Product Datasheet

HDAC2 Rabbit mAb

Catalog No: #58563

Package Size: #58563-1 50ul #58563-2 100ul

Orders: order@signalwayantibody.com
Support: tech@signalwayantibody.com

Description

Product Name	HDAC2 Rabbit mAb
Host Species	Rabbit
Clonality	Monoclonal
Isotype	Rabbit IgG
Purification	Affinity-chromatography
Applications	WB IHC ICC/IF IP FC
Species Reactivity	Human Mouse Rat
Specificity	HDAC2 Antibody detects endogenous levels of total HDAC2
Immunogen Description	A synthesized peptide derived from human HDAC2
Other Names	HDAC2; HD2; Histone deacetylase 2; RPD3; YAF1; YY1 associated factor 1;
Accession No.	Uniprot:Q92769
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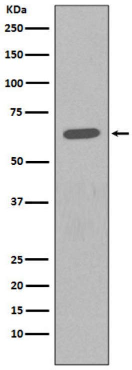
Formulation	Rabbit IgG in phosphate buffered saline , pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol.
Storage	Store at +4°C short term. Store at -20°C long term. Avoid freeze / thaw cycle.

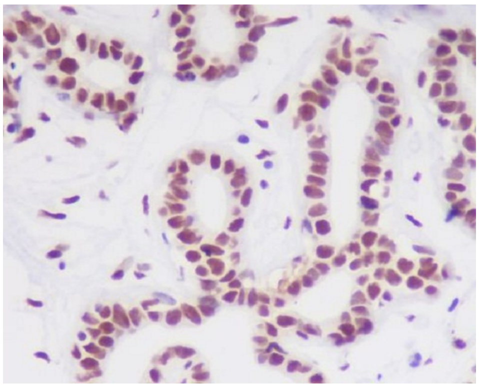
Application Details

WB 1:1000~1:2000 IHC 1:50~1:100 ICC/IF 1:50~1:100 IP 1:30 FC 1:50

Images



Western blot analysis of HDAC2 expression in K562 cell lysate.



Immunohistochemical analysis of paraffin-embedded human breast, using HDAC2 Antibody.

Product Description

In the intact cell, DNA closely associates with histones and other nuclear proteins to form chromatin. The remodeling of chromatin is believed to be a critical component of transcriptional regulation and a major source of this remodeling is brought about by the acetylation of nucleosomal histones. Acetylation of lysine residues in the amino-terminal tail domain of histone results in an allosteric change in the nucleosomal conformation and an increased accessibility to transcription factors by DNA.

Background

In the intact cell, DNA closely associates with histones and other nuclear proteins to form chromatin. The remodeling of chromatin is believed to be a critical component of transcriptional regulation and a major source of this remodeling is brought about by the acetylation of nucleosomal histones. Acetylation of lysine residues in the amino-terminal tail domain of histone results in an allosteric change in the nucleosomal conformation and an increased accessibility to transcription factors by DNA.