Product datasheet

Anti-SIRT1 antibody [E104] ab32441

Overview

Product name
Anti-SIRT1 antibody [E104]

Description
Rabbit monoclonal [E104] to SIRT1

Host species
Rabbit

Specificity
The antibody does not cross-react with other sirtuin family members. Expression levels of the target protein vary with sample type and some optimisation may be required. For western blotting, more concentrated lysates may be required when using tissues samples.

Tested applications
Suitable for: ICC/IF, IHC-Fr, WB, IP, IHC-P, Flow Cyt

Species reactivity
Reacts with: Human

Immunogen
Synthetic peptide within Human SIRT1 aa 700-800 (C terminal). The exact sequence is proprietary.

Positive control
WB: HeLa, Jurkat, HEK293, SW480 and A549 cell lysates. IHC-P: Human colon carcinoma and human lung squamous carcinoma tissues. Flow: HeLa cells. IP: Jurkat whole cell lysate (ab7899).

General notes
Rat: We have preliminary internal testing data to indicate this antibody may not react with these species. Please contact us for more information.

Our RabMab® technology is a patented hybridoma-based technology for making rabbit monoclonal antibodies. For details on our patents, please refer to RabMab® patents

We are constantly working hard to ensure we provide our customers with best in class antibodies. As a result of this work we are pleased to now offer this antibody in purified format. We are in the process of updating our datasheets. The purified format is designated 'PUR' on our product labels. If you have any questions regarding this update, please contact our Scientific Support team.

This product is a recombinant rabbit monoclonal antibody.

Properties

Form
Liquid

Storage instructions
Shipped at 4°C. Upon delivery aliquot and store at -20°C. Avoid freeze / thaw cycles.

Storage buffer
pH: 7.20
Preservative: 0.01% Sodium azide
 Constituents: 59% PBS, 40% Glycerol, 0.05% BSA
Purity: Protein A purified
Clonality: Monoclonal
Clone number: E104
Isotype: IgG

Applications

Our Abpromise guarantee covers the use of ab32441 in the following tested applications. The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

<table>
<thead>
<tr>
<th>Application</th>
<th>Abreviews</th>
<th>Notes</th>
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<tbody>
<tr>
<td>ICC/IF</td>
<td></td>
<td>1/150.</td>
</tr>
<tr>
<td>IHC-Fr</td>
<td></td>
<td>Use at an assay dependent concentration. PubMed: 21098725</td>
</tr>
<tr>
<td>WB</td>
<td>★★★★★</td>
<td>1/20000. Detects a band of approximately 110 kDa (predicted molecular weight: 82 kDa). <strong>For unpurified, use 1/5000.</strong> Detects a band of approximately 110 kDa (110-121 kDa) which is likely to be due to post translational glycosylation. SIRT1 is known to bind to several other proteins, and the 121kDa band could also be due to the presence of one of these complexes (ensure samples are adequately reduced and denatured).</td>
</tr>
<tr>
<td>IP</td>
<td></td>
<td>1/30.</td>
</tr>
<tr>
<td>IHC-P</td>
<td>★★★★★</td>
<td>1/150.</td>
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<tr>
<td>Flow Cyt</td>
<td></td>
<td>1/200.</td>
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Target

Function: NAD-dependent protein deacetylase that links transcriptional regulation directly to intracellular energetics and participates in the coordination of several separated cellular functions such as cell cycle, response to DNA damage, metabolism, apoptosis and autophagy. Can modulate chromatin function through deacetylation of histones and can promote alterations in the methylation of histones and DNA, leading to transcriptional repression. Deacetylates a broad range of transcription factors and coregulators, thereby regulating target gene expression positively and negatively. Serves as a sensor of the cytosolic ratio of NAD(+)/NADH which is altered by glucose deprivation and metabolic changes associated with caloric restriction. Is essential in skeletal muscle cell differentiation and in response to low nutrients mediates the inhibitory effect on skeletal myoblast differentiation which also involves 5'-AMP-activated protein kinase (AMPK) and nicotinamide phosphoribosyltransferase (NAMPT). Component of the eNoSC (energy-dependent nucleolar silencing) complex, a complex that mediates silencing of rDNA in response to intracellular energy status and acts by recruiting histone-modifying enzymes. The eNoSC complex is able to sense the energy status of cell: upon glucose starvation, elevation of NAD(+)NADP(+) ratio activates SIRT1, leading to histone H3 deacetylation followed by dimethylation of H3 at 'Lys-9' (H3K9me2) by SUV39H1 and the formation of silent chromatin in the rDNA locus. Deacetylates 'Lys-266' of SUV39H1, leading to its activation. Inhibits skeletal muscle differentiation by deacetylating PCAF and MYOD1. Deacetylates H2A and 'Lys-26' of HIST1H1E.
Deacetylates 'Lys-16' of histone H4 (in vitro). Involved in NR0B2/SHP corepression function through chromatin remodeling: Recruited to LRH1 target gene promoters by NR0B2/SHP thereby stimulating histone H3 and H4 deacetylation leading to transcriptional repression. Proposed to contribute to genomic integrity via positive regulation of telomere length; however, reports on localization to pericentromeric heterochromatin are conflicting. Proposed to play a role in constitutive heterochromatin (CH) formation and/or maintenance through regulation of the available pool of nuclear SUV39H1. Upon oxidative/metabolic stress decreases SUV39H1 degradation by inhibiting SUV39H1 polyubiquitination by MDM2. This increase in SUV39H1 levels enhances SUV39H1 turnover in CH, which in turn seems to accelerate renewal of the heterochromatin which correlates with greater genomic integrity during stress response.

