Product name:	SMAP45 Rabbit Polyclonal Antibody
Cat number:	ABN18004
Conjugate:	Unconjugated
Size:	100μL
Clone:	Polyclonal
Concentration:	1mg/ml
Host:	Rabbit
Isotype:	IgG
Immunogen:	The antiserum was produced against synthesized peptide derived from human HDAC3. AA range:379-428
Reactivity:	Human,Mouse,Rat,Monkey
Applications:	WB 1:500-1:2000,IHC 1:100-1:300,ICC/IF 1:200-1:1000,ELISA 1:10000-1:20000
Molecular Weight:	50kDa
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 the histone deacetylase/acuc/apha family. It has histone deacetylase activity and represses transcription when tethered to a promoter. It may participate in the regulation of transcription through its binding with the zinc-finger transcription factor YY1. This protein can also down-regulate p53 function and thus modulate cell growth and apoptosis. This gene is regarded as a potential tumor suppressor gene. [provided by RefSeq, Jul 2008],catalytic activity:Hydrolysis of an N(6)-acetyl-lysine residue of a histone to yield a deacetylated histone.,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. Probably participates in the regulation of transcription through its binding to the zinc-finger transcription factor YY1; increases YY1 repression activity. Required to repress transcription of the POU1F1 transcription factor.,PTM:Sumoylated in vitro.,similarity:Belongs to the histone deacetylase family. Type 1 subfamily.,subunit:Interacts with HDAC7 and HDAC9. Forms a heterologous complex at least with YY1. Interacts with DAXX, HDAC10 and DACH1. Found in a complex with NCOR1 and NCOR2. Component of the N-Cor repressor complex, at least composed of NCOR1, NCOR2, HDAC3, TBL1X, TBL1R, CORO2A and GPS2. Interacts with BCOR, MJD2A/JHDM3A, NRIP1, PRDM6 and SRY. Interacts with BTBD14B. Interacts with GLIS2 (By similarity). Interacts with CBFA2T3.,tissue specificity:Widely expressed.,