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SIRT7 Antibody
Purified Rabbit Polyclonal Antibody
Catalog # ABV11620

Specification

SIRT7 Antibody - Product Information

Application	**WB**
Primary Accession	Q9NRC8
Reactivity	**Human**
Host	**Rabbit**
Clonality	**Polyclonal**
Isotype	**Rabbit IgG**
Calculated MW	**44898**

SIRT7 Antibody - Additional Information

Gene ID 51547

Other Names
SIR2; Sirtuin 7; Silent Information Regulator 7

Target/Specificity
SIRT7

Formulation
50 µg of antibody in 100 µl PBS containing 0.2% gelatin and 0.05% sodium azide

Handling
The antibody solution should be gently mixed before use.

Background Descriptions

Precautions
SIRT7 Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

SIRT7 Antibody - Protein Information

Name SIRT7 {ECO:0000303|PubMed:22722849, ECO:0000312|HGNC:HGNC:14935}

Function
NAD-dependent protein-lysine deacylase that can act both as a deacetylase or deacylase (desuccinylase, depropionylase, deglutarylase and dedecanoylase), depending on the context (PubMed:22722849, PubMed:26907567, PubMed:30653310, PubMed:31542297, PubMed:35939806).

Specifically mediates deacetylation of histone H3 at 'Lys-18' (H3K18Ac) (PubMed:22722849, PubMed:30420520, PubMed:35939806). In contrast to other histone deacetylases, displays strong preference for a specific histone mark, H3K18Ac, directly linked to control of gene expression (PubMed:22722849, PubMed:30653310). H3K18Ac is mainly present around the transcription start site of genes and has been linked to activation of nuclear hormone receptors; SIRT7 thereby acts as a transcription repressor (PubMed:22722849). Moreover, H3K18 hypoacetylation has been reported as a marker of malignancy in various cancers and seems to maintain the transformed phenotype of cancer cells (PubMed:22722849). Also able to mediate deacetylation of histone H3 at 'Lys-36' (H3K36Ac) in the context of nucleosomes (PubMed:30653310). Also mediates deacetylation of non-histone proteins, such as ATM, CDK9, DDX21, DDB1, FBL, FKBP5/FKBP51, GABPB1, RAN, RRP9/U3-55K and POLR1E/PAF53 (PubMed:24207024, PubMed:26867678, PubMed:28147277, PubMed:28886238, PubMed:28426094, PubMed:30540930, PubMed:31075303, PubMed:30944854, PubMed:28790157). Enriched in nucleolus where it stimulates transcription activity of the RNA polymerase I complex (PubMed:16618798, PubMed:19174463, PubMed:24207024). Acts by mediating the deacetylation of the RNA polymerase I subunit POLR1E/PAF53, thereby promoting the association of RNA polymerase I with the rDNA promoter region and coding region (PubMed:16618798, PubMed:19174463, PubMed:24207024). In response to metabolic stress, SIRT7 is released from nucleoli leading to hyperacetylation of POLR1E/PAF53 and decreased RNA polymerase I transcription (PubMed:24207024). Required to restore the transcription of ribosomal RNA (rRNA) at the exit from mitosis (PubMed:19174463). Promotes pre-ribosomal RNA (pre-rRNA) cleavage at the 5'-terminal processing site by mediating deacetylation of RRP9/U3- 55K, a core subunit of the U3 snoRNP complex (PubMed:26867678). Mediates 'Lys-37' deacetylation of Ran, thereby regulating the nuclear export of NF-kappa-B subunit RELA/p65 (PubMed:31075303). Acts as a regulator of DNA damage repair by mediating deacetylation of ATM during the late stages of DNA damage response, promoting ATM dephosphorylation and deactivation (PubMed:30944854). Suppresses the activity of the DCX (DDB1-CUL4-X-box) E3 ubiquitin-protein ligase complexes by mediating deacetylation of DDB1, which prevents the interaction between DDB1 and CUL4 (CUL4A or CUL4B) (PubMed:28886238). Activates RNA polymerase II transcription by mediating deacetylation of CDK9, thereby promoting 'Ser-2' phosphorylation of the C-terminal domain (CTD) of RNA polymerase II (PubMed:28426094). Deacetylates FBL, promoting histone- glutamine methyltransferase activity of FBL (PubMed:<a

