SANTA CRUZ BIOTECHNOLOGY, INC.

SATB2 siRNA (m): sc-76457

BACKGROUND

SATB2 (special AT-rich sequence-binding protein 2) is a nuclear matrix protein that influences craniofacial formation mechanisms, such as jaw and palate development, and is part of a transcriptional network regulating skeletal development and osteoblast differentiation. Highly expressed in adult and fetal brain, SATB2 contains two CUT DNA-binding domains and one homeobox domain and is closely related to SATB1, a transcriptional repressor. SATB2 is thought to bind to matrix attachment regions (MARs) and regulate MAR-dependent transcription of various genes, including HoxA2 and ATF-4 (CREB-2), involved in skeletal development. Functioning as both a transcriptional activator and repressor, SATB2 can also act as a protein scaffold that can enhance the activity of other DNA-binding proteins. Defects in the gene encoding SATB2 are the cause of cleft palate manifested in conjunction with severe mental retardation.

REFERENCES

1. FitzPatrick, D.R., et al. 2003. Identification of SATB2 as the cleft palate gene on 2q32-q33. Hum. Mol. Genet. 12: 2491-2501.
2. Dobreva, G., et al. 2003. SUMO modification of a novel MAR-binding protein, SATB2, modulates immunoglobulin μ gene expression. Genes Dev. 17: 3048-3061.
3. Britanova, O., et al. 2005. Novel transcription factor SATB2 interacts with matrix attachment region DNA elements in a tissue-specific manner and demonstrates cell-type-dependent expression in the developing mouse CNS. Eur. J. Neurosci. 21: 658-668.
4. Szemes, M., et al. 2006. Isolation and characterization of SATB2, a novel AT-rich DNA-binding protein expressed in development- and cell-specific manner in the rat brain. Neurochem. Res. 31: 237-246.
5. Beaty, T.H., et al. 2006. Analysis of candidate genes on chromosome 2 in oral cleft case-parent trios from three populations. Hum. Genet. 120: 501-518.
6. Britanova, O., et al. 2006. SATB2 haploinsufficiency phenocopies 2q32-q33 deletions, whereas loss suggests a fundamental role in the coordination of jaw development. Am. J. Hum. Genet. 79: 668-678.

CHROMOSOMAL LOCATION

Genetic locus: Satb2 (mouse) mapping to 1 C1.3.

PRODUCT

SATB2 siRNA (m) is a pool of 3 target-specific 19-25 nt siRNAs designed to knock down gene expression. Each vial contains 3.3 nmol of lyophilized siRNA, sufficient for a 10 µM solution once resuspended using protocol below. Suitable for 50-100 transfections. Also see SATB2 shRNA Plasmid (m): sc-76457-SH and SATB2 shRNA (m) Lentiviral Particles: sc-76457-V as alternate gene silencing products.

For independent verification of SATB2 (m) gene silencing results, we also provide the individual siRNA duplex components. Each is available as 3.3 nmol of lyophilized siRNA. These include: sc-76457A, sc-76457B and sc-76457C.

STORAGE AND RESUSPENSION

Store lyophilized siRNA duplex at -20° C with desiccant. Stable for at least one year from the date of shipment. Once resuspended, store at -20° C, avoid contact with RNAses and repeated freeze thaw cycles.

Resuspend lyophilized siRNA duplex in 330 µl of the RNAse-free water provided. Resuspension of the siRNA duplex in 330 µl of RNAse-free water makes a 10 µM solution in a 10 µM Tris-HCl, pH 8.0, 20 mM NaCl, 1 mM EDTA buffered solution.

APPLICATIONS

SATB2 siRNA (m) is recommended for the inhibition of SATB2 expression in mouse cells.

SUPPORT REAGENTS

For optimal siRNA transfection efficiency, Santa Cruz Biotechnology's siRNA Transfection Reagent: sc-29528 (0.3 ml), siRNA Transfection Medium: sc-36868 (20 ml) and siRNA Dilution Buffer: sc-29527 (1.5 ml) are recommended. Control siRNAs or Fluorescein Conjugated Control siRNAs are available as 10 µM in 66 µl. Each contain a scrambled sequence that will not lead to the specific degradation of any known cellular mRNA. Fluorescein Conjugated Control siRNAs include: sc-36869, sc-44239, sc-44240 and sc-44241. Control siRNAs include: sc-37007, sc-44230, sc-44231, sc-44232, sc-44233, sc-44234, sc-44235, sc-44236, sc-44237 and sc-44238.

GENE EXPRESSION MONITORING

SATB2 (SATBA4B10): sc-81376 is recommended as a control antibody for monitoring of SATB2 gene expression knockdown by Western Blotting (starting dilution 1:200, dilution range 1:100-1:1000) or immunofluorescence (starting dilution 1:50, dilution range 1:50-1:500).

To ensure optimal results, the following support reagents are recommended: 1) Western Blotting: use m-IgGκ BP-HRP: sc-516102 or m-IgGκ BP-HRP (Cruz Marker): sc-516102-CM (dilution range: 1:1000-1:10000), Cruz Marker™ Molecular Weight Standards: sc-2035, UltraCruz® Blocking Reagent: sc-516214 and Western Blotting Luminol Reagent: sc-2048. 2) Immunofluorescence: use m-IgGκ BP-FITC: sc-516140 or m-IgGκ BP-PE: sc-516141 (dilution range: 1:50-1:200) with UltraCruz® Mounting Medium: sc-24941 or UltraCruz® Hard-set Mounting Medium: sc-359850.

RT-PCR REAGENTS

Semi-quantitative RT-PCR may be performed to monitor SATB2 gene expression knockdown using RT-PCR Primer: SATB2 (m)-PR: sc-76457-PR (20 µl, 585 bp). Annealing temperature for the primers should be 55-60° C and the extension temperature should be 68-72° C.

SELECT PRODUCT CITATIONS

1. Zhang, J., et al. 2011. Roles of SATB2 in osteogenic differentiation and bone regeneration. Tissue Eng. Part A 17: 1767-1776.

RESEARCH USE

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