SignalSilence® Bmi1 siRNA I

#6442 Store at -20°C

☑ 10 µM in 300 µl
(100 transfections)

Cell Signaling TECHNOLOGY®

Orders ■ 877-616-CELL (2355)
orders@cellsignal.com
Support ■ 877-678-TECH (8324)
info@cellsignal.com
Web ■ www.cellsignal.com

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

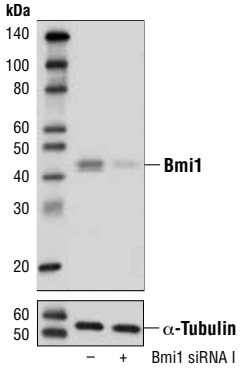
Species Cross-Reactivity: H

Description: SignalSilence® Bmi1 siRNA I from Cell Signaling Technology (CST) allows the researcher to specifically inhibit Bmi1 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: The polycomb group (PcG) of proteins contributes to the maintenance of cell identity, stem cell self-renewal, cell cycle regulation, and oncogenesis by maintaining the silenced state of genes that promote cell lineage specification, cell death, and cell-cycle arrest (1-4). PcG proteins exist in two complexes that cooperate to maintain long-term gene silencing through epigenetic chromatin modifications. The first complex, EED-EZH2, is recruited to genes by DNA-binding transcription factors and methylates histone H3 on Lys27. This histone methyltransferase activity requires the Ezh2, Eed, and Suz12 subunits of the complex (5). Histone H3 methylation at Lys27 facilitates the recruitment of the second complex, PRC1, which ubiquitinylates histone H2A on Lys119 (6). Bmi1 is a component of the PRC1 complex, which together with Ring1 strongly enhances the E3 ubiquitin ligase activity of the Ring2 catalytic subunit (7). Bmi1 plays an important role in the regulation of cell proliferation and senescence through repression of the p16 INK4A and p19 ARF genes and is required for maintenance of adult hematopoietic and neural stem cells (3,4,8-10).

Directions for Use: CST recommends transfection with 100 nM Bmi1 siRNA I 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 (-) or SignalSilence® Bmi1 siRNA I (+), using Bmi1 (D20B7) XP® Rabbit mAb #6964 (upper) or α-Tubulin (11H10) Rabbit mAb #2125 (lower). The Bmi1 (D20B7) XP® Rabbit mAb confirms silencing of Bmi1 expression, while the α-Tubulin (11H10) Rabbit mAb is used as a loading control.

Entrez-Gene ID #648
Swiss-Prot Acc. #P35226

Storage: Bmi1 siRNA I is supplied in RNAse-free water. *Aliquot and store at -20ºC.*

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

Background References:

(1) Boyer, L.A. et al. (2006) *Nature* 441, 349-53.
(2) Lee, T.I. et al. (2006) *Cell* 125, 301-13.
(3) Park, I.K. et al. (2003) *Nature* 423, 302-5.
(4) Molofsky, A.V. et al. (2003) *Nature* 425, 962-7.
(5) Cao, R. and Zhang, Y. (2004) *Mol Cell* 15, 57-67.
(6) Wang, H. et al. (2004) *Nature* 431, 873-8.
(7) Cao, R. et al. (2005) *Mol Cell* 20, 845-54.
(8) Molofsky, A.V. et al. (2005) *Genes Dev* 19, 1432-7.
(9) Jacobs, J.J. et al. (1999) *Nature* 397, 164-8.
(10) Jacobs, J.J. et al. (1999) *Genes Dev* 13, 2678-90.

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.