

SPT16 (H-300): sc-28734

BACKGROUND

Expression of protein-coding genes requires the association of specific transcription factors, RNA polymerase and various accessory factors. These accessory factors are distinguished as either histone acetyltransferases or ATP-dependent chromatin-remodeling enzymes, which include FACT (for facilitates chromatin transcription), and they facilitate transcription initiation on DNA packaged into chromatin. FACT is a chromatin-specific elongation factor required for transcription of chromatin templates, and it specifically interacts with nucleosomes and histone H2A/H2B dimers, to promote nucleosome disassembly upon transcription. FACT represents a complex between SPT16, a homologue of the *Saccharomyces cerevisiae* Spt16/Cdc68 protein, and the high-mobility group (HMG)-1-like protein structure-specific recognition protein-1 (SSRP-1). Similar to other (HMG) domain containing proteins, which are characterized by their ability to bend target DNAs, SSRP1 and the murine ortholog T160, physically interact with serum response factors (SRF) and function as a positive co regulatory proteins involved in modulating SRF-dependent gene expression.

CHROMOSOMAL LOCATION

Genetic locus: SUPT16H (human) mapping to 14q11.2; Supt16h (mouse) mapping to 14 C2.

SOURCE

SPT16 (H-300) is a rabbit polyclonal antibody raised against amino acids 748-1047 mapping at the C-terminus of SPT16 of human origin.

PRODUCT

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

APPLICATIONS

SPT16 (H-300) is recommended for detection of SPT16 of mouse, rat and human origin by Western Blotting (starting dilution 1:200, dilution range 1:100-1:1000), immunoprecipitation [1-2 µg per 100-500 µg of total protein (1 ml of cell lysate)], immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500) and solid phase ELISA (starting dilution 1:30, dilution range 1:30-1:3000).

SPT16 (H-300) is also recommended for detection of SPT16 in additional species, including equine, canine, bovine and porcine.

Suitable for use as control antibody for SPT16 siRNA (h): sc-37875, SPT16 siRNA (m): sc-37876, SPT16 shRNA Plasmid (h): sc-37875-SH, SPT16 shRNA Plasmid (m): sc-37876-SH, SPT16 shRNA (h) Lentiviral Particles: sc-37875-V and SPT16 shRNA (m) Lentiviral Particles: sc-37876-V.

Molecular Weight of SPT: 140 kDa.

Positive Controls: K-562 nuclear extract: sc-2130, HeLa nuclear extract: sc-2120 or Jurkat nuclear extract: sc-2132.

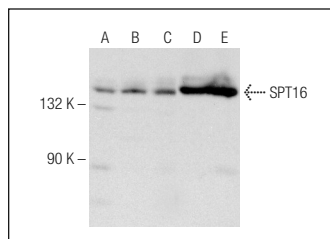
RESEARCH USE

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

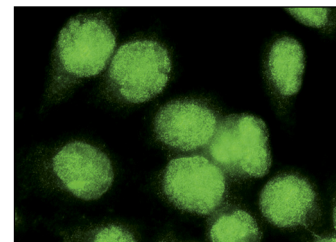
STORAGE

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

DATA



SPT16 (H-300): sc-28734. Western blot analysis of SPT16 expression in HeLa (A), A549 (B), SH-SY5Y (C), K-562 (D) and Jurkat (E) nuclear extracts.



SPT16 (H-300): sc-28734. Immunofluorescence staining of methanol-fixed UV-treated HeLa cells showing nuclear localization.

SELECT PRODUCT CITATIONS

- Vernimmen, D., et al. 2007. Long-range chromosomal interactions regulate the timing of the transition between poised and active gene expression. *EMBO J.* 26: 2041-2051.
- Birch, J.L., et al. 2009. FACT facilitates chromatin transcription by RNA polymerases I and III. *EMBO J.* 28: 854-865.
- Egloff, S., et al. 2009. Chromatin structure is implicated in "late" elongation checkpoints on the U2 snRNA and β -actin genes. *Mol. Cell. Biol.* 29: 4002-4013.
- Gautier, V.W., et al. 2009. *In vitro* nuclear interactome of the HIV-1 Tat protein. *Retrovirology* 6: 47.
- Lachapelle, S., et al. 2011. Proteome-wide identification of WRN-interacting proteins in untreated and nuclease-treated samples. *J. Proteome Res.* 10: 1216-1227.
- Kari, V., et al. 2011. The H2B ubiquitin ligase RNF40 cooperates with SUPT16H to induce dynamic changes in chromatin structure during DNA double-strand break repair. *Cell Cycle* 10: 3495-3504.
- Bender, M.A., et al. 2012. The hypersensitive sites of the murine β -globin locus control region act independently to affect nuclear localization and transcriptional elongation. *Blood* 119: 3820-3827.
- Carvalho, S., et al. 2013. Histone methyltransferase SETD2 coordinates FACT recruitment with nucleosome dynamics during transcription. *Nucleic Acids Res.* 41: 2881-2893.


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Try **SPT16 (D-3): sc-377028** or **SPT16 (H-4): sc-165989**, our highly recommended monoclonal alternatives to SPT16 (H-300).