

**Anti-SIRT7 Picoband Antibody**  
Catalog # ABO12049**Specification****Anti-SIRT7 Picoband Antibody - Product Information**

Application	<b>WB, IHC</b>
Primary Accession	<a href="#">O9NRC8</a>
Host	<b>Rabbit</b>
Reactivity	<b>Human, Mouse, Rat</b>
Clonality	<b>Polyclonal</b>
Format	<b>Lyophilized</b>

**Description**

Rabbit IgG polyclonal antibody for NAD-dependent protein deacetylase sirtuin-7(SIRT7) detection. Tested with WB, IHC-P in Human;Mouse;Rat.

**Reconstitution**

Add 0.2ml of distilled water will yield a concentration of 500ug/ml.

**Anti-SIRT7 Picoband Antibody - Additional Information**

**Gene ID** 51547

**Other Names**

NAD-dependent protein deacetylase sirtuin-7, 3.5.1.-, Regulatory protein SIR2 homolog 7, SIR2-like protein 7, SIRT7, SIR2L7

**Calculated MW**

44898 MW KDa

**Application Details**

Immunohistochemistry(Paraffin-embedded Section), 0.5-1 µg/ml, Mouse, Rat, Human, By Heat<br>Western blot, 0.1-0.5 µg/ml, Human, Rat<br>

**Subcellular Localization**

Cytoplasm. Nucleus, nucleolus. Located close to the nuclear membrane when in the cytoplasm. Associated with chromatin. Associated with rDNA promoter and transcribed region. Associated with nucleolar organizer regions during mitosis.

**Protein Name**

NAD-dependent protein deacetylase sirtuin-7

**Contents**

Each vial contains 5mg BSA, 0.9mg NaCl, 0.2mg Na<sub>2</sub>HPO<sub>4</sub>, 0.05mg Na<sub>3</sub>.

**Immunogen**

E.coli-derived human SIRT7 recombinant protein (Position: R8-G350). Human SIRT7 shares 96% and 95% amino acid (aa) sequence identity with mouse and rat SIRT7, respectively.

**Purification**

Immunogen affinity purified.

**Cross Reactivity**

No cross reactivity with other proteins.

**Storage**

**At -20°C for one year. After r<sup>o</sup>Constitution, at 4°C for one month. It<sup>o</sup>Can also be aliquotted and stored frozen at -20°C for a longer time.Avoid repeated freezing and thawing.**

**Sequence Similarities**

Belongs to the sirtuin family. Class IV subfamily.

**Anti-SIRT7 Picoband Antibody - Protein Information**

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

**Function**

NAD-dependent protein-lysine deacetylase that can act both as a deacetylase or deacylase (desuccinylase, depropionylase, deglutarylase and dedecanoylase), depending on the context (PubMed:<a href="http://www.uniprot.org/citations/22722849" target="\_blank">22722849</a>, PubMed:<a href="http://www.uniprot.org/citations/26907567" target="\_blank">26907567</a>, PubMed:<a href="http://www.uniprot.org/citations/30653310" target="\_blank">30653310</a>, PubMed:<a href="http://www.uniprot.org/citations/31542297" target="\_blank">31542297</a>, PubMed:<a href="http://www.uniprot.org/citations/35939806" target="\_blank">35939806</a>). Specifically mediates deacetylation of histone H3 at 'Lys-18' (H3K18Ac) (PubMed:<a href="http://www.uniprot.org/citations/22722849" target="\_blank">22722849</a>, PubMed:<a href="http://www.uniprot.org/citations/30420520" target="\_blank">30420520</a>, PubMed:<a href="http://www.uniprot.org/citations/35939806" target="\_blank">35939806</a>). In contrast to other histone deacetylases, displays strong preference for a specific histone mark, H3K18Ac, directly linked to control of gene expression (PubMed:<a href="http://www.uniprot.org/citations/22722849" target="\_blank">22722849</a>, PubMed:<a href="http://www.uniprot.org/citations/30653310" target="\_blank">30653310</a>). 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:<a href="http://www.uniprot.org/citations/22722849" target="\_blank">22722849</a>). 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:<a href="http://www.uniprot.org/citations/22722849" target="\_blank">22722849</a>). Also able to mediate deacetylation of histone H3 at 'Lys-36' (H3K36Ac) in the context of nucleosomes (PubMed:<a href="http://www.uniprot.org/citations/30653310" target="\_blank">30653310</a>). 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:<a href="http://www.uniprot.org/citations/24207024" target="\_blank">24207024</a>, PubMed:<a href="http://www.uniprot.org/citations/26867678" target="\_blank">26867678</a>, PubMed:<a href="http://www.uniprot.org/citations/28147277" target="\_blank">28147277</a>, PubMed:<a href="http://www.uniprot.org/citations/28426094" target="\_blank">28426094</a>, PubMed:<a href="http://www.uniprot.org/citations/28790157" target="\_blank">28790157</a>, PubMed:<a href="http://www.uniprot.org/citations/28886238" target="\_blank">28886238</a>, PubMed:<a href="http://www.uniprot.org/citations/30540930" target="\_blank">30540930</a>, PubMed:<a href="http://www.uniprot.org/citations/30944854" target="\_blank">30944854</a>, PubMed:<a href="http://www.uniprot.org/citations/31075303" target="\_blank">31075303</a>). Enriched in nucleolus where it stimulates transcription activity of the RNA polymerase I complex (PubMed:<a href="http://www.uniprot.org/citations/16618798" target="\_blank">16618798</a>, PubMed:<a href="http://www.uniprot.org/citations/19174463" target="\_blank">19174463</a>, PubMed:<a

