

Product datasheet

Recombinant Human SIRT7 protein ab176933

1 Image

Overview

Product name	Recombinant Human SIRT7 protein
Protein length	Protein fragment

Description

Nature	Recombinant
Source	Escherichia coli
Amino Acid Sequence	
Accession	Q9NRC8
Species	Human

Sequence	<p>AAGGLSRSERKAAERVRLREEQQRERLRQVSRILRK AAAERSAEEGRLL AESADLVTELQGRSRRREGLKRRQEEVCDDPEELRG KVRELASAVRNAKY LVVYTGAGISTAASIPDYRGPNGVWTLQKGRSVSAAD LSEAEPTLTHMS ITRLHEQKLVQHVVVSQNC DGLHLRSGLPRTAISELHGN MYIEVCTSCVPN REYVRVFDVTERTALHRHQTGRTCHKCGTQLRDTIVHF GERGTLGQPLNW EAATEAASRADTILCLGSSLKVLKKYPRLWCMTKPPS RRPKLYMNLQWT PKDDWAALKLHGKCDDVMRLLMAELGLEIPAYSRWQ DIFSLATPLRAGE EGSHSRKSLCRSREEAPPGDRGAPLSSAPILGGWFG RGCTKRTRKRVKVT</p>
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Molecular weight	49 kDa including tags
Amino acids	2 to 400
Tags	His tag N-Terminus

Specifications

Our [Abpromise guarantee](#) covers the use of **ab176933** in the following tested applications.

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

Applications	SDS-PAGE
Purity	>= 85 % SDS-PAGE.
Form	Liquid

Preparation and Storage

Stability and Storage	Shipped on Dry Ice. Store at -80°C. Avoid freeze / thaw cycle.
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General Info

Function	NAD-dependent protein deacetylase that specifically mediates deacetylation of histone H3 at 'Lys-18' (H3K18Ac). In contrast to other histone deacetylases, displays selectivity for a single histone mark, H3K18Ac, directly linked to control of gene expression. 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. Moreover, H3K18 hypoacetylation has been reported as a marker of malignancy in various cancers and seems to maintain the transformed phenotype of cancer cells. These data suggest that SIRT7 may play a key role in oncogenic transformation by suppresses expression of tumor suppressor genes by locus-specific deacetylation of H3K18Ac at promoter regions. Also required to restore the transcription of ribosomal RNA (rRNA) at the exit from mitosis: promotes the association of RNA polymerase I with the rDNA promoter region and coding region. Stimulates transcription activity of the RNA polymerase I complex. May also deacetylate p53/TP53 and promotes cell survival, however such data need additional confirmation.
Sequence similarities	Belongs to the sirtuin family. Class IV subfamily. Contains 1 deacetylase sirtuin-type domain.
Post-translational modifications	Phosphorylated during mitosis.
Cellular 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.

Images



SDS-PAGE analysis of ab176933.

Lane 1: 1 µg of ab176933

Lane 2: 2 µg of ab176933

Lane 3: 5 µg of ab176933

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