SANTA CRUZ BIOTECHNOLOGY, INC.

QAPRTase siRNA (h): sc-62914

BACKGROUND

Quinolinate phosphoribosyltransferase (QPRTase) is a major enzyme in the catabolism of quinolinate. Quinolinate is an intermediate in the tryptophan-nicotinamide adenine dinucleotide (NAD) pathway, leading to the production of nicotinic acid, carbon dioxide, and pyrophosphate. Catabolism of quinolinate is vital due to the quinolinate's neurotoxicity. Increased levels of quinolinate have been linked to neurodegenerative symptoms associated with meningitis and AIDS. QAPRTase has a seven-stranded α/β-barrel domain which is similar in structure to the eight-stranded α/β-barrel enzymes. The protein possesses a novel fold in comparison to other members of the PRTase family. This fold comprises a structure combining two domains. The structure is part α/β barrel-like domain, and part α/β N-terminal domain.

REFERENCES

1. Eads, J.C., et al. 1997. A new function for a common fold: the crystal structure of quinolinic acid phosphoribosyltransferase. Structure 5: 47-58.
2. Cao, H., et al. 2002. Quinolinate phosphoribosyltransferase: kinetic mechanism for a type II PRTase. Biochemistry 41: 3520-3528.
3. Kim, M.K., et al. 2003. Crystallization and preliminary X-ray crystallographic analysis of quinolinate phosphoribosyltransferase of *Helicobacter pylori*. Acta Crystallogr. D Biol. Crystallogr. 59: 1265-1266.
4. Connor, S.C., et al. 2004. Development of a multivariate statistical model to predict peroxisome proliferation in the rat, based on urinary 1H-NMR spectral patterns. Biomarkers 9: 364-385.
5. Schwarzenbacher, R., et al. 2004. Crystal structure of a type II quinolic acid phosphoribosyltransferase (TM1645) from *Thermotoga maritima* at 2.50 A resolution. Proteins 55: 768-771.
6. Delaney, J., et al. 2005. Tryptophan-NAD^+ pathway metabolites as putative biomarkers and predictors of peroxisome proliferation. Arch. Toxicol. 79: 208-223.
7. Wang, T., et al. 2006. Structure of Nampt/PBEF/visfatin, a mammalian NAD^+ biosynthetic enzyme. Nat. Struct. Mol. Biol. 13: 661-662.
8. Kim, M.K., et al. 2006. Crystal structure of quinolinic acid phosphoribosyltransferase from *Helicobacter pylori*. Proteins 63: 252-255.

CHROMOSOMAL LOCATION

Genetic locus: QPRT (human) mapping to 16p11.2.

PRODUCT

QAPRTase siRNA (h) is a pool of 2 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 QAPRTase shRNA Plasmid (h): sc-62914-SH and QAPRTase shRNA (h) Lentiviral Particles: sc-62914-V as alternate gene silencing products.

For independent verification of QAPRTase (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-62914A and sc-62914B.

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

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

QAPRTase (ZN-17): sc-100809 is recommended as a control antibody for monitoring of QAPRTase 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 QAPRTase gene expression knockdown using RT-PCR Primer: QAPRTase (h)-PR: sc-62914-PR (20 µl). Annealing temperature for the primers should be 55-60° C and the extension temperature should be 68-72° C.

SELECT PRODUCT CITATIONS

1. Liu, L., et al. 2018. Quantitative analysis of NAD synthesis-breakdown fluxes. Cell Metab. 27: 1067-1080.

RESEARCH USE

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