href="http://www.uniprot.org/citations/24207024" target="\_blank">24207024</a>). 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:<a href="http://www.uniprot.org/citations/16618798" target="\_blank">16618798</a>, PubMed:<a href="http://www.uniprot.org/citations/19174463" target="\_blank">19174463</a>, PubMed:<a href="http://www.uniprot.org/citations/24207024" target="\_blank">24207024</a>). In response to metabolic stress, SIRT7 is released from nucleoli leading to hyperacetylation of POLR1E/PAF53 and decreased RNA polymerase I transcription (PubMed:<a href="http://www.uniprot.org/citations/24207024" target="\_blank">24207024</a>). Required to restore the transcription of ribosomal RNA (rRNA) at the exit from mitosis (PubMed:<a href="http://www.uniprot.org/citations/19174463" target="\_blank">19174463</a>). 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:<a href="http://www.uniprot.org/citations/26867678" target="\_blank">26867678</a>). Mediates 'Lys-37' deacetylation of Ran, thereby regulating the nuclear export of NF-kappa-B subunit RELA/p65 (PubMed:<a href="http://www.uniprot.org/citations/31075303" target="\_blank">31075303</a>). 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:<a href="http://www.uniprot.org/citations/30944854" target="\_blank">30944854</a>). 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:<a href="http://www.uniprot.org/citations/28886238" target="\_blank">28886238</a>). 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:<a href="http://www.uniprot.org/citations/28426094" target="\_blank">28426094</a>). Deacetylates FBL, promoting histone- glutamine methyltransferase activity of FBL (PubMed:<a href="http://www.uniprot.org/citations/30540930" target="\_blank">30540930</a>). 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:<a href="http://www.uniprot.org/citations/28147277" target="\_blank">28147277</a>). 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:<a href="http://www.uniprot.org/citations/28790157" target="\_blank">28790157</a>). In addition to protein deacetylase activity, also acts as a protein-lysine deacylase (PubMed:<a href="http://www.uniprot.org/citations/27436229" target="\_blank">27436229</a>, PubMed:<a href="http://www.uniprot.org/citations/27997115" target="\_blank">27997115</a>, PubMed:<a href="http://www.uniprot.org/citations/31542297" target="\_blank">31542297</a>). 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:<a href="http://www.uniprot.org/citations/31542297" target="\_blank">31542297</a>). 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:<a href="http://www.uniprot.org/citations/27436229" target="\_blank">27436229</a>). 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:<a href="http://www.uniprot.org/citations/31226208" target="\_blank">31226208</a>). Required to stabilize ribosomal DNA (rDNA) heterochromatin and prevent cellular senescence induced by rDNA instability (PubMed:<a href="http://www.uniprot.org/citations/29728458" target="\_blank">29728458</a>). Acts as a negative regulator of SIRT1 by preventing

autodeacetylation of SIRT1, restricting SIRT1 deacetylase activity (By similarity).

