

Mouse anti-Human SIRT1 Monoclonal Antibody | anti-SIRT1 antibody

SIRT1 Antibody

CATALOG #	HOST	REACTIVITY	APPLICATIONS
AAA290497	Mouse	Human	Immunoprecipitation, Western Blot

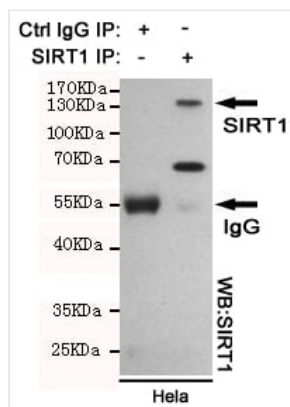
PRODUCT SYNONYMS

SIRT1; Monoclonal Antibody; SIRT1 Antibody; Purified Mouse Monoclonal Antibody (Mab); 75SirT1; BA57G10.4; hSIR2; hSIRT1; HST2; S. cerevisiae; homolog of; NAD dependent deacetylase SIRT1; NAD dependent deacetylase sirtuin 1; NAD dependent protein deacetylase sirtuin 1; OTTHUMP00000198111; OTTHUMP00000198112; Regulatory protein SIR2 homolog 1; SIR1_HUMAN; SIR2 like 1; SIR2 like protein 1; SIR2; S.cerevisiae; homolog-like 1; SIR2-like protein 1; SIR2ALPHA; SIR2alpha protein; SIR2L1; SIRT 1; Sirt1; SIRT1 Sir like proteins (siruitins) type 1; SIRT1: sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae); SirtT1 75 kDa fragment; sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae); Sirtuin 1; sirtuin; Sirtuin type 1; Sirtuin type 1.; anti-SIRT1 antibody

PRODUCT SPECIFICATIONS

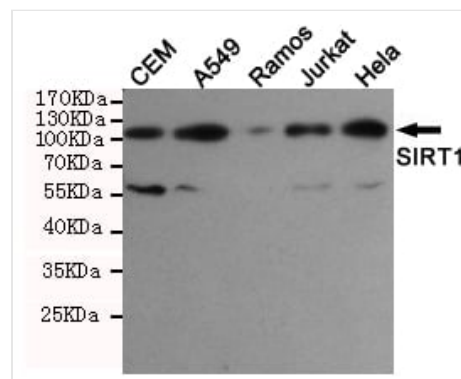
Host	Mouse
Reactivity	Human
Clonality	Monoclonal
Form/Format	Purified mouse monoclonal antibody in PBS(pH 7.4) containing with 0.02% sodium azide and 50% glycerol.
Sequence Length	452
Applicable Applications for anti-SIRT1 antibody	IP (Immunoprecipitation), WB (Western Blot)
Antigen Source	Human
Antigen Type	Recombinant Protein
Preparation and Storage	Maintain refrigerated at 2-8 degree C for up to 6 months. For long term storage store at -20 degree C in small aliquots to prevent freeze-thaw cycles.

IMAGES



IP (Immunoprecipitation)

Immunoprecipitation analysis of HeLa cell lysates using SIRT1 mouse mAb.



WB (Western Blot)

Western blot detection of SIRT1 in HeLa, Jurkat, Ramos, A549 and CEM cell lysates using SIRT1 mouse mAb (1:1000 diluted). Predicted band size: 120KDa. Observed band size: 120KDa.

Related Product Information for anti-SIRT1 antibody

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 proteasomal 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 proteasomal degradation and results in cholesterol efflux; a promoter clearing mechanism after each 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 PPARG 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,

Product Categories/Family for anti-SIRT1 antibody	Cell Biology; Metabolism; Microbiology
References	Frye R.A.,et al.Biochem. Biophys. Res. Commun. 260:273-279(1999). Takata T.,et al.Biochem. Biophys. Res. Commun. 301:250-257(2003). Deloukas P.,et al.Nature 429:375-381(2004). Vaziri H.,et al.Cell 107:149-159(2001). Langley E.,et al.EMBO J. 21:2383-2396(2002).

NCBI AND UNIPROT INFORMATION

NCBI GI #	215982798
NCBI GeneID	23411
NCBI Accession #	NP_001135970.1
NCBI GenBank Nucleotide #	NM_001142498.1
UniProt Accession #	Q96EB6; Q2XNF6; Q5JVVQ0; Q9GZR9; Q9Y6F0
Molecular Weight	81681
NCBI Official Full Name	NAD-dependent protein deacetylase sirtuin-1 isoform b
NCBI Official Synonym Full Names	sirtuin 1
NCBI Official Symbol	SIRT1
NCBI Official Synonym Symbols	SIR2; SIR2L1; SIR2alpha
NCBI Protein Information	NAD-dependent protein deacetylase sirtuin-1
UniProt Protein Name	NAD-dependent protein deacetylase sirtuin-1
UniProt Gene Name	SIRT1
UniProt Synonym Gene Names	SIR2L1; hSIRT1; hSIR2; 75SirT1
UniProt Entry Name	SIR1_HUMAN

For Research Use Only. Not for use in diagnostic or therapeutic procedures. Small volumes of product may become entrapped in the seal of the vial during shipment and storage; if necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the cap.

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Online datasheet: <https://stage.aaabiotech.com/monoclonal/sirt1-antibody-immunoprecipitation-western-blot-elisa/290497>