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Beta catenin Recombinant Rabbit mAb

Catalog # AP96637

Product Information

Application	WB, IHC-P, IHC-F, IF
Primary Accession	Q02248
Other Accession	Q02248
Reactivity	Rat, Human, Mouse
Host	Rabbit
Clonality	Recombinant
Calculated MW	85471
Physical State	Liquid
Immunogen	A synthesized peptide derived from human beta Catenin
Epitope Specificity	30-90
Isotype	IgG
Purity	Affinity Purification
Buffer	PBS with 100 □g/ml BSA,0.15% ProClin300 and 50% glycerol.
SIMILARITY	Belongs to the beta-catenin family.Contains 12 ARM repeats.
SUBUNIT	Two separate complex-associated pools are found in the cytoplasm. The majority is present as component of an E-cadherin/ catenin adhesion complex composed of at least E-cadherin/CDH1 and beta-catenin/CTNNB1, and possibly alpha-catenin/CTNNA1; the complex is located to adherens junctions. The stable association of CTNNA1 is controversial as CTNNA1 was shown not to bind to F-actin when assembled in the complex. Alternatively, the CTNNA1-containing complex may be linked to F-actin by other proteins such as LIMA1. Another cytoplasmic pool is part of a large complex containing AXIN1, AXIN2, APC, CSNK1A1 and GSK3B that promotes phosphorylation on N-terminal Ser and Thr residues and ubiquitination of CTNNB1 via BTRC and its subsequent degradation by the proteasome. Wnt-dependent activation of DVL antagonizes the action of GSK3B. When GSK3B activity is inhibited the complex dissociates, CTNNB1 is dephosphorylated and is no longer targeted for destruction. The stabilized protein translocates to the nucleus, where it binds TCF/LEF-1 family members, TBP, BCL9 and possibly also RUVBL1 and CHD8. Binds CTNNBIP and EP300. CTNNB1 forms a ternary complex with LEF1 and EP300 that is disrupted by CTNNBIP1 binding (By similarity). Interacts with TAX1BP3 (via the PDZ domain); this interaction inhibits the transcriptional activity of CTNNB1 (By similarity). Interacts with AJAP1, BAIAP1, CARM1, CTNNA3, CXADR and PCDH11Y. Binds SLC9A3R1. Interacts with GLIS2 and MUC1. Interacts with SLC30A9. Interacts with XIRP1 (By similarity). Interacts directly with AXIN1; the interaction is regulated by CDK2 phosphorylation of AXIN1 (By similarity). Interacts with SCRIB (By similarity). Interacts with PTPRU (via the cytoplasmic juxtamembrane domain). Interacts with EMD. Interacts with TNIK and TCF7L2. Interacts with SESTD1 and TRPC4. Interacts with CAV1. Interacts with TRPV4. The TRPV4 and CTNNB1 complex can interact with CDH1. Interacts with VCL (By similarity). Interacts with PTPRJ. Interacts with PKT7 and CDK2. Interacts with FAT1 (via the cytoplasmic domain) (By similarity). Interacts with NANOS1 and NDRG2. Interacts with isoform 1 of NEK2. Interacts with both isoform 1 and isoform 2 of CDK5. Interacts with PTK6. Interacts with SOX7; this interaction may lead to