#### Cellular Location

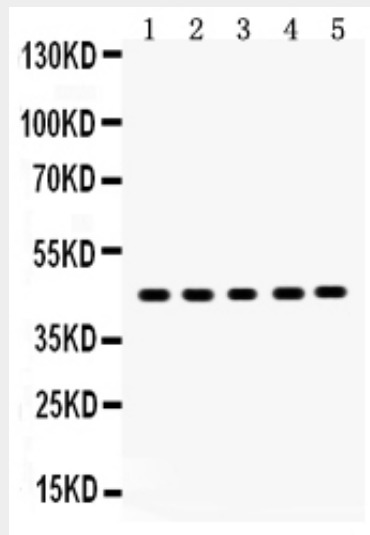
Nucleus, nucleolus. Nucleus, nucleoplasm. Chromosome. Cytoplasm. Note=Mainly localizes in the nucleolus and nucleoplasm (PubMed:24207024, PubMed:28790157, PubMed:28886238, PubMed:31075303). Associated with rDNA promoter and transcribed region (PubMed:16079181, PubMed:19174463). Associated with nucleolar 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 (Probable) (PubMed:27436229). Located close to the nuclear membrane when in the cytoplasm (PubMed:11953824).

#### Anti-SIRT7 Picoband Antibody - Protocols

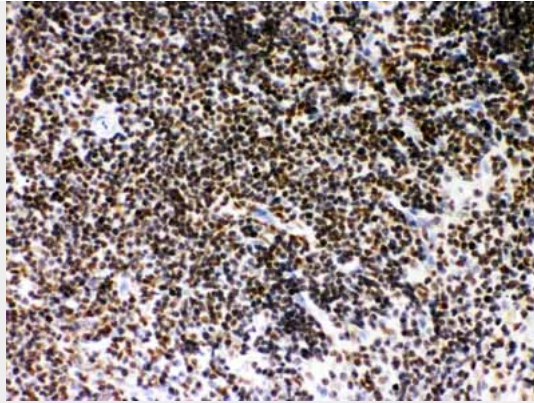
Provided below are standard protocols that you may find useful for product applications.

- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

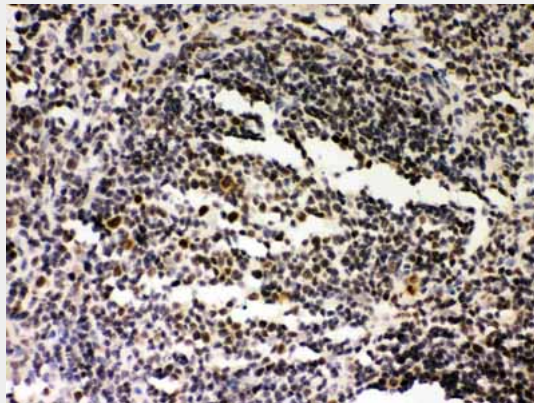
#### Anti-SIRT7 Picoband Antibody - Images



Anti- SIRT7 Picoband antibody, ABO12049, Western blottingAll lanes: Anti SIRT7 (ABO12049) at 0.5ug/mlLane 1: Rat Spleen Tissue Lysate at 50ugLane 2: Rat Brain Tissue Lysate at 50ugLane 3: Rat Intestine Tissue Lysate at 50ugLane 4: SMMC Whole Cell Lysate at 40ugLane 5: JURKAT Whole Cell Lysate at 40ugPredicted bind size: 45KDObserved bind size: 45KD



Anti- SIRT7 Picoband antibody, ABO12049, IHC(P)IHC(P): Mouse Spleen Tissue



Anti- SIRT7 Picoband antibody, ABO12049, IHC(P)IHC(P): Rat Spleen Tissue

#### **Anti-SIRT7 Picoband Antibody - Background**

SIRT7 is also known as SIR2L7. This gene encodes a member of the sirtuin family of proteins, homologs to the yeast Sir2 protein. Members of the sirtuin family are characterized by a sirtuin core domain and grouped into four classes. The functions of human sirtuins have not yet been determined; however, yeast sirtuin proteins are known to regulate epigenetic gene silencing and suppress recombination of rDNA. Studies suggest that the human sirtuins may function as intracellular regulatory proteins with mono-ADP-ribosyltransferase activity. The protein encoded by this gene is included in class IV of the sirtuin family.