Deacetylates 'Lys-382' of p53/TP53 and impairs its ability to induce transcription-dependent proapoptotic program and modulate cell senescence. Deacetylates TAF1B and thereby represses rDNA transcription by the RNA polymerase I. Deacetylates MYC, promotes the association of MYC with MAX and decreases MYC stability leading to compromised transformational capability. Deacetylates FOXO3 in response to oxidative stress thereby increasing its ability to induce cell cycle arrest and resistance to oxidative stress but inhibiting FOXO3-mediated induction of apoptosis transcriptional activity; also leading to FOXO3 ubiquitination and proteosomal degradation. Appears to have a similar effect on MLLT7/FOXO4 in regulation of transcriptional activity and apoptosis. Deacetylates DNMT1; thereby impairs DNMT1 methyltransferase-independent transcription repressor activity, modulates DNMT1 cell cycle regulatory function and DNMT1-mediated gene silencing. Deacetylates RELA/NF-kappa-B p65 thereby inhibiting its transactivating potential and augments apoptosis in response to TNF-alpha.

Deacetylates HIF1A, KAT5/TIP60, RB1 and HIC1. Deacetylates FOXO1 resulting in its nuclear retention and enhancement of its transcriptional activity leading to increased gluconeogenesis in liver. Inhibits E2F1 transcriptional activity and apoptotic function, possibly by deacetylation. Involved in HES1- and HEY2-mediated transcriptional repression. In cooperation with MYCN seems to be involved in transcriptional repression of DUSP6/MAPK3 leading to MYCN stabilization by phosphorylation at 'Ser-62'. Deacetylates MEF2D. Required for antagonist-mediated transcription suppression of AR-dependent genes which may be linked to local deacetylation of histone H3. Represses HNF1A-mediated transcription. Required for the repression of ESRRG by CREBZF. Modulates AP-1 transcription factor activity. Deacetylates NR1H3 AND NR1H2 and deacetylation of NR1H3 at 'Lys-434' positively regulates transcription of NR1H3:RXR target genes, promotes NR1H3 proteosomal degradation and results in cholesterol efflux; a promoter clearing mechanism after reach round of transcription is proposed. Involved in lipid metabolism. Implicated in regulation of adipogenesis and fat mobilization in white adipocytes by repression of PPARG which probably involves association with NCOR1 and SMRT/NCOR2. Deacetylates ACSS2 leading to its activation, and HMGCS1. Involved in liver and muscle metabolism. Through deacetylation and activation of PPARGC1A is required to activate fatty acid oxidation in skeletal muscle under low-glucose conditions and is involved in glucose homeostasis. Involved in regulation of PPARA and fatty acid beta-oxidation in liver. Involved in positive regulation of insulin secretion in pancreatic beta cells in response to glucose; the function seems to imply transcriptional repression of UCP2. Proposed to deacetylate IRS2 thereby facilitating its insulin-induced tyrosine phosphorylation. Deacetylates SREBF1 isoform SREBP-1C thereby decreasing its stability and transactivation in lipogenic gene expression. Involved in DNA damage response by repressing genes which are involved in DNA repair, such as XPC and TP73, deacetylating XRCC6/Ku70, and facilitating recruitment of additional factors to sites of damaged DNA, such as SIRT1-deacetylated NBN can recruit ATM to initiate DNA repair and SIRT1-deacetylated XPA interacts with RPA2. Also involved in DNA repair of DNA double-strand breaks by homologous recombination and specifically single-strand annealing independently of XRCC6/Ku70 and NBN. Transcriptional suppression of XPC probably involves an E2F4:RBL2 suppressor complex and protein kinase B (AKT) signaling. Transcriptional suppression of TP73 probably involves E2F4 and PCAF. Deacetylates WRN thereby regulating its helicase and
exonuclease activities and regulates WRN nuclear translocation in response to DNA damage.

