its covalent attachment to other proteins. In vitro catalyzes 'Lys-48'-linked polyubiquitination. Cooperates with the E2 UBCH5C and the SCF(FBXW11) E3 ligase complex for the polyubiquitination of NFKBIA leading to its subsequent proteasomal degradation. Performs ubiquitin chain elongation building ubiquitin chains from the UBE2D3-primed NFKBIA-linked ubiquitin. UBE2D3 acts as an initiator E2, priming the phosphorylated NFKBIA target at positions 'Lys-21' and/or 'Lys-22' with a monoubiquitin. Cooperates with the SCF(SKP2) E3 ligase complex to regulate cell proliferation through ubiquitination and degradation of MYBL2 and KIP1. Involved in ubiquitin conjugation and degradation of CREM isoform ICERIIgamma and ATF15 resulting in abrogation of ICERIIgamma and ATF5-mediated repression of cAMP-induced transcription during both meiotic and mitotic cell cycles. Involved in the regulation of the cell cycle G2/M phase through its targeting of the WEE1 kinase for ubiquitination and degradation. Also involved in the degradation of beta-catenin. Is target of human herpes virus 1 protein ICP0, leading to ICP0-dependent dynamic interaction with proteasomes.

**Subcellular location:** Cytoplasm. Nucleus. *NOTE:* The phosphorylation of the C-terminal tail plays an important role in mediating nuclear localization. Colocalizes with beta-tubulin on mitotic spindles in anaphase.

**Tissue specificity:** Expressed in testes during spermatogenesis to regulate repression of cAMP-induced transcription.

**Two antibodies: CDC34-1 and CDC34-2 were tested. Both were approved for IHC, CDC34-2 was selected for full protein profiling.**



## CDC34-2 (CAB047311)

OK

### Immunohistochemistry

**IHC protocol:** HIER pH 6, Dilution 1:325

**IHC test staining:** Cytoplasmic staining of varying intensity in all tissues. .

### IHC Annotators comments

Most normal tissues showed weak to moderate cytoplasmic positivity. Stomach, small intestine, heart and skeletal muscle exhibited strong immunoreactivity. Pneumocytes, salivary gland, bile duct cells and glial cells were in general negative.

### Immunofluorescence

**IF Overlay:** antibody (green), anti-tubuline (red) and DAPI (blue)

**IF Localization:** Positivity in nucleus but not nucleoli & cytoplasm.

**IF Validation:** The subcellular location is supported by literature.

### Western blot

**WB Size markers (kDa):** 250, 130, 95, 72, 55, 36, 28, 17, 11

**WB Lanes:** Marker(1), RT-4(2), U251 MG(3), Plasma(4), Liver(5), Tonsil(6)

**WB Target weight (kDa):** 27

**WB Validation:** Not supportive (Weak band of predicted size but with additional bands of higher intensity also present)