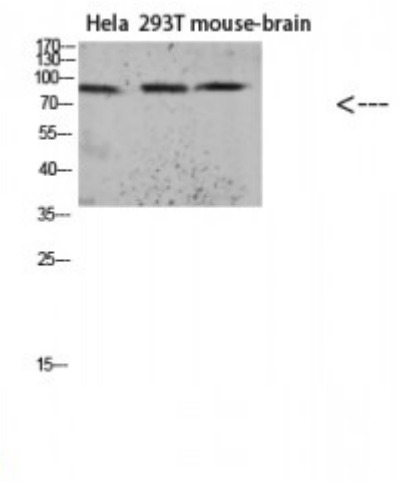
Anti-Tau (Acetyl Lys174) antibody



Description	Rabbit polyclonal to Tau (Acetyl Lys174).

Model	STJ98828
Host	Rabbit
Reactivity	Human, Mouse, Rat
Applications	ELISA, WB
Immunogen	Synthetic Acetyl peptide from human Tau (Acetyl Lys174) protein.
Immunogen Region	174 aa
Gene ID	4137
Gene Symbol	MAPT
Dilution range	WB 1:500-2000ELISA 1:5000-20000
Specificity	The antibody detects endogenous Tau when Acetyl occurs at Lys174.
Tissue Specificity	Expressed in neurons. Isoform PNS-tau is expressed in the peripheral nervous system while the others are expressed in the central nervous system.
Purification	The antibody was affinity-purified from rabbit serum by affinity-chromatography using specific immunogen.
Note	For Research Use Only (RUO).
Protein Name	Microtubule-associated protein tau Neurofibrillary tangle protein Paired helical filament-tau PHF-tau
Molecular Weight	80kDa
Clonality	Polyclonal

Conjugation	Unconjugated
Isotype	IgG
Formulation	PBS, pH 7.4, containing 0.02% sodium azide as Preservative and 50% Glycerol.
Concentration	1 mg/ml
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Database Links	HGNC:6893OMIM:157140
Alternative Names	Microtubule-associated protein tau Neurofibrillary tangle protein Paired helical filament-tau PHF-tau
Function	Promotes microtubule assembly and stability, and might be involved in the establishment and maintenance of neuronal polarity. The C-terminus binds axonal microtubules while the N-terminus binds neural plasma membrane components, suggesting that tau functions as a linker protein between both. Axonal polarity is predetermined by TAU/MAPT localization (in the neuronal cell) in the domain of the cell body defined by the centrosome. The short isoforms allow plasticity of the cytoskeleton whereas the longer isoforms may preferentially play a role in its stabilization.
Sequence and Domain Family	The tau/MAP repeat binds to tubulin. Type I isoforms contain 3 repeats while type II isoforms contain 4 repeats.
Cellular Localization	Cytoplasm, cytosol Cell membrane Cytoplasm, cytoskeleton Cell projection, axon. Mostly found in the axons of neurons, in the cytosol and in association with plasma membrane components.
Post-translational Modifications	Phosphorylation at serine and threonine residues in S-P or T-P motifs by proline-directed protein kinases (PDPK1: CDK1, CDK5, GSK3, MAPK) (only 2-3 sites per protein in interphase, seven-fold increase in mitosis, and in the form associated with paired helical filaments (PHF-tau)), and at serine residues in K-X-G-S motifs by MAP/microtubule affinity-regulating kinase (MARK1 or MARK2), causing detachment from microtubules, and their disassembly. Phosphorylation decreases with age. Phosphorylation within tau/MAP's repeat domain or in flanking regions seems to reduce tau/MAP's interaction with, respectively, microtubules or plasma membrane components. Phosphorylation on Ser-610, Ser-622, Ser-641 and Ser-673 in several isoforms during mitosis. Phosphorylation at Ser-548 by GSK3B reduces ability to bind and stabilize microtubules. Phosphorylation at Ser-579 by BRSK1 and BRSK2 in neurons affects ability to bind microtubules and plays a role in neuron polarization. Phosphorylated at Ser-554, Ser-579, Ser-602, Ser-606 and Ser-669 by PHK. Phosphorylation at Ser-214 by SGK1 mediates microtubule depolymerization and neurite formation in hippocampal neurons. There is a reciprocal down-regulation of phosphorylation and O-GlcNAcylation. Phosphorylation on Ser-717 completely abolishes the O-GlcNAcylation on this site, while phosphorylation on Ser-713 and Ser-721 reduces glycosylation by a factor of 2 and 4 respectively. Phosphorylation on Ser-721 is reduced by about 41.5% by GlcNAcylation on Ser-717. Dephosphorylated at several serine and threonine residues by the serine/threonine phosphatase PPP5C. Polyubiquitinated. Requires functional TRAF6 and may provoke SQSTM1-dependent degradation by the proteasome . PHF-tau can be modified by three different forms of polyubiquitination.

'Lys-48'-linked polyubiquitination is the major form, 'Lys-6'-linked and 'Lys-11'-linked polyubiquitination also occur. O-glycosylated. O-GlcNAcylation content is around 8.2%. There is reciprocal down-regulation of phosphorylation and O-GlcNAcylation. Phosphorylation on Ser-717 completely abolishes the O-GlcNAcylation on this site, while phosphorylation on Ser-713 and Ser-721 reduces O-GlcNAcylation by a factor of 2 and 4 respectively. O-GlcNAcylation on Ser-717 decreases the phosphorylation on Ser-721 by about 41.5%. Glycation of PHF-tau, but not normal brain TAU/MAPT. Glycation is a non-enzymatic post-translational modification that involves a covalent linkage between a sugar and an amino group of a protein molecule forming ketoamine. Subsequent oxidation, fragmentation and/or cross-linking of ketoamine leads to the production of advanced glycation endproducts (AGES). Glycation may play a role in stabilizing PHF aggregation leading to tangle formation in AD.