SignalSilence® HDAC4 siRNA II

#7609 Store at -20°C

☑ 10µM in 300 µl
(100 transfections)

Cell Signaling TECHNOLOGY®

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

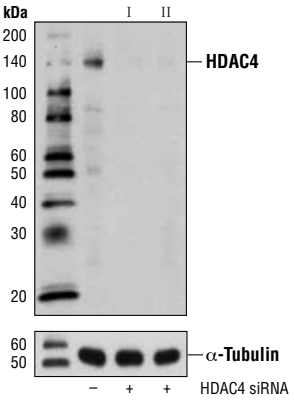
Species Cross-Reactivity: H

Description: SignalSilence® HDAC4 siRNA II from Cell Signaling Technology (CST) allows the researcher to specifically inhibit HDAC4 expression using RNA interference, a method whereby gene expression can be selectively silenced through the delivery of double stranded RNA molecules into the cell. All SignalSilence® siRNA products from CST are rigorously tested in-house and have been shown to reduce target protein expression by western analysis.

Background: Acetylation of the histone tail causes chromatin to adopt an "open" conformation, allowing increased accessibility of transcription factors to DNA. The identification of histone acetyltransferases (HATs) and their large multiprotein complexes has yielded important insights into how these enzymes regulate transcription (1,2). HAT complexes interact with sequence-specific activator proteins to target specific genes. In addition to histones, HATs can acetylate nonhistone proteins, suggesting multiple roles for these enzymes (3). In contrast, histone deacetylation promotes a "closed" chromatin conformation and typically leads to repression of gene activity (4). Mammalian histone deacetylases can be divided into three classes on the basis of their similarity to various yeast deacetylases (5). Class I proteins (HDACs 1, 2, 3 and 8) are related to the yeast Rpd3-like proteins, those in class II (HDACs 4, 5, 6, 7, 9 and 10) are related to yeast Hda1-like proteins, and class III proteins are related to the yeast protein Sir2. Inhibitors of HDAC activity are now being explored as potential therapeutic cancer agents (6,7).

Directions for Use: CST recommends transfection with 100 nM HDAC4 siRNA II 48 to 72 hours prior to cell lysis. For transfection procedure, follow protocol provided by the transfection reagent manufacturer. Please feel free to contact CST with any questions on use.

Quality Control: Oligonucleotide synthesis is monitored base by base through trityl analysis to ensure appropriate coupling efficiency. The oligo is subsequently purified by affinity-solid phase extraction. The annealed RNA duplex is further analyzed by mass spectrometry to verify the exact composition of the duplex. Each lot is compared to the previous lot by mass spectrometry to ensure maximum lot-to-lot consistency.



Western blot analysis of extracts from HeLa cells, transfected with 100 nM SignalSilence® Control siRNA (Unconjugated) #6568 (-), SignalSilence® HDAC4 siRNA I #7595 (+) or SignalSilence® HDAC4 siRNA II (+), using HDAC4 (D15C3) Rabbit mAb #7628 (upper) or α-Tubulin (11H10) Rabbit mAb #2125 (lower). The HDAC4 (D15C3) Rabbit mAb confirms silencing of HDAC4 expression, while the α-Tubulin (11H10) Rabbit mAb is used as a loading control.

Entrez-Gene ID #9759
Swiss-Prot Acc. #P56524

Storage: HDAC4 siRNA II is supplied in RNAse-free water. *Aliquot and store at -20°C.*

Please visit www.cellsignal.com for a complete listing of recommended companion products.

Background References:

(1) Marmorstein, R. (2001) *Cell Mol Life Sci* 58, 693-703.

(2) Gregory, P.D. et al. (2001) *Exp Cell Res* 265, 195-202.

(3) Liu, Y. et al. (2000) *Mol Cell Biol* 20, 5540-53.

(4) Cress, W.D. and Seto, E. (2000) *J Cell Physiol* 184, 1-16.

(5) Gray, S.G. and Ekström, T.J. (2001) *Exp Cell Res* 262, 75-83.

(6) Thiagalingam, S. et al. (2003) *Ann. N.Y. Acad. Sci.* 983, 84-100.

(7) Vigushin, D.M. and Coombes, R.C. (2004) *Curr. Cancer Drug Targets* 4, 205-218.

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.