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HDAC2 (phospho Ser394) Polyclonal Antibody

Catalog # AP67214

Product Information

Application	WB, E
Primary Accession	Q92769
Reactivity	Human, Mouse, Rat, Monkey
Host	Rabbit
Clonality	Polyclonal
Calculated MW	55364

Additional Information

Gene ID	3066
Other Names	HDAC2; Histone deacetylase 2; HD2
Dilution	WB~~Western Blot: 1/500 - 1/2000. ELISA: 1/20000. Not yet tested in other applications. E~~N/A
Format	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.09% (W/V) sodium azide.
Storage Conditions	-20℃

Protein Information

Name	HDAC2 {ECO:0000303|PubMed:10545197, ECO:0000312|HGNC:HGNC:4853}
Function	Histone deacetylase that catalyzes the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4) (PubMed:28497810). Histone deacetylation gives a tag for epigenetic repression and plays an important role in transcriptional regulation, cell cycle progression and developmental events (By similarity). Histone deacetylases act via the formation of large multiprotein complexes (By similarity). Forms transcriptional repressor complexes by associating with MAD, SIN3, YY1 and N-COR (PubMed:12724404). Component of a RCOR/GFI/KDM1A/HDAC complex that suppresses, via histone deacetylase (HDAC) recruitment, a number of genes implicated in multilineage blood cell development (By similarity). Acts as a component of the histone deacetylase NuRD complex which participates in the remodeling of chromatin (PubMed:16428440, PubMed:28977666). Component of the SIN3B complex that represses transcription and counteracts the histone acetyltransferase activity of EP300 through the recognition H3K27ac marks by PHF12 and the activity of the histone deacetylase HDAC2 (PubMed:37137925). Also deacetylates non-histone targets: deacetylates TSHZ3, thereby regulating its transcriptional repressor activity (PubMed:19343227). May be involved in the transcriptional

repression of circadian target genes, such as PER1, mediated by CRY1 through histone deacetylation (By similarity). Involved in MTA1-mediated transcriptional corepression of TFF1 and CDKN1A (PubMed:21965678). In addition to protein deacetylase activity, also acts as a protein-lysine deacylase by recognizing other acyl groups: catalyzes removal of (2E)-butenoyl (crotonyl), lactoyl (lactyl) and 2-hydroxyisobutanoyl (2-hydroxyisobutyryl) acyl groups from lysine residues, leading to protein decrotonylation, delactylation and de-2-hydroxyisobutyrylation, respectively (PubMed:28497810, PubMed:29192674, PubMed:35044827).

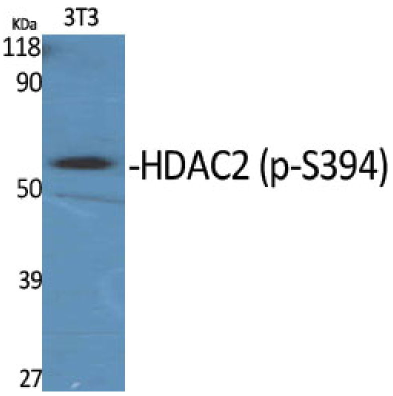
Cellular Location Nucleus. Cytoplasm

Tissue Location Widely expressed; lower levels in brain and lung.

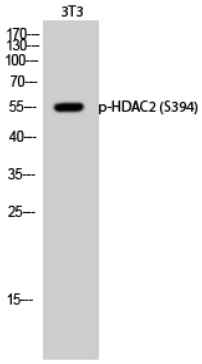
Background

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. Forms transcriptional repressor complexes by associating with MAD, SIN3, YY1 and N-COR. Interacts in the late S-phase of DNA-replication with DNMT1 in the other transcriptional repressor complex composed of DNMT1, DMAP1, PCNA, CAF1. Deacetylates TSHZ3 and regulates its transcriptional repressor activity. Component of a RCOR/GFI/KDM1A/HDAC complex that suppresses, via histone deacetylase (HDAC) recruitment, a number of genes implicated in multilineage blood cell development. May be involved in the transcriptional repression of circadian target genes, such as PER1, mediated by CRY1 through histone deacetylation. Involved in MTA1-mediated transcriptional corepression of TFF1 and CDKN1A.

Images



Western Blot analysis of various cells using Phospho-HDAC2 (S394) Polyclonal Antibody



Western Blot analysis of 3T3 cells using Phospho-HDAC2 (S394) Polyclonal Antibody