SANTA CRUZ BIOTECHNOLOGY, INC.

Vav siRNA (h): sc-29517

BACKGROUND

The Vav gene was originally identified on the basis of its oncogenic activation during the course of gene transfer assays. The major translational product of the Vav proto-oncogene has been identified as a protein containing an array of structural motifs. This protein, known as Vav, Vav1 or p95Vav, contains an N-terminal helix-loop-helix domain and a leucine zipper motif similar to that of Myc family proteins that, if deleted, causes oncogenic activation. In addition, Vav contains an SH2 domain, which could indicate its role as a substrate for tyrosine kinases. Expression of Vav is limited exclusively to cells of hematopoietic origin, including those of the erythroid, lymphoid and myeloid lineages. These results suggest that Vav may represent a new type of signal transduction molecule involved in the transduction of tyrosine phosphorylation signaling into transcriptional events.

CHROMOSOMAL LOCATION

Genetic locus: VAV1 (human) mapping to 19p13.3.

PRODUCT

Vav 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 Vav shRNA Plasmid (h): sc-29517-SH and Vav shRNA (h) Lentiviral Particles: sc-29517-V as alternate gene silencing products.

For independent verification of Vav (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-29517A, sc-29517B and sc-29517C.

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

Vav siRNA (h) is recommended for the inhibition of Vav 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

Vav (D-7): sc-8039 is recommended as a control antibody for monitoring of Vav 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 Vav gene expression knockdown using RT-PCR Primer: Vav (h)-PR: sc-29517-PR (20 µl, 523 bp). Annealing temperature for the primers should be 55-60° C and the extension temperature should be 68-72° C.

SELECT PRODUCT CITATIONS

1. Sekine, Y., et al. 2009. Signal-transducing adaptor protein-2 regulates stromal cell-derived factor-1 α-induced chemotaxis in T cells. J. Immunol. 183: 7966-7974.
2. Bertagnolo, V., et al. 2011. Nuclear proteome analysis reveals a role of Vav1 in modulating RNA processing during maturation of tumoral promyelocytes. J. Proteomics 75: 398-409.
3. Grassilli, S., et al. 2014. High nuclear level of Vav1 is a positive prognostic factor in early invasive breast tumors: a role in modulating genes related to the efficiency of metastatic process. Oncotarget 5: 4320-4336.
4. Grassilli, S., et al. 2016. A network including PU.1, Vav1 and miR-142-3p sustains ATRA-induced differentiation of acute promyelocytic leukemia cells—a short report. Cell. Oncol. 39: 483-489.
5. Vezzali, F., et al. 2018. Vav1 is necessary for PU.1 mediated upmodulation of miR-29b in acute myeloid leukaemia-derived cells. J. Cell. Mol. Med. 22: 3149-3158.
6. Brugnoli, F., et al. 2021. Vav1 sustains the *in vitro* differentiation of normal and tumor precursors to Insulin producing cells induced by all-*trans* retinoic acid (ATRA). Stem Cell Rev. Rep. 17: 673-684.
7. Grassilli, S., et al. 2022. Vav1 selectively down-regulates Akt2 through miR-29b in certain breast tumors with triple negative phenotype. J. Pers. Med. 12: 993.

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.