SANTA CRUZ BIOTECHNOLOGY, INC.

MTA2 siRNA (h): sc-35983

BACKGROUND

MTA1 (metastasis-associated protein 1) is a component of the NURD (nucleosome remodeling and histone deacetylation) complex, which is associated with ATP-dependent chromatin-remodeling and histone deacetylase activity. MTA1 functions in conjunction with other components of NURD to mediate transcriptional repression as it facilitates the association of repressor molecules with the chromatin. Structurally, MTA1 contains a single SH3-binding motif and a zinc finger domain, along with a region similar to the co-repressor protein N-Cor. MTA1 is normally expressed at low levels in various tissues and is more highly expressed in testis. Overexpression of MTA1 correlates with tumor invasion and metastasis in various carcinomas including colorectal, gastrointestinal and breast carcinomas. Elevation of MTA1 levels in these tumors appears to enhance the metastases to lymph nodes, increase mammary cell motility and potentiate growth, and therefore may be an indicator for assessing the potential malignancies of various tumors. A similar protein, MTA2, also designated MTA1-L1 (MTA1-like protein 1), shares more than 55% sequence homology with MTA1 and is ubiquitously expressed.

REFERENCES

1. Toh, Y., et al. 1994. A novel candidate metastasis-associated gene, MTA1, differentially expressed in highly metastatic mammary adenocarcinoma cell lines. cDNA cloning, expression and protein analyses. J. Biol. Chem. 269: 22958-22963.
2. Toh, Y., et al. 1995. Analysis of the complete sequence of the novel metastasis-associated candidate gene, MTA1, differentially expressed in mammary adenocarcinoma and breast cancer cell lines. Gene 159: 97-104.
3. Toh, Y., et al. 1997. Overexpression of the MTA1 gene in gastrointestinal carcinomas: correlation with invasion and metastasis. Int. J. Cancer 74: 459-463.
4. Paterno, G.D., et al. 1997. cDNA cloning of a novel, developmentally regulated immediate early gene activated by fibroblast growth factor and encoding a nuclear protein. J. Biol. Chem. 272: 25591-25595.
5. Heinzel, T., et al. 1997. A complex containing N-CoR, mSin3 and histone deacetylase mediates transcriptional repression. Nature 387: 43-48.

CHROMOSOMAL LOCATION

Genetic locus: MTA2 (human) mapping to 11q12.3.

PRODUCT

MTA2 siRNA (h) 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 MTA2 shRNA Plasmid (h): sc-35983-SH and MTA2 shRNA (h) Lentiviral Particles: sc-35983-V as alternate gene silencing products.

For independent verification of MTA2 (h) gene silencing results, we also provide the individual siRNA duplex components. Each is available as 3.3 nmol of lyophilized siRNA. These include: sc-35983A, sc-35983B and sc-35983C.

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

MTA2 siRNA (h) is recommended for the inhibition of MTA2 expression in human 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

MTA2 (F-9): sc-55566 is recommended as a control antibody for monitoring of MTA2 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 MTA2 gene expression knockdown using RT-PCR Primer: MTA2 (h)-PR: sc-35983-PR (20 µl, 465 bp). Annealing temperature for the primers should be 55-60° C and the extension temperature should be 68-72° C.

RESEARCH USE

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

PROTOCOLS

See our web site at www.scbt.com for detailed protocols and support products.