Deacetylates APEX1 at 'Lys-6' and 'Lys-7' and stimulates cellular AP endonuclease activity by
promoting the association of APEX1 to XRCC1. Increases p53/TP53-mediated transcription-

independent apoptosis by blocking nuclear translocation of cytoplasmic p53/TP53 and probably
redirecting it to mitochondria. Deacetylates XRCC6/Ku70 at 'Lys-539' and 'Lys-542' causing it to
sequester BAX away from mitochondria thereby inhibiting stress-induced apoptosis. Is involved in
autophagy, presumably by deacetylating ATG5, ATG7 and MAP1LC3B/ATG8. Deacetylates

AKT1 which leads to enhanced binding of AKT1 and PDK1 to PIP3 and promotes their activation.

Proposed to play role in regulation of STK11/LBK1-dependent AMPK signaling pathways
implicated in cellular senescence which seems to involve the regulation of the acetylation status of
STK11/LBK1. Can deacetylate STK11/LBK1 and thereby increase its activity, cytoplasmic
localization and association with STRAD; however, the relevance of such activity in normal cells is
unclear. In endothelial cells is shown to inhibit STK11/LBK1 activity and to promote its
degradation. Deacetylates SMAD7 at 'Lys-64' and 'Lys-70' thereby promoting its degradation.

Deacetylates CIITA and augments its MHC class II transactivation and contributes to its stability.

Deacetylates MECOM/EVI1. Deacetylates PML at 'Lys-487' and this deacetylation promotes
PML control of PER2 nuclear localization. During the neurogenic transition, repress selective
NOTCH1-target genes through

Isoform 2: Isoform 2 is shown to deacetylate 'Lys-382' of p53/TP53, however with lower activity
than isoform 1. In combination, the two isoforms exert an additive effect. Isoform 2 regulates
p53/TP53 expression and cellular stress response and is in turn repressed by p53/TP53
presenting a SIRT1 isomorf-dependent auto-regulatory loop.

(Microbial infection) In case of HIV-1 infection, interacts with and deacetylates the viral Tat protein.
The viral Tat protein inhibits SIRT1 deacetylation activity toward RELA/NF-kappa-B p65, thereby
potentiates its transcriptional activity and SIRT1 is proposed to contribute to T-cell hyperactivation
during infection.

SirtT1 75 kDa fragment: catalytically inactive 75SirT1 may be involved in regulation of apoptosis.
May be involved in protecting chondrocytes from apoptotic death by associating with cytochrome
C and interfering with apoptosome assembly.

Tissue specificity
Widely expressed.

Sequence similarities
Belongs to the sirtuin family. Class I subfamily.
Contains 1 deacetylase sirtuin-type domain.

Post-translational
modifications
Methylated on multiple lysine residues; methylation is enhanced after DNA damage and is
dispensable for deacetylase activity toward p53/TP53.
Phosphorylated. Phosphorylated by STK4/MST1, resulting in inhibition of SIRT1-mediated
p53/TP53 deacetylation. Phosphorylation by MAPK8/JNK1 at Ser-27, Ser-47, and Thr-530 leads
to increased nuclear localization and enzymatic activity. Phosphorylation at Thr-530 by DYRK1A
and DYRK3 increases deacetylase activity and promotes cell survival. Phosphorylation by
mammalian target of rapamycin complex 1 (mTORC1) at Ser-47 inhibits deacetylation activity.
Phosphorylated by CaMK2, leading to increased p53/TP53 and NF-kappa-B p65/RELA
deacetylation activity (By similarity). Phosphorylation at Ser-27 implicating MAPK9 is linked to
protein stability. There is some ambiguity for some phosphosites: Ser-159/Ser-162 and Thr-
544/Ser-545.

Proteolytically cleaved by cathepsin B upon TNF-alpha treatment to yield catalytic inactive but
stable SirtT1 75 kDa fragment (75SirT1).
S-nitrosylated by GAPDH, leading to inhibit the NAD-dependent protein deacetylase activity.

Cellular localization
Cytoplasm. Mitochondrion and Nucleus, PML body. Cytoplasm. Nucleus. Recruited to the nuclear
bodies via its interaction with PML (PubMed:12006491). Colocalized with APEX1 in the nucleus
(PubMed:19934257). May be found in nucleolus, nuclear euchromatin, heterochromatin and inner
membrane (PubMed:15469825). Shuttles between nucleus and cytoplasm (By similarity).
Colocalizes in the nucleus with XBP1 isoform 2 (PubMed:20955178).

