

SirT2 (D4S6J) Rabbit mAb

✓ 100 µl
 (10 western blots)



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New 03/13

For Research Use Only. Not For Use In Diagnostic Procedures.

| Applications W Endogenous | Species Cross-Reactivity* H, M, R, Mk | Molecular Wt. 39, 43 kDa | Isotype Rabbit IgG** |
|---------------------------------|--|-----------------------------|-------------------------|
|---------------------------------|--|-----------------------------|-------------------------|

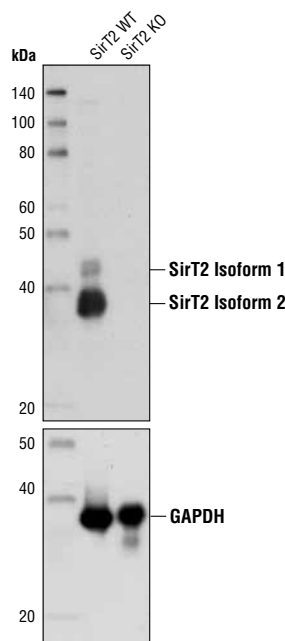
Background: The Silent Information Regulator (SIRT) family of genes is a highly conserved group of genes that encode nicotinamide adenine dinucleotide (NAD)-dependent protein deacetylases, also known as Class III histone deacetylases. The first discovered and best characterized of these genes is *Saccharomyces cerevisiae* SIR2, which is involved in silencing of mating type loci, telomere maintenance, DNA damage response, and cell aging (1). SirT2, a mammalian homolog of Sir2, deacetylates α -tubulin at Lys40 and histone H4 at Lys16 and has been implicated in cytoskeletal regulation and progression through mitosis (2,3). SirT2 protein is mainly cytoplasmic and is associated with microtubules and HDAC6, another tubulin deacetylase (2). Deacetylation of α -tubulin decreases its stability and may be required for proper regulation of cell shape, intracellular transport, cell motility, and cell division (2,4). The abundance and phosphorylation state of SirT2 increase at the G2/M transition of the cell cycle, and SirT2 relocates to chromatin during mitosis when histone H4 Lys16 acetylation levels decrease (3,5). Overexpression of SirT2 prolongs mitosis, while overexpression of the CDC14B phosphatase results in both decreased phosphorylation and abundance of SirT2, allowing for proper mitotic exit (5). Thus, the deacetylation of both histone H4 and α -tubulin by SirT2 may be critical for proper chromatin and cytoskeletal dynamics required for completion of mitosis.

Specificity/Sensitivity: SirT2 (D4S6J) Rabbit mAb recognizes endogenous levels of total SirT2 protein. This antibody does not cross-react with other sirtuin proteins.

Source/Purification: Monoclonal antibody is produced by immunizing animals with a recombinant protein specific to human SirT2 protein.

Background References:

- (1) Guarente, L. (1999) *Nat. Genet.* 23, 281-285.
- (2) North, B.J. et al. (2003) *Mol. Cell* 11, 437-444.
- (3) Vaquero, A. et al. (2006) *Genes Dev.* 20, 1256-1261.
- (4) Nogales, E. (2000) *Annu. Rev. Biochem.* 69, 277-302.
- (5) Dryden, S.C. et al. (2003) *Mol. Cell Biol.* 23, 3173-3185.



Western blot analysis of extracts from SirT2 wild-type (WT) and knockout (KO) mouse brain using SirT2 (D4S6J) Rabbit mAb (upper) or GAPDH (D16H11) XP® Rabbit mAb #5174 (lower). SirT2 WT and KO mouse brain extracts were kindly provided by Dr. Gizem Donmez, Tufts University School of Medicine.

Entrez-Gene ID #22933
 Swiss-Prot Acc. #Q8IXJ6

Storage: Supplied in 10 mM sodium HEPES (pH 7.5), 150 mM NaCl, 100 µg/ml BSA, 50% glycerol and less than 0.02% sodium azide. Store at -20°C. Do not aliquot the antibody.

*Species cross-reactivity is determined by western blot.

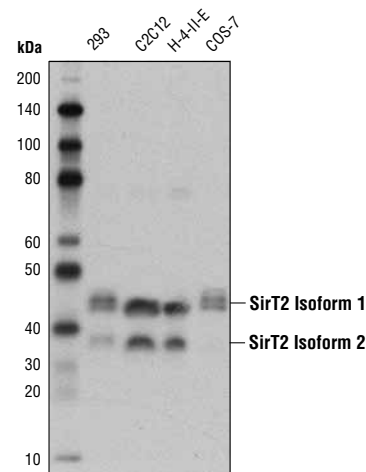
**Anti-rabbit secondary antibodies must be used to detect this antibody.

Recommended Antibody Dilutions:

Western blotting 1:1000

For product specific protocols please see the web page for this product at www.cellsignaling.com.

Please visit www.cellsignaling.com for a complete listing of recommended complementary products.



Western blot analysis of extracts from various cell lines using SirT2 (D4S6J) Rabbit mAb.

IMPORTANT: For western blots, incubate membrane with diluted antibody in 5% w/v BSA, 1X TBS, 0.1% Tween-20 at 4°C with gentle shaking, overnight.

Applications Key: W—Western IP—Immunoprecipitation IHC—Immunohistochemistry ChIP—Chromatin Immunoprecipitation IF—Immunofluorescence F—Flow cytometry E-P—ELISA-Peptide
Species Cross-Reactivity Key: H—human M—mouse R—rat Hm—hamster Mk—monkey Mi—mink C—chicken Dm—D. melanogaster X—Xenopus Z—zebrafish B—bovine
 Dg—dog Pg—pig Sc—S. cerevisiae Ce—C. elegans Hr—horse All—all species expected Species enclosed in parentheses are predicted to react based on 100% homology.