

SIRT7 Antibody

Purified Mouse Monoclonal Antibody

Catalog # AO2123a

Product Information

Application	WB, FC, E
Primary Accession	Q9NRC8
Reactivity	Human
Host	Mouse
Clonality	Monoclonal
Clone Names	1E2B2
Isotype	IgG1
Calculated MW	44898
Description	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.
Immunogen	Purified recombinant fragment of human SIRT7 (AA: 1-105) expressed in E. Coli.
Formulation	Purified antibody in PBS with 0.05% sodium azide

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
Dilution	WB~~1/500 - 1/2000 FC~~1/200 - 1/400 E~~1/10000
Storage	Maintain refrigerated at 2-8°C for up to 6 months. For long term storage store at -20°C in small aliquots to prevent freeze-thaw cycles.
Precautions	SIRT7 Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

Protein Information

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

References

1.Clin Cancer Res. 2014 Apr 1;20(7):1741-6. 2.Mol Cell Proteomics. 2014 Jan;13(1):73-83.

Images