	proteasomal degradation of active CTNNB1 and thus inhibition of Wnt/beta-catenin-stimulated transcription. Identified in a complex with HINT1 and MITF. Interacts with FHIT. The CTNNB1 and TCF4 complex interacts with PML (isoform PML-4). Interacts with FERMT2. Identified in a complex with TCF4 and FERMT2.
Post-translational modifications	Phosphorylation at Ser-552 by AMPK promotes stabilizion of the protein, enhancing TCF/LEF-mediated transcription. Phosphorylation by GSK3B requires prior phosphorylation of Ser-45 by another kinase. Phosphorylation proceeds then from Thr-41 to Ser-37 and Ser-33. Phosphorylated by NEK2. EGF stimulates tyrosine phosphorylation. Phosphorylation on Tyr-654 decreases CDH1 binding and enhances TBP binding. Phosphorylated on Ser-33 and Ser-37 by HIPK2. This phosphorylation triggers proteasomal degradation. Phosphorylation on Ser-191 and Ser-246 by CDK5. Phosphorylation by CDK2 regulates insulin internalization. Phosphorylation by PTK6 at Tyr-64, Tyr-142, Tyr-331 and/or Tyr-333 with the predominant site at Tyr-64 is not essential for inhibition of transcriptional activity. Ubiquitinated by the SCF(BTRC) E3 ligase complex when phosphorylated by GSK3B, leading to its degradation. Ubiquitinated by a E3 ubiquitin ligase complex containing UBE2D1, SIAH1, CACYBP/SIP, SKP1, APC and TBL1X, leading to its subsequent proteasomal degradation (By similarity). S-nitrosylation at Cys-619 within adherens junctions promotes VEGF-induced, NO-dependent endothelial cell permeability by disrupting interaction with E-cadherin, thus mediating disassembly adherens junctions.
DISEASE	Colorectal cancer (CRC) [MIM:114500]: A complex disease characterized by malignant lesions arising from the inner wall of the large intestine (the colon) and the rectum. Genetic alterations are often associated with progression from premalignant lesion (adenoma) to invasive adenocarcinoma. Risk factors for cancer of the colon and rectum include colon polyps, long-standing ulcerative colitis, and genetic family history. Note=The gene represented in this entry may be involved in disease pathogenesis. Note=Activating mutations in CTNNB1 have oncogenic activity resulting in tumor development. Somatic mutations are found in various tumor types, including colon cancers, ovarian and prostate carcinomas, hepatoblastoma (HB), hepatocellular carcinoma (HCC). HBs are malignant embryonal tumors mainly affecting young children in the first three years of life. Pilomatrixoma (PTR) [MIM:132600]: Common benign skin tumor. Note=The disease is caused by mutations affecting the gene represented in this entry. Medulloblastoma (MDB) [MIM:155255]: Malignant, invasive embryonal tumor of the cerebellum with a preferential manifestation in children. Note=The gene represented in this entry may be involved in disease pathogenesis. Ovarian cancer (OC) [MIM:167000]: The term ovarian cancer defines malignancies originating from ovarian tissue. Although many histologic types of ovarian tumors have been described, epithelial ovarian carcinoma is the most common form. Ovarian cancers are often asymptomatic and the recognized signs and symptoms, even of late-stage disease, are vague. Consequently, most patients are diagnosed with advanced disease. Note=Disease susceptibility is associated with variations affecting the gene represented in this entry. Note=A chromosomal aberration involving CTNNB1 is found in salivary gland pleiomorphic adenomas, the most common benign epithelial tumors of the salivary gland. Translocation t(3;8)(p21;q12) with PLAG1. Mesothelioma, malignant (MESOM) [MIM:156240]: An aggressive neoplasm of the serosal lining of the chest. It appears as broad sheets of cells, with some regions containing spindle-shaped, sarcoma-like cells and other regions showing adenomatous patterns. Pleural mesotheliomas have been linked to exposure to asbestos. Note=The gene represented in this entry may be involved in disease pathogenesis.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	Key downstream component of the canonical Wnt signaling pathway. In the absence of Wnt, forms a complex with AXIN1, AXIN2, APC, CSNK1A1 and

GSK3B that promotes phosphorylation on N-terminal Ser and Thr residues and ubiquitination of CTNNB1 via BTRC and its subsequent degradation by the proteasome. In the presence of Wnt ligand, CTNNB1 is not ubiquitinated and accumulates in the nucleus, where it acts as a coactivator for transcription factors of the TCF/LEF family, leading to activate Wnt responsive genes.

