

HDAC4 + 5 + 9 Rabbit pAb

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Catalog # AP54308

Product Information

Application	IHC-P, IHC-F, IF, E
Primary Accession	P56524
Predicted	
Host	Human, Mouse, Rat, Pig, Horse, Rabbit
Clonality	Polyclonal
Calculated MW	119040
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human HDAC4 + 5 + 9
Epitope Specificity	651-750/1084
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SUBCELLULAR LOCATION	Nucleus. Cytoplasm. Note=Shuttles between the nucleus and the cytoplasm. Upon muscle cells differentiation, it accumulates in the nuclei of myotubes, suggesting a positive role of nuclear HDAC4 in muscle differentiation. The export to cytoplasm depends on the interaction with a 14-3-3 chaperone protein and is due to its phosphorylation at Ser-246, Ser-467 and Ser-632 by CaMK4 and SIK1. The nuclear localization probably depends on sumoylation. Belongs to the histone deacetylase family. HD type 2 subfamily. Interacts with HDAC7. Homodimer. Homodimerization via its N-terminal domain. Interacts with MEF2C, AHRR, and NR2C1. Interacts with a 14-3-3 chaperone protein in a phosphorylation dependent manner. Interacts with BTBD14B. Interacts with KDM5B. Interacts with MYOCD. Interacts with MORC2. Interacts with ANKRA2. Phosphorylated by CaMK4 at Ser-246, Ser-467 and Ser-632. Phosphorylation at other residues by CaMK2D is required for the interaction with 14-3-3. Phosphorylation at Ser-350 impairs the binding of ANKRA2 but generates a high-affinity docking site for 14-3-3. Sumoylation on Lys-559 is promoted by the E3 SUMO-protein ligase RANBP2, and prevented by phosphorylation by CaMK4. Brachydactyly-mental retardation syndrome (BDMR) [MIM:600430]: A syndrome resembling the physical anomalies found in Albright hereditary osteodystrophy. Common features are mild facial dysmorphism, congenital heart defects, distinct brachydactyly type E, mental retardation, developmental delay, seizures, autism spectrum disorder, and stocky build. Soft tissue ossification is absent, and there are no abnormalities in parathyroid hormone or calcium metabolism. Note=The disease is caused by mutations affecting the gene represented in this entry. This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications. Histones play a critical role in transcriptional regulation, cell cycle progression, and developmental events. Histone acetylation/deacetylation alters chromosome structure and affects transcription factor access to DNA.
SIMILARITY	
SUBUNIT	
Post-translational modifications	
DISEASE	
Important Note	
Background Descriptions	

The protein encoded by this gene belongs to class II of the histone deacetylase/acuc/apha family. It possesses histone deacetylase activity and represses transcription when tethered to a promoter. This protein does not bind DNA directly, but through transcription factors MEF2C and MEF2D. It seems to interact in a multiprotein complex with RbAp48 and HDAC3. [provided by RefSeq, Jul 2008].

Additional Information

Gene ID	9759
Other Names	Histone deacetylase 4, HD4, 3.5.1.98, HDAC4 (HGNC:14063), KIAA0288
Target/Specificity	Ubiquitous.
Dilution	IHC-P=1:100-500,IHC-F=1:100-500,ICC/IF=1:100-500,IF=1:100-500,ELISA=1:500 0-10000
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	HDAC4 (HGNC:14063)
Synonyms	KIAA0288
Function	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. Involved in muscle maturation via its interaction with the myocyte enhancer factors such as MEF2A, MEF2C and MEF2D. Involved in the MTA1-mediated epigenetic regulation of ESR1 expression in breast cancer. Deacetylates HSPA1A and HSPA1B at 'Lys-77' leading to their preferential binding to co-chaperone STUB1 (PubMed: 27708256).
Cellular Location	Nucleus. Cytoplasm. Note=Shuttles between the nucleus and the cytoplasm. Upon muscle cells differentiation, it accumulates in the nuclei of myotubes, suggesting a positive role of nuclear HDAC4 in muscle differentiation. The export to cytoplasm depends on the interaction with a 14-3-3 chaperone protein and is due to its phosphorylation at Ser-246, Ser-467 and Ser-632 by CaMK4 and SIK1. The nuclear localization probably depends on sumoylation Interaction with SIK3 leads to HDAC4 retention in the cytoplasm (By similarity). {ECO:0000250 UniProtKB:Q6NZM9}
Tissue Location	Ubiquitous.

Background

Histones play a critical role in transcriptional regulation, cell cycle progression, and developmental events. Histone acetylation/deacetylation alters chromosome structure and affects transcription factor access to DNA. The protein encoded by this gene belongs to class II of the histone deacetylase/acuc/apha family. It

possesses histone deacetylase activity and represses transcription when tethered to a promoter. This protein does not bind DNA directly, but through transcription factors MEF2C and MEF2D. It seems to interact in a multiprotein complex with RbAp48 and HDAC3. [provided by RefSeq, Jul 2008].

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