Data Sheet (Cat.No.TMAH-00537)

TargetMol

Anti-HDAC6 Antibody (2F772)

Product Details

Ig Type:	Rabbit IgG
Reactivity:	Human
Conjugation:	Unconjugated
Clone:	2F772
Purification:	Affinity-chromatography

Applications

Verified Activity:	1. Western Blot -Positive WB detected in: Hela whole cell lysate, MCF-7 whole cell lysate, HepG2 whole cell lysate, K562 whole cell lysate, Jurkat whole cell lysate -All lanes: HDAC6 antibody at 1.1μg/ml -Secondary: Goat polyclonal to rabbit IgG at 1/50000 dilution -Predicted band size: 132, 115 KDa -Observed band size: 160 KDa 2. IHC image of TMAH-00537 diluted at 1:112.5 and staining in paraffin-embedded human liver cancer performed on a Leica BondTM system. After dewaxing and hydration, antigen retrieval was mediated by high pressure in a citrate buffer (pH 6.0). Section was blocked with 10% normal goat serum 30min at RT. Then primary antibody (1% BSA) was incubated at 4°C overnight. The primary is detected by a biotinylated secondary antibody and visualized using an HRP conjugated SP system. 3. Immunoprecipitating HDAC6 in HepG2 whole cell lysate -Lane 1: Rabbit control IgG instead of TMAH-00537 in HepG2 whole cell lysate. For western blotting, a HRP-conjugated Protein G antibody was used as the secondary antibody (1/2000) -Lane 2: TMAH-00537 (3μg) + HepG2 whole cell lysate (500μg) -Lane 3: HepG2 whole cell lysate (20μg)
Application:	ELISA,IHC,IP,WB
Recommended	WB:1:500-1:5000; IHC:1:50-1:200; IP:1:200-1:1000.

Properties

Stability & Storage:	Store at -20°C or -80°C for 12 months. Avoid repeated freeze-thaw cycles.
Shipping:	Shipping with blue ice.

Antigen Details

Immunogen:	A synthetic peptide: Human HDAC6
Antigen Species:	Human
Gene ID:	10013
Uniprot ID:	Q9UBN7
Biology Area:	Epigenetics and Nuclear Signaling

Research Background

Responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events. Histone deacetylases act via the formation of large multiprotein complexes. In addition to histones, deacetylates other proteins: plays a central role in microtubule-dependent cell motility by mediating deacetylation of tubulin. Promotes deacetylation of CTTN, leading to actin polymerization, promotion of autophagosome-lysosome fusion and completion of autophagy. Involved in the MTA1-mediated epigenetic regulation of ESR1 expression in breast cancer. In addition to its protein deacetylase activity, plays a key role in the degradation of misfolded proteins: when misfolded proteins are too abundant to be degraded by the chaperone refolding system and the ubiquitin-proteasome, mediates the transport of misfolded proteins to a cytoplasmic juxtanuclear structure called aggresome. Probably acts as an adapter that recognizes polyubiquitinated misfolded proteins and target them to the aggresome, facilitating their clearance by autophagy.

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