Additional Information

Gene ID 12387

Other Names CTNNB; EVR7; MRD19; NEDSDV; armadillo; Bfc; Catnb; Mesc; CTNB1_HUMAN; CTNNB1; Beta-catenin; CTNB1_MOUSE; CTNB1_RAT; catenin beta 1; catenin (cadherin-associated protein), beta 1 (88kD); catenin (cadherin-associated protein), beta 1, 88kDa; catenin (cadherin-associated protein), beta 1

Dilution WB=1:1000-5000,IHC-P=1:200-800,IF=1:200-800,IHC-F=1:200-800

Storage Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

Protein Information

Name Ctnnb1 {ECO:0000312|MGI:MGI:88276}

Function Key downstream component of the canonical Wnt signaling pathway (PubMed:15132997). In the absence of Wnt, forms a complex with AXIN1, AXIN2, APC, CSNK1A1 and GSK3B that promotes phosphorylation on N-terminal Ser and Thr residues and ubiquitination of CTNNB1 via BTRC and its subsequent degradation by the proteasome. In the presence of Wnt ligand, CTNNB1 is not ubiquitinated and accumulates in the nucleus, where it acts as a coactivator for transcription factors of the TCF/LEF family, leading to activate Wnt responsive genes (By similarity). Also acts as a coactivator for other transcription factors, such as NR5A2 (By similarity). Promotes epithelial to mesenchymal transition/mesenchymal to epithelial transition (EMT/MET) via driving transcription of CTNNB1/TCF-target genes (By similarity). Involved in the regulation of cell adhesion, as component of an E-cadherin:catenin adhesion complex (PubMed:16325582, PubMed:18093941). Acts as a negative regulator of centrosome cohesion. Involved in the CDK2/PTPN6/CTNNB1/CEACAM1 pathway of insulin internalization. Blocks anoikis of malignant kidney and intestinal epithelial cells and promotes their anchorage-independent growth by down-regulating DAPK2. Disrupts PML function and PML-NB formation by inhibiting RANBP2- mediated sumoylation of PML (By similarity). Promotes neurogenesis by maintaining sympathetic neuroblasts within the cell cycle (PubMed:21325504). Involved in chondrocyte differentiation via interaction with SOX9: SOX9-binding competes with the binding sites of TCF/LEF within CTNNB1, thereby inhibiting the Wnt signaling (PubMed:15132997). Acts as a positive regulator of odontoblast differentiation during mesenchymal tooth germ formation, via promoting the transcription of differentiation factors such as LEF1, BMP2 and BMP4 (PubMed:29148101). Activity is repressed in a MSX1-mediated manner at the bell stage of mesenchymal tooth germ formation which prevents premature differentiation of odontoblasts (PubMed:29148101).

Cellular Location Cytoplasm. Nucleus. Cytoplasm, cytoskeleton. Cell junction, adherens

	junction. Cell junction. Cell membrane. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome {ECO:0000250|UniProtKB:P35222} Cytoplasm, cytoskeleton, spindle pole {ECO:0000250|UniProtKB:P35222} Synapse. Cytoplasm, cytoskeleton, cilium basal body. Note=Colocalized with RAPGEF2 and TJP1 at cell-cell contacts (By similarity). Cytoplasmic when it is un-stable (highly phosphorylated) or bound to CDH1. Translocates to the nucleus when it is stabilized (low level of phosphorylation) Interaction with GLIS2 and MUC1 promotes nuclear translocation Interaction with EMD inhibits nuclear localization. The majority of CTNNB1 is localized to the cell membrane. In interphase, colocalizes with CROCC between CEP250 puncta at the proximal end of centrioles, and this localization is dependent on CROCC and CEP250. In mitosis, when NEK2 activity increases, it localizes to centrosomes at spindle poles independent of CROCC. Colocalizes with CDK5 in the cell-cell contacts and plasma membrane of undifferentiated and differentiated neuroblastoma cells. Interaction with FAM53B promotes translocation to the nucleus (By similarity). Translocates to the nucleus in the presence of SNAIL1 (By similarity). Ca(2+)-mediated localization to the cell membrane in dental epithelial cells is inhibited via WNT3A (PubMed:27015268). Localizes to cell-cell contacts as keratinocyte differentiation progresses (PubMed:27375112) {ECO:0000250|UniProtKB:B6V8E6, ECO:0000250|UniProtKB:P35222, ECO:0000269|PubMed:27015268, ECO:0000269|PubMed:27375112}
Tissue Location	Expressed in cerebellar granule neurons (at protein level) (PubMed:21623382). Expressed in the intestinal epithelium (at protein level) (PubMed:22510880). Abundantly expressed in the tooth, skin, lung, kidney, eye and brain with weak expression in the liver and heart (PubMed:27015268).

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