href="http://www.uniprot.org/citations/30540930" target="_blank">30540930). Acts as a regulator of mitochondrial function by catalyzing deacetylation of GABPB1 (By similarity). Regulates Akt/AKT1 activity by mediating deacetylation of FKBP5/FKBP51 (PubMed:28147277). Required to prevent R- loop-associated DNA damage and transcription-associated genomic instability by mediating deacetylation and subsequent activation of DDX21, thereby overcoming R-loop-mediated stalling of RNA polymerases (PubMed:28790157). In addition to protein deacetylase activity, also acts as a protein-lysine deacylase (PubMed:27436229, PubMed:27997115, PubMed:31542297). Acts as a protein depropionylase by mediating depropionylation of Osterix (SP7), thereby regulating bone formation by osteoblasts (By similarity). Acts as a histone deglutarylase by mediating deglutarylation of histone H4 on 'Lys-91' (H4K91glu); a mark that destabilizes nucleosomes by promoting dissociation of the H2A-H2B dimers from nucleosomes (PubMed:31542297). Acts as a histone desuccinylase: in response to DNA damage, recruited to DNA double- strand breaks (DSBs) and catalyzes desuccinylation of histone H3 on 'Lys-122' (H3K122succ), thereby promoting chromatin condensation and DSB repair (PubMed:27436229). Also promotes DSB repair by promoting H3K18Ac deacetylation, regulating non-homologous end joining (NHEJ) (By similarity). Along with its role in DNA repair, required for chromosome synapsis during prophase I of female meiosis by catalyzing H3K18Ac deacetylation (By similarity). Involved in transcriptional repression of LINE-1 retrotransposon via H3K18Ac deacetylation, and promotes their association with the nuclear lamina (PubMed:31226208). Required to stabilize ribosomal DNA (rDNA) heterochromatin and prevent cellular senescence induced by rDNA instability (PubMed:29728458). Acts as a negative regulator of SIRT1 by preventing autodeacetylation of SIRT1, restricting SIRT1 deacetylase activity (By similarity).

Cellular Location
Nucleus, nucleolus. Nucleus, nucleoplasm. Chromosome. Cytoplasm. Note=Mainly localizes in the nucleolus and nucleoplasm (PubMed:24207024, PubMed:28886238, PubMed:28790157, PubMed:31075303). Associated with rDNA promoter and transcribed region (PubMed:16079181, PubMed:19174463). Associated with nucleolar organizer regions during mitosis (PubMed:16079181, PubMed:19174463). In response to stress, released from nucleolus to nucleoplasm (PubMed:24207024) Associated with chromatin (PubMed:22722849). In response to DNA damage, recruited to DNA double-strand breaks (DSBs) sites (PubMed:27436229) (Probable). Located close to the nuclear membrane when in the cytoplasm (PubMed:11953824).

SIRT7 Antibody - Protocols

Provided below are standard protocols that you may find useful for product applications.

- Western Blot
- Blocking Peptides
- Dot Blot
- Immunohistochemistry
- Immunofluorescence
- Immunoprecipitation
- Flow Cytomety
- Cell Culture

SIRT7 Antibody - Images

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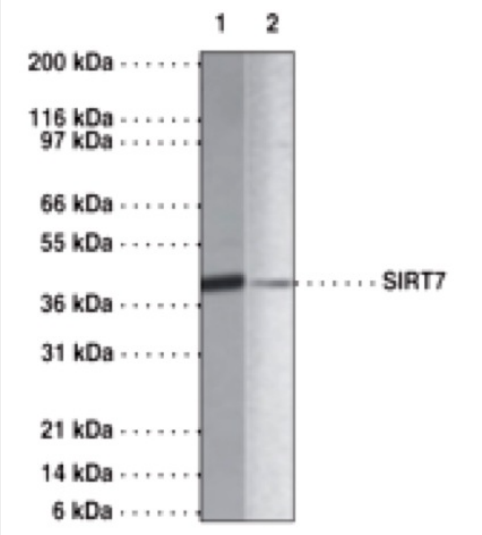

WB using SIRT7 pAb. Lane1. Human liver homogenate; Lane2. PBMC lysate.

SIRT7 Antibody - Background

The sirtuins represent a distinct class of trichostatin A-insensitive lysyl-deacetylases (class III HDACs) and have been shown to catalyze a reaction that couples lysine deacetylation to the formation of nicotinamide and O-acetyl-ADP-ribose from NAD+ and the abstracted acetyl group. SIRT7 is a member of this family of proteins and is present in prokaryotes and eukaryotes. All SIR2-like proteins have a sirtuin core domain, which contains a series of sequence motifs conserved in organisms ranging from bacteria to humans. Bacterial, yeast, and mammalian sirtuins are able to metabolize NAD+ and several act as mono-ADP-ribosyltransferases. The enzymatic function of sirtuins is not yet completely understood but as mentioned above, recent reports of histone-activated SIR2-mediated NAD+ metabolism and NAD+-activated SIR2-mediated histone deacetylation s µggest a possible coupled reciprocal activation mechanism involving interactions of SIR2 with NAD+ and the N-ε-acetyl-lysine groups of acetylated histone.