Images

**All lanes** : Anti-SIRT1 antibody [E104] (ab32441) at 1/20000 dilution (purified)

* Lane 1 : Jurkat cell lysate
* Lane 2 : HeLa cell lysate
* Lane 3 : HEK293 cell lysate
* Lane 4 : A549 cell lysate
* Lane 5 : SW480 cell lysate

Lysates/proteins at 20 µg per lane.

**Secondary**

* All lanes : HRP goat anti-rabbit IgG (H+L) at 1/1000 dilution

**Predicted band size**: 82 kDa

**Additional bands at**: 110 kDa (possible glycosylated form)

Blocking buffer and concentration: 5% NFDM/TBST.

Diluting buffer and concentration: 5% NFDM /TBST.

IHC image of SIRT1 staining in a section of formalin-fixed paraffin-embedded normal human colon* performed on a Leica BOND™ system using the standard protocol F. The section was pre-treated using heat mediated antigen retrieval with sodium citrate buffer (pH6, epitope retrieval solution 1) for 20mins. The section was then incubated with ab32441, 1/250 dilution, for 15 mins at room temperature and detected using an HRP conjugated compact polymer system. DAB was used as the chromogen. The section was then counterstained with haematoxylin and mounted with DPX.

For other IHC staining systems (automated and non-automated) customers should optimize variable parameters such as antigen retrieval conditions, primary antibody concentration and antibody incubation times.

*Tissue obtained from the Human Research Tissue Bank, supported by the NIHR Cambridge Biomedical Research Centre
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For other IHC staining systems (automated and non-automated) customers should optimize variable parameters such as antigen retrieval conditions, primary antibody concentration and antibody incubation times.

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Immunohistochemical staining of paraffin embedded human cerebral cortex with purified ab32441 at a working dilution of 1 in 150. The secondary antibody used is a HRP polymer for rabbit IgG. The sample is counter-stained with hematoxylin. Antigen retrieval was performed using Tris-EDTA buffer, pH 9.0. PBS was used instead of the primary antibody as the negative control, and is shown in the inset.
Immunofluorescence staining of SH-SY5Y cells with purified ab32441 at a working dilution of 1 in 150, counter-stained with DAPI. The secondary antibody was Alexa Fluor® 488 goat anti-rabbit (ab150077), used at a dilution of 1 in 500. The cells were fixed in 4% PFA and permeabilized using 0.1% Triton X 100. The negative control is shown in bottom right hand panel - for the negative control, purified ab32441 was used at a dilution of 1/200 followed by an Alexa Fluor® 594 goat anti-mouse antibody (ab150120) at a dilution of 1/500.

Flow cytometry analysis of HeLa (human cervix adenocarcinoma) cells labeling SIRT1 (red) with ab32441 at a 1/200 dilution. Cells were fixed with 4% paraformaldehyde and permeabilized with 90% methanol. A goat anti-rabbit IgG (Alexa Fluor® 488) (ab150077) was used as the secondary antibody at a 1/2000 dilution. Black - Rabbit monoclonal IgG (ab172730). Blue (unlabeled control) - Cells without incubation with the primary and secondary antibodies.
ab32441 (purified) at 1/30 immunoprecipitating SIRT1 in Jurkat cells (Lane 1). For western blotting, a HRP-conjugated anti-rabbit IgG (H+L) was used as the secondary antibody (1/1000).

Blocking buffer and concentration: 5% NFDM/TBST.

Diluting buffer and concentration: 5% NFDM /TBST.

All lanes: Anti-SIRT1 antibody [E104] (ab32441) at 1/20000 dilution

Lane 1: HeLa whole cell lysate
Lane 2: HepG2 whole cell lysate
Lane 3: Human Testis tissue lysate
Lane 4: Human Colon tissue lysate

Lysates/proteins at 20 µg per lane.

Secondary
All lanes: Goat Anti-Rabbit IgG H&L (HRP) preadsorbed at 1/10000 dilution

Developed using the ECL technique.

Performed under reducing conditions.

Predicted band size: 82 kDa
Observed band size: 110 kDa why is the actual band size different from the predicted?

Exposure time: 150 seconds
This blot was produced using a 4-12% Bis-tris gel under the MOPS buffer system. The gel was run at 200V for 50 minutes before being transferred onto a Nitrocellulose membrane at 30V for 70 minutes. The membrane was then blocked for an hour using 3% Milk before being incubated with ab32441 overnight at 4°C. Antibody binding was detected using an anti-rabbit antibody conjugated to HRP, and visualised using ECL development solution.

Immunohistochemical analysis of paraffin-embedded human colon carcinoma using unpurified ab32441 at 1/100 dilution.

Immunohistochemical analysis of paraffin-embedded human lung squamous carcinoma using unpurified ab32441 at 1/100 dilution.

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