



HDAC8 Rabbit mAb

Catalog No	YP-rAb-17761
Isotype	IgG
Reactivity	Human,Mouse,Rat
Applications	WB,IHC,IF,IP,ELISA
Gene Name	HDAC8
Protein Name	Histone deacetylase 8
Purification Process	Protein A
Specificity	Endogenous
Formulation	PBS, 50% glycerol, 0.05% Proclin 300, 0.05%BSA
Source	Monoclonal, Rabbit,IgG
Dilution	IHC 1:200-1:500; WB 1:2000-1:10000; IF 1:200-1:1000; ELISA 1:5000-1:20000; IP 1:50-1:200; Note: For IHC, we suggest antigen retrieval with TE buffer pH 9.0
Concentration	0.5 mg/ml
Purity	≥90%
Storage Stability	-15 ° C to -25 ° C/1 year(Do not lower than -25 ° C)
Synonyms	HDAC8;Histone deacetylase 8;HDAC8 ; HDACL1 ; CDA07 ; Histone deacetylase 8 ; HD8
Observed Band	44kD
Calculated Molecular Weight	42kD
Cell Pathway	Nucleus . Chromosome . Cytoplasm . Excluded from the nucleoli (PubMed:10748112). Found in the cytoplasm of cells showing smooth muscle differentiation (PubMed:15772115, PubMed:16538051). .
Tissue Specificity	Weakly expressed in most tissues. Expressed at higher level in heart, brain, kidney and pancreas and also in liver, lung, placenta, prostate and kidney.
Function	Catalytic activity:Hydrolysis of an N(6)-acetyl-lysine residue of a histone to yield a deacetylated histone.,Caution:The sequence shown here is derived from an Ensembl automatic analysis pipeline and should be considered as preliminary data.,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.,miscellaneous:Its activity is inhibited by trichostatin A (TSA) and butyrate, two well known histone deacetylase inhibitors.,similarity:Belongs to the histone deacetylase family. Type 1 subfamily.,subcellular location:Excluded from the nucleoli.,subunit:Interacts with PEPB2-MYH11, a fusion protein consisting of



the 165 N-terminal residues of CBF-beta (PEPB2) with the tail region of MYH11 produced by the inversion Inv(16)(p13q22), a translocation associated with acute myeloid leukemia of M4EO subtype. The PEPB2-MYH1 fusion protein also interacts with RUNX1, a well known transcriptional regulator, suggesting that the interaction with HDAC8 may participate in the conversion of RUNX1 into a constitutive transcriptional repressor. Interacts with CBFA2T3.,tissue specificity:Weakly expressed in most tissues. Expressed at higher level in heart, brain, kidney and pancreas.,

Background

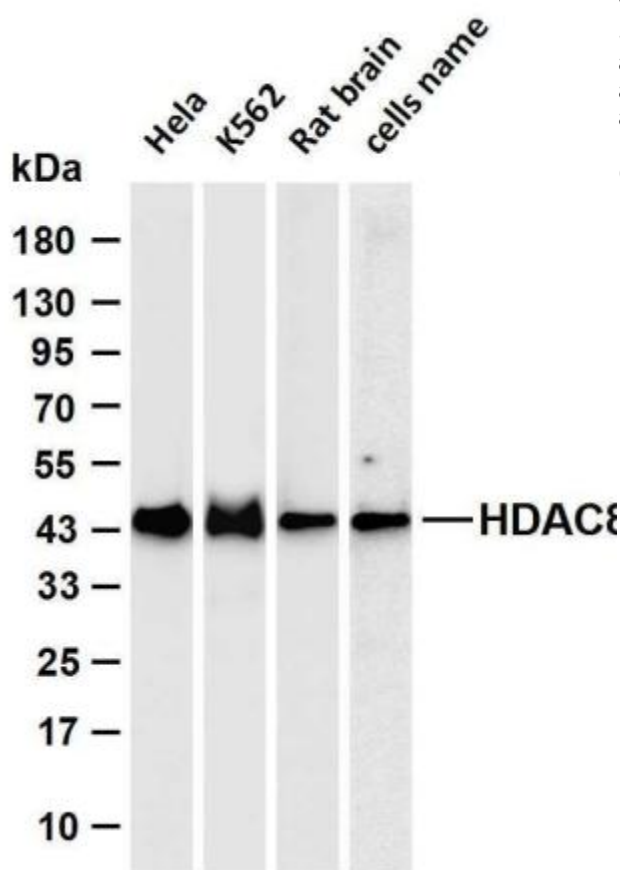
Histones play a critical role in transcriptional regulation, cell cycle progression, and developmental events. Histone acetylation/deacetylation alters chromosome structure and affects transcription factor access to DNA. The protein encoded by this gene belongs to class I of the histone deacetylase family. It catalyzes the deacetylation of lysine residues in the histone N-terminal tails and represses transcription in large multiprotein complexes with transcriptional co-repressors . Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Oct 2009],

matters needing attention

Avoid repeated freezing and thawing!

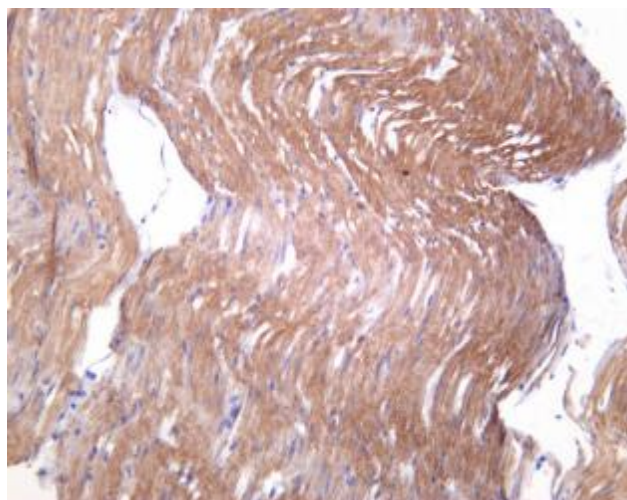
Usage suggestions

This product can be used in immunological reaction related experiments. For more information, please consult technical personnel.



Various whole cell lysates were separated by 4-20% SDS-PAGE, and the membrane was blotted with anti-HDAC8 antibody. The HRP-conjugated Goat anti-Rabbit IgG (H + L) antibody was used to detect the antibody. Lane 1: Hela Lane 2: K562 Lane 3: Rat brain Lane 4: Mouse brain Predicted band size: 42kDa Observed band size: 44kDa





Human smooth muscle was stained with anti-HDAC8 Rabbit antibody

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