

Product datasheet for **RN201201**

Sirt2 (NM_001008368) Rat Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: Sirt2 (NM_001008368) Rat Untagged Clone
Tag: Tag Free
Symbol: Sirt2
Synonyms: MGC105900
Vector: pCMV6-Entry (PS100001)
E. coli Selection: Kanamycin (25 ug/mL)
Cell Selection: Neomycin
Fully Sequenced ORF: >RN201201 representing NM_001008368
Red=Cloning site **Blue**=ORF **Orange**=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC
GCC**GCGATCGCC**

ATGGACTTCTACGGAATTTATTCACCCAGACCCTGGGCCTGGGTCCCAGAAGGAGCGTCTGCTGGACG
AGCTGACCCTTGAAGGAGTGACACGCTACATGCAGAGCGAGCGCTGTCGAGGGTCATCTGTTTGGTGGG
AGCTGGAATCTCCACATCCGAGGAATCCCTGACTTCCGCTCCCCATCCACTGGCCTCTATGCAAACCTG
GAGAAATACCACCTTCCATACCCAGAGGCCATCTTTGAGATCAGCTACTTCAAGAAACATCCAGAACCTT
TCTTTGCCCTTGCTAAGGAGCTCTATCCTGGGCAGTTCAGCCGACCATCTGCCACTACTTCATCCGCCCT
GCTGAAGGAGAAGGGGCTGCTGCTGCGCTGCTACACGCAGAATATTGACACTCTGGAACGAGTGGCAGGG
CTGGAGCCCCAGGACCTGGTGGAGGCCACGGCACCTTACACATCACACTGTGTCAACACCTCCTGTG
GAAAAGAGTACACGATGAGCTGGATGAAAGAGAAGATCTTCTCAGAAGCAACTCCCAAGTGTGAGAAGTG
TCAGAAATGTGGTAAAGCCGATATCGTGTTCGCTGAGAACCTCCACCGCCTTCTTCTCCTGCATG
CAGTCAGACTTCTCAAAGGTGGACCTCCTCATCATCATGGGCACCTCCCTGCAGGTGCAGCCCTTCGCT
CCCTCATCAGCAAGGCACCACTAGCCACCCACGACTGCTCATTAAACAAGGAGAAGACAGGCCAGACGGA
TCCCTTCCCTGGGATGATGATGGGCTTGGGAGGCGCATGGATTTTGACTCCAAGAAGGCTTACAGGGAC
GTGGCCTGGCTGGGTGACTGTGACCAAGGCTGCCTGGCTCTCGCTGACCTCCTGGGATGGAAGGAGCTGG
AAGACCTTGTCCGGAGGGAGCATGCCAACATAGATGCCAGTCAGGGTACAGGCCCTCAACCCAGCGC
TACCGTCTCCCCTAGAAAGTCCCACCTCCTGCCAAGGAGGCGCCAGGACCAAAGAGAAAGAGGAACAC
TAG

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTTAA

Restriction Sites: SgfI-MluI
ACCN: NM_001008368



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Insert Size:	1053 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).
Reconstitution Method:	<ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	NM_001008368.1 , NP_001008369.1
RefSeq Size:	2070 bp
RefSeq ORF:	1053 bp
Locus ID:	361532
UniProt ID:	Q5R1Q4
Cytogenetics:	1q21
Gene Summary:	<p>NAD-dependent protein deacetylase, which deacetylates internal lysines on histone and alpha-tubulin as well as many other proteins such as key transcription factors (PubMed:17344398). Participates in the modulation of multiple and diverse biological processes such as cell cycle control, genomic integrity, microtubule dynamics, cell differentiation, metabolic networks, and autophagy. Plays a major role in the control of cell cycle progression and genomic stability. Functions in the antephasic checkpoint preventing precocious mitotic entry in response to microtubule stress agents, and hence allowing proper inheritance of chromosomes. Positively regulates the anaphase promoting complex/cyclosome (APC/C) ubiquitin ligase complex activity by deacetylating CDC20 and FZR1, then allowing progression through mitosis. Associates both with chromatin at transcriptional start sites (TSSs) and enhancers of active genes. Plays a role in cell cycle and chromatin compaction through epigenetic modulation of the regulation of histone H4 'Lys-20' methylation (H4K20me1) during early mitosis. Specifically deacetylates histone H4 at 'Lys-16' (H4K16ac) between the G2/M transition and metaphase enabling H4K20me1 deposition by KMT5A leading to ulterior levels of H4K20me2 and H4K20me3 deposition throughout cell cycle, and mitotic S-phase progression. Deacetylates KMT5A modulating KMT5A chromatin localization during the mitotic stress response. Deacetylates also histone H3 at 'Lys-57' (H3K56ac) during the mitotic G2/M transition. During oocyte meiosis progression, may deacetylate histone H4 at 'Lys-16' (H4K16ac) and alpha-tubulin, regulating spindle assembly and chromosome alignment by influencing microtubule dynamics and kinetochore function.</p>

Deacetylates histone H4 at 'Lys-16' (H4K16ac) at the VEGFA promoter and thereby contributes to regulate expression of VEGFA, a key regulator of angiogenesis. Deacetylates alpha-tubulin at 'Lys-40' and hence controls neuronal motility, oligodendroglial cell arbor projection processes and proliferation of non-neuronal cells. Phosphorylation at Ser-368 by a G1/S-specific cyclin E-CDK2 complex inactivates SIRT2-mediated alpha-tubulin deacetylation, negatively regulating cell adhesion, cell migration and neurite outgrowth during neuronal differentiation. Deacetylates PARD3 and participates in the regulation of Schwann cell peripheral myelination formation during early postnatal development and during postinjury remyelination. Involved in several cellular metabolic pathways. Plays a role in the regulation of blood glucose homeostasis by deacetylating and stabilizing phosphoenolpyruvate carboxykinase PCK1 activity in response to low nutrient availability. Acts as a key regulator in the pentose phosphate pathway (PPP) by deacetylating and activating the glucose-6-phosphate G6PD enzyme, and therefore, stimulates the production of cytosolic NADPH to counteract oxidative damage. Maintains energy homeostasis in response to nutrient deprivation as well as energy expenditure by inhibiting adipogenesis and promoting lipolysis. Attenuates adipocyte differentiation by deacetylating and promoting FOXO1 interaction to PPARG and subsequent repression of PPARG-dependent transcriptional activity. Plays a role in the regulation of lysosome-mediated degradation of protein aggregates by autophagy in neuronal cells. Deacetylates FOXO1 in response to oxidative stress or serum deprivation, thereby negatively regulating FOXO1-mediated autophagy (By similarity). Deacetylates a broad range of transcription factors and co-regulators regulating target gene expression. Deacetylates transcriptional factor FOXO3 stimulating the ubiquitin ligase SCF(SKP2)-mediated FOXO3 ubiquitination and degradation (By similarity). Deacetylates HIF1A and therefore promotes HIF1A degradation and inhibition of HIF1A transcriptional activity in tumor cells in response to hypoxia. Deacetylates RELA in the cytoplasm inhibiting NF-kappaB-dependent transcription activation upon TNF-alpha stimulation. Inhibits transcription