10320 Camino Santa Fe, Suite G
San Diego, CA 92121
Tel: 858.875.1900 Fax: 858.875.1999

UBR5 Antibody

Purified Rabbit Polyclonal Antibody (Pab)
Catalog # AP51600

Product Information

Application	WB, IHC-P
Primary Accession	O95071
Reactivity	Human, Mouse
Host	Rabbit
Clonality	Polyclonal
Calculated MW	309352

Additional Information

Gene ID	51366
Other Names	E3 ubiquitin-protein ligase UBR5, 632-, E3 ubiquitin-protein ligase, HECT domain-containing 1, Hyperplastic discs protein homolog, hHYD, Progestin-induced protein, UBR5, EDD, EDD1, HYD, KIAA0896
Target/Specificity	KLH-conjugated synthetic peptide encompassing a sequence within the N-term region of human UBR5. The exact sequence is proprietary.
Dilution	WB~~1:1000 IHC-P~~N/A
Format	0.01M PBS, pH 7.2, 0.09% (W/V) Sodium azide, Glycerol 50%
Storage	Store at -20 °C.Stable for 12 months from date of receipt

Protein Information

Name	UBR5
Function	E3 ubiquitin-protein ligase involved in different protein quality control pathways in the cytoplasm and nucleus (PubMed:29033132, PubMed:33208877, PubMed:37478846, PubMed:37478862). Mainly acts as a ubiquitin chain elongator that extends pre-ubiquitinated substrates (PubMed:29033132, PubMed:37409633). Component of the N-end rule pathway: ubiquitinates proteins bearing specific N-terminal residues that are destabilizing according to the N-end rule, leading to their degradation (By similarity). Recognizes type-1 N-degrons, containing positively charged amino acids (Arg, Lys and His) (By similarity). Together with UBR4, part of a cytoplasm protein quality control pathway that prevents protein aggregation by catalyzing assembly of heterotypic 'Lys-11'-/'Lys-48'-linked branched ubiquitin chains on aggregated proteins, leading to substrate recognition by the segregase p97/VCP and degradation by the proteasome: UBR5 is probably branching multiple 'Lys-48'-linked chains of substrates initially modified with

	mixed conjugates by UBR4 (PubMed:29033132). Together with ITCH, catalyzes 'Lys-48'-/'Lys-63'-branched ubiquitination of TXNIP, leading to its degradation: UBR5 mediates branching of 'Lys-48'-linked chains of substrates initially modified with 'Lys-63'-linked conjugates by ITCH (PubMed:29378950). Catalytic component of a nuclear protein quality control pathway that mediates ubiquitination and degradation of unpaired transcription factors (i.e. transcription factors that are not assembled into functional multiprotein complexes): specifically recognizes and binds degrons that are not accessible when transcription regulators are associated with their coactivators (PubMed:37478846, PubMed:37478862). Ubiquitinates various unpaired transcription regulator (MYC, SUPT4H1, SUPT5H, CDC20 and MCRS1), as well as ligand- bound nuclear receptors (ESR1, NR1H3, NR3C1, PGR, RARA, RXRA AND VDR) that are not associated with their nuclear receptor coactivators (NCOAs) (PubMed:33208877, PubMed:37478846, PubMed:37478862). Involved in maturation and/or transcriptional regulation of mRNA by mediating polyubiquitination and activation of CDK9 (PubMed:21127351). Also acts as a regulator of DNA damage response by acting as a suppressor of RNF168, an E3 ubiquitin-protein ligase that promotes accumulation of 'Lys-63'-linked histone H2A and H2AX at DNA damage sites, thereby acting as a guard against excessive spreading of ubiquitinated chromatin at damaged chromosomes (PubMed:22884692). Regulates DNA topoisomerase II binding protein (TopBP1) in the DNA damage response (PubMed:11714696). Ubiquitinates acetylated PCK1 (PubMed:21726808). Acts as a positive regulator of the canonical Wnt signaling pathway by mediating (1) ubiquitination and stabilization of CTNNB1, and (2) 'Lys- 48'-linked ubiquitination and degradation of TLE3 (PubMed:21118991, PubMed:28689657). Promotes disassembly of the mitotic checkpoint complex (MCC) from the APC/C complex by catalyzing ubiquitination of BUB1B, BUB3 and CDC20 (PubMed:35217622). Plays an essential role in extraembryonic development (By similarity). Required for the maintenance of skeletal tissue homeostasis by acting as an inhibitor of hedgehog (HH) signaling (By similarity).
Cellular Location	Nucleus. Cytoplasm
Tissue Location	Widely expressed. Most abundant in testis and expressed at high levels in brain, pituitary and kidney

Background

E3 ubiquitin-protein ligase which is a component of the N-end rule pathway. Recognizes and binds to proteins bearing specific N-terminal residues that are destabilizing according to the N-end rule, leading to their ubiquitination and subsequent degradation (By similarity). Involved in maturation and/or transcriptional regulation of mRNA by activating CDK9 by polyubiquitination. May play a role in control of cell cycle progression. May have tumor suppressor function. Regulates DNA topoisomerase II binding protein (TopBP1) in the DNA damage response. Plays an essential role in extraembryonic development. Ubiquitinates acetylated PCK1. Also acts as a regulator of DNA damage response by acting as a suppressor of RNF168, an E3 ubiquitin-protein ligase that promotes accumulation of 'Lys-63'- linked histone H2A and H2AX at DNA damage sites, thereby acting as a guard against excessive spreading of ubiquitinated chromatin at damaged chromosomes.

References

Callaghan M.J.,et al.Oncogene 17:3479-3491(1998).
Honda Y.,et al.J. Biol. Chem. 277:3599-3605(2002).
Nagase T.,et al.DNA Res. 5:355-364(1998).
Nakajima D.,et al.DNA Res. 9:99-106(2002).
Ohara O.,et al.Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.