Product name:	HDAC8 (phospho Ser39) Rabbit Polyclonal Antibody
Cat number:	ABN04768
Conjugate:	Unconjugated
Size:	100µL
Clone:	Polyclonal
Concentration:	1mg/ml
Host:	Rabbit
Isotype:	IgG
Immunogen:	The antiserum was produced against synthesized peptide derived from human HDAC8 around the phosphorylation site of Ser39. AA range:5-54
Reactivity:	Human,Mouse,Rat
Applications:	WB 1:500-1:2000,IHC 1:100-1:300,ICC/IF 1:50-1:200,ELISA 1:10000-1:20000
Purification:	Affinity purification
Form:	Liquid
Buffer:	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% New type preservative N.
Storage:	Store at 4°C short term. Aliquot and store at -20°C for 12 months. Avoid freeze/thaw cycles.

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],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.,