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phospho-APBB1 (Ser347) Rabbit pAb

Catalog # AP99109

Product Information

Application	WB, IHC-P, IHC-F, IF
Primary Accession	O00213
Other Accession	O00213
Reactivity	Rat, Human, Mouse
Predicted	Pig, Rabbit, Dog, Horse
Host	Rabbit
Clonality	Polyclonal
Calculated MW	77244
Physical State	Liquid
Immunogen	KLH conjugated Synthesised phosphopeptide derived from human APBB1 around the phosphorylation site of Ser347
Epitope Specificity	SL(p-S)PE
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Contains 2 PID domains.Contains 1 WW domain.
SUBUNIT	Component of a complex, at least composed of APBB1,RASD1/DEXRAS1 and APP. Interacts (via PID domain 2) with APP (withthe intracellular domain of the beta-amyloid precursor protein).Interacts (via PID domain 2) with RASD1/DEXRAS1; impairs thetrancription activation activity. Interacts (via PID domain 1) withKAT5/TIP60. Interacts (via the WW domain) with the proline-richregion of APBB1IP. Interacts with TSHZ1 and TSHZ2 (By similarity).Interacts (via the WW domain) with histone H2AX (whenphosphorylated on 'Tyr-142') and the proline-rich region of ENAH.Interacts with MAPK8. Interacts (via PID domain 1) with TSHZ3 (viahomeobox domain). Interacts with SET. Found in a trimeric complexwith HDAC1 and TSHZ3; the interaction between HDAC1 and APBB1 ismediated by TSHZ3. Interacts (via WWW domain) with NEK6. Interacts(via WWW domain) with ABL1.
Post-translational modifications	Phosphorylation at Ser-610 by SGK1 promotes its localizationto the nucleus (By similarity). Phosphorylated following nucleartranslocation. Phosphorylation at Tyr-547 by ABL1 enhancestranscriptional activation activity and reduces the affinity forRASD1/DEXRAS1.
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	The protein encoded by this gene is a member of the Fe65 protein family. It is an adaptor protein localized in the nucleus. It interacts with the Alzheimer's disease amyloid precursor protein (APP), transcription factor CP2/LSF/LBP1 and the low-density lipoprotein receptor-related protein. APP functions as a cytosolic anchoring site that can prevent the gene product's nuclear translocation. This encoded protein could play an important role in the pathogenesis of Alzheimer's disease. It is thought to regulate transcription. Also it is observed to block cell cycle progression by downregulating thymidylate synthase expression. Multiple alternatively spliced transcript variants encoding different isoforms have been described for this gene.

Additional Information

Gene ID	322
Other Names	FE65; MGC:9072; RIR; APBB1_HUMAN; APBB1; Amyloid-beta A4 precursor protein-binding family B member 1; Protein Fe65; APBB1_MOUSE; APBB1_RAT; amyloid beta precursor protein binding family B member 1; amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65); APBB1 (phospho-S347); p-APBB1; phospho-APBB1; APBB1 (phospho-Ser347)
Dilution	WB=1:500-2000,IHC-P=1:100-500,IHC-F=1:100-500,IF=1:100-500
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	APBB1 (HGNC:581)
Function	Transcription coregulator that can have both coactivator and corepressor functions (PubMed:15031292, PubMed:18468999, PubMed:18922798, PubMed:25342469, PubMed:33938178). Adapter protein that forms a transcriptionally active complex with the gamma-secretase- derived amyloid precursor protein (APP) intracellular domain (PubMed:15031292, PubMed:18468999, PubMed:18922798, PubMed:25342469). Plays a central role in the response to DNA damage by translocating to the nucleus and inducing apoptosis (PubMed:15031292, PubMed:18468999, PubMed:18922798, PubMed:25342469). May act by specifically recognizing and binding histone H2AX phosphorylated on 'Tyr-142' (H2AXY142ph) at double-strand breaks (DSBs), recruiting other pro-apoptosis factors such as MAPK8/JNK1 (PubMed:19234442). Required for histone H4 acetylation at double-strand breaks (DSBs) (PubMed:19234442). Its ability to specifically bind modified histones and chromatin modifying enzymes such as KAT5/TIP60, probably explains its transcription activation activity (PubMed:33938178). Functions in association with TSHZ3, SET and HDAC factors as a transcriptional repressor, that inhibits the expression of CASP4 (PubMed:19343227). Associates with chromatin in a region surrounding the CASP4 transcriptional start site(s) (PubMed:19343227). Involved in hippocampal neurite branching and neuromuscular junction formation, as a result plays a role in spatial memory functioning (By similarity). Plays a role in the maintenance of lens transparency (By similarity). May play a role in muscle cell strength (By similarity). Acts as a molecular adapter that functions in neurite outgrowth by activating the RAC1-ARF6 axis upon insulin treatment (PubMed:36250347).
Cellular Location	Cell membrane. Cytoplasm. Nucleus. Cell projection, growth cone {ECO:0000250|UniProtKB:P46933}. Nucleus speckle. Note=Colocalizes with TSHZ3 in axonal growth cone (By similarity). Colocalizes with TSHZ3 in the nucleus (PubMed:19343227). In normal conditions, it mainly localizes to the cytoplasm, while a small fraction is tethered to the cell membrane via its interaction with APP (PubMed:18468999). Following exposure to DNA damaging agents, it is released from cell membrane and translocates to the nucleus (PubMed:18468999). Nuclear translocation is under the regulation of APP (PubMed:18468999). Colocalizes with NEK6 at the nuclear speckles (PubMed:17512906). Phosphorylation at Ser-610 by SGK1 promotes its

	localization to the nucleus (By similarity) {ECO:0000250|UniProtKB:P46933, ECO:0000269|PubMed:17512906, ECO:0000269|PubMed:18468999, ECO:0000269|PubMed:19343227}
Tissue Location	Highly expressed in brain; strongly reduced in post-mortem elderly subjects with Alzheimer disease

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