

# Sir2 (yN-19): sc-6666

## BACKGROUND

Telomeric DNA is bound by the transcription regulator Rap1 (repressor activator protein 1, also designated Grf1). In addition to playing a role in silencing the HM mating-type loci, Rap1 is involved in the repression of genes located adjacent to the telomeres, a phenomenon known as telomere position effect (TPE). The silent information regulator proteins Sir2 (also designated Mar1), Sir3 (also designated Mar2, Ste8 or Cmt1) and Sir4 (also designated Ste9, Asd1 or Uth2) form a complex with Rap1. These proteins are essential for TPE silencing and HM structure. Sir1 is essential for silencing the HM mating-type loci, but it has no effect on TPE. Tel1, a member of the PI 3-kinase family and a homolog of the human ataxia telangiectasia protein, is involved in controlling telomere length. Hdf1 (also referred to as Ku-70), a homolog of the mammalian Ku-70, also plays a role in maintaining telomere length.

## REFERENCES

1. Kyrion, G., et al. 1993. Rap1 and telomere structure regulate telomere position effects in *Saccharomyces cerevisiae*. *Genes Dev.* 7: 1146-1159.
2. Palladino, F., et al. 1993. Sir3 and Sir4 proteins are required for the positioning and integrity of yeast telomeres. *Cell* 75: 543-555.
3. Cockell, M., et al. 1995. The carboxy-termini of Sir4 and Rap1 affect Sir3 localization: evidence for a multicomponent complex required for yeast telomeric silencing. *J. Cell Biol.* 129: 909-924.
4. Greenwell, P.W., et al. 1995. Tel1, a gene involved in controlling telomere length in *S. cerevisiae*, is homologous to the human ataxia telangiectasia gene. *Cell* 82: 823-829.
5. Porter, S.E., et al. 1996. The DNA-binding protein Hdf1p (a putative Ku homologue) is required for maintaining normal telomere length in *Saccharomyces cerevisiae*. *Nucl. Acids Res.* 24: 582-585.
6. Tsukamoto, Y., et al. 1997. Silencing factors participate in DNA repair and recombination in *Saccharomyces cerevisiae*. *Nature* 388: 900-903.

## SOURCE

Sir2 (yN-19) is an affinity purified goat polyclonal antibody raised against a peptide mapping at the N-terminus of Sir2 of *Saccharomyces cerevisiae* origin.

## PRODUCT

Each vial contains 200 µg IgG in 1.0 ml of PBS with < 0.1% sodium azide and 0.1% gelatin.

Blocking peptide available for competition studies, sc-6666 P, (100 µg peptide in 0.5 ml PBS containing < 0.1% sodium azide and 0.2% BSA).

## STORAGE

Store at 4° C, **\*\*DO NOT FREEZE\*\***. Stable for one year from the date of shipment. Non-hazardous. No MSDS required.

## RESEARCH USE

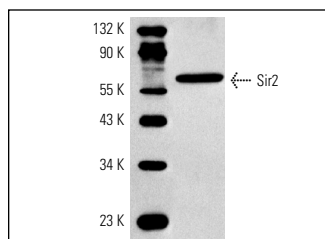
For research use only, not for use in diagnostic procedures.

## APPLICATIONS

Sir2 (yN-19) is recommended for detection of Sir2 of *Saccharomyces cerevisiae* origin by Western Blotting (starting dilution 1:200, dilution range 1:100-1:1000).

Molecular Weight of Sir2: 70 kDa.

## DATA



Sir2 (yN-19): sc-6666. Western blot analysis of Sir2 expression in yeast extract.

## SELECT PRODUCT CITATIONS

1. van Leeuwen, F., et al. 2002. Dot1p modulates silencing in yeast by methylation of the nucleosome core. *Cell* 109: 745-756.
2. Lahue, E., et al. 2005. The *Saccharomyces cerevisiae* Sub2 protein suppresses heterochromatic silencing at telomeres and subtelomeric genes. *Yeast* 22: 537-551.
3. Fry, C.J., et al. 2006. The LRS and SIN domains: two structurally equivalent but functionally distinct nucleosomal surfaces required for transcriptional silencing. *Mol. Cell. Biol.* 26: 9045-9059.
4. Jin, Y., et al. 2007. Simultaneous mutation of methylated lysine residues in Histone H3 causes enhanced gene silencing, cell cycle defects, and cell lethality in *Saccharomyces cerevisiae*. *Mol. Cell. Biol.* 27: 6832-6841.
5. Blank, H.M., et al. 2008. An increase in mitochondrial DNA promotes nuclear DNA replication in yeast. *PLoS Genet.* 4: e1000047.
6. Chaudhuri, S., et al. 2009. Histone H3 Lys 79 methylation is required for efficient nucleotide excision repair in a silenced locus of *Saccharomyces cerevisiae*. *Nucleic Acids Res.* 37: 1690-1700.
7. Mazor, Y., et al. 2009. Developmentally regulated MAPK pathways modulate heterochromatin in *Saccharomyces cerevisiae*. *Nucleic Acids Res.* 37: 4839-4849.
8. Park, J.H. and Ahn, S.H. 2010. IMP dehydrogenase is recruited to the transcription complex through serine 2 phosphorylation of RNA polymerase II. *Biochem. Biophys. Res. Commun.* 392: 588-592.
9. De Vos, D., et al. 2011. Progressive methylation of ageing histones by Dot1 functions as a timer. *EMBO Rep.* 12: 956-962.
10. Sorolla, M.A., et al. 2011. Sir2 is induced by oxidative stress in a yeast model of Huntington disease and its activation reduces protein aggregation. *Arch. Biochem. Biophys.* 510: 27-34.