SIRT1 Antibody – Rabbit Monoclonal

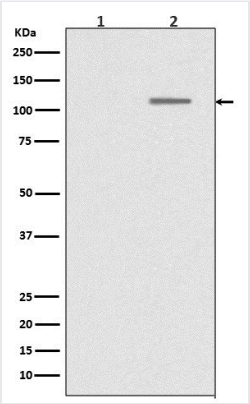
PRODUCT OVERVIEW

Product Name	SIRT1, Monoclonal Antibody
Full Product Name	Anti-Phospho-SIRT1 (S47) Rabbit Monoclonal Antibody
Product Gene Name	anti-SIRT1 antibody
Product Synonym Names	NAD-dependent protein deacetylase sirtuin-1; hSIRT1; 3.5.1.-; Regulatory protein SIR2 homolog 1; SIR2-like protein 1; hSIR2; SirtT1 75 kDa fragment; 75SirT1; SIRT1; SIR2L1
Clonality	Monoclonal
Host	Rabbit
Species Reactivity	Human
Form/Format	Liquid
Purity/Purification	Affinity-chromatography
Preparation and Storage	Store at -20 degree C for one year. After reconstitution, at 4 degree C for one month. It can also be aliquotted and stored frozen at -20 degree C for a longer time. Avoid repeated freezing and thawing.
Molecular Weight	81681 MW
OMIM	AF083106 mRNA
3D Structure	ModBase 3D Structure for Q96EB6
Immunogen	A synthesized peptide derived from human Phospho-SIRT1 (S47)
Subcellular Localization	Nucleus, PML body. Cytoplasm. Nucleus. Recruited to the nuclear bodies via its interaction with PML. Colocalized with APEX1 in the nucleus. May be found in nucleolus, nuclear euchromatin, heterochromatin and inner membrane. Shuttles between nucleus and cytoplasm (By similarity). Colocalizes in the nucleus with XBP1 isoform 2 (PubMed: 20955178).
Tissue Specificity	Widely expressed.
Contents	Rabbit IgG in phosphate buffered saline, pH 7.4, 150mM NaCl, 0.02% sodium azide and 50% glycerol.
Product Categories/Family for anti-SIRT1 antibody	Cell Biology; Apoptosis; Intracellular; p53 Pathway; Epigenetics and Nuclear Signaling; Chromatin Modifying Enzymes; Acetylation; Microbiology; Interspecies Interaction; Host Virus Interaction; Tags & Cell Markers; Subcellular Markers; Nucleus; Other Nucl
ISO Certification	Manufactured in an ISO 13485:2003 and EN ISO 13485:2012 Certified Laboratory.
Applications Tested/Suitable for anti-SIRT1 antibody	Immunofluorescence (IF), Immunohistochemistry (IHC), Immunocytochemistry (ICC), Western Blot (WB)
Application Notes for anti-SIRT1 antibody	WB: 1:1000-1:2000 IHC: 1:50-1:200 ICC/IF: 1:50-1:200

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, metobolism, 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 protesomal 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 deacteylation and activation of PPARGC1A is required to activate fatty acid oxidation in skeletel 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 faciliting 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 Recombinantion 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

Other Notes	Small volumes of anti-SIRT1 antibody vial(s) may occasionally become entrapped in the seal of the product vial during shipment and storage. If necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the container`s cap. Certain products may require to ship with dry ice and additional dry ice fee may apply.
Searchable Terms for SIRT1 purchase	MBS1750182 is an antibody targeting SIRT1. Also known as Anti-Phospho-SIRT1 (S47) Rabbit Monoclonal Antibody. Reactive in Human. Host: Rabbit.



Western Blot (WB) of anti-SIRT1 antibody
Western blot analysis of Phospho-SIRT1 (S47) expression in (1) HEK293 cell lysate; (2) HEK293 cell lysate treated with LP (MBS1750182).Electrophoresis was performed on a 5-20% SDS-PAGE gel at 70V (Stacking gel) / 90V (Resolving gel) for 2-3 hours. The sample well of each lane was loaded with 50ug of sample under reducing conditions. After Electrophoresis, proteins were transferred to a Nitrocellulose membrane at 150mA for 50-90 minutes. Blocked the membrane with 5% Non-fat Milk/ TBS for 1.5 hour at RT. The membrane was incubated with rabbit anti-SIRT1 monoclonal antibody overnight at 4 degree C, then washed with TBS-0.1%Tween 3 times with 5 minutes each and probed with a goat anti-rabbit IgG-HRP secondary antibody at a dilution of 1:10000 for 1.5 hour at RT. The signal is developed using an Enhanced Chemiluminescent detection (ECL) kit with Tanon 5200 system. A specific band was detected for SIRT1

ADDITIONAL DETAILS

NCBI/Uniprot data below describe general gene information for SIRT1. It may not necessarily be applicable to this product.

NCBI GI #	215982798
NCBI GeneID	23411
NCBI Accession #	NP_001135970.1
UniProt Primary Accession #	Q96EB6
UniProt Secondary Accession #	Q2XNF6; Q5JVQ0; Q9GZR9; Q9Y6F0
UniProt Related Accession #	Q96EB6
GenBank Nucleotide #	NM_001142498.1
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
UniProt Protein Name	NAD-dependent protein deacetylase sirtuin-1
UniProt Synonym Protein Names	Regulatory protein SIR2 homolog 1; SIR2-like protein 1; hSIR2
Protein Family	NAD-dependent protein deacetylase sirtuin
UniProt Gene Name	SIRT1

UniProt Synonym Gene Names	SIR2L1; hSIRT1; hSIR2; 75SirT1
NCBI Protein Information	NAD-dependent protein deacetylase sirtuin-1
NCBI Summary for SIRT1	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 I of the sirtuin family. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Dec 2008]

UniProt Comments for SIRT1

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Research Articles on SIRT1	**1.** miR-212 facilitates macrophage foam cell formation and suppresses ABCA1-dependent cholesterol efflux through downregulation of SIRT1.
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