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SIRT7 Rabbit pAb

Catalog # AP99841

Product Information

Application	WB, IHC-P, IHC-F, IF
Primary Accession	Q9NRC8
Other Accession	Q9NRC8
Reactivity	Mouse
Predicted	Rat, Pig, Human, Chicken, Dog
Host	Rabbit
Clonality	Polyclonal
Calculated MW	44898
Physical State	Liquid
Immunogen	KLH conjugated synthetic peptide derived from human SIRT7
Epitope Specificity	231-330/400
Isotype	IgG
Purity	affinity purified by Protein A
Buffer	0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol.
SIMILARITY	Belongs to the sirtuin family. Class IV subfamily.Contains 1 deacetylase sirtuin-type domain.
SUBUNIT	Interacts with UBTF and the RNA polymerase I complex. Interacts with histone H2A and/or histone H2B.
Post-translational modifications	Phosphorylated during mitosis (Probable).
Important Note	This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.
Background Descriptions	SIRT7 is 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.

Additional Information

Gene ID	51547
Other Names	SIR2L7; SIR7_BOVIN; SIRT7; NAD-dependent protein deacylase sirtuin-7; Regulatory protein SIR2 homolog 7; SIR2-like protein 7; 2.3.1.286; SIR7_HUMAN; SIR7_MOUSE; sirtuin 7; sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 7; sirtuin (silent mating type information regulation 2 homolog) 7 (S. cerevisiae)
Dilution	WB=1:500-2000,IHC-P=1:100-500,IHC-F=1:100-500,IF=1:100-500,Flow-Cyt=1 μg/Test

Storage	Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

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:28426094, PubMed:28790157, PubMed:28886238, PubMed:30540930, PubMed:30944854, PubMed:31075303). 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: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: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).

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