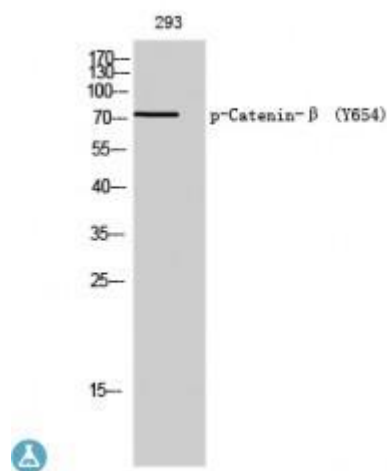


Anti-Phospho-Catenin-beta (Y654) antibody

Cat# NB-22-0209 (100 µl)

Cat# NB-22-0209-S (20 µl)

Cat# NB-22-0209-200ul (200 µl)



Description

Rabbit polyclonal to Phospho-Catenin-beta (Y654).

Product informations

Model	NB-22-0209
Host	Rabbit
Reactivity	Human, Mouse, Rat
Applications	ELISA, IHC, WB
Immunogen	Synthesized peptide derived from human Catenin-beta around the phosphorylation site of Y654.
Immunogen Region	590-670 aa
Gene ID	1499
Gene Symbol	CTNNB1
Dilution range	WB 1:500-1:2000IHC 1:100-1:300ELISA 1:40000
Specificity	Phospho-Catenin-beta (Y654) Polyclonal Antibody detects endogenous levels of Catenin-beta protein only when phosphorylated at Y654.
Tissue Specificity	Expressed in several hair follicle cell types: basal and peripheral matrix cells, and cells of the outer and inner root sheaths. Expressed in colon. Present in cortical neurons (at protein level).
Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
Note	For Research Use Only (RUO).

Protein Name	Catenin beta-1 Beta-catenin
Molecular Weight	75 kDa
Clonality	Polyclonal
Conjugation	Unconjugated
Isotype	IgG
Formulation	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
Concentration	1 mg/ml
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Database Links	HGNC:2514OMIM:114500
Alternative Names	Catenin beta-1 Beta-catenin
Function	<p>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. Involved in the regulation of cell adhesion, as component of an E-cadherin:catenin adhesion complex. 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 . Promotes neurogenesis by maintaining sympathetic neuroblasts within the cell cycle .</p>
Cellular Localization	<p>Cytoplasm Nucleus Cytoplasm, cytoskeleton Cell junction, adherens junction Cell junction Cell membrane Cytoplasm, cytoskeleton, microtubule organizing center, centrosome. Cytoplasm, cytoskeleton, spindle pole. Cell junction, synapse. Colocalized with RAPGEF2 and TJP1 at cell-cell contacts . Cytoplasmic when it is unstabilized (high level of phosphorylation) 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 beta-catenin 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.</p>

Post-translational Modifications

Phosphorylation at Ser-552 by AMPK promotes stabilization 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 and GSK3B, 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. 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. O-glycosylation at Ser-23 decreases nuclear localization and transcriptional activity, and increases localization to the plasma membrane and interaction with E-cadherin CDH1. Deacetylated at Lys-49 by SIRT1.

