miR-26A microRNAs bind PTEN mRNA


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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references


Reactome database release: 83

This document contains 1 reaction (see Table of Contents)

https://reactome.org
miR-26A microRNAs bind PTEN mRNA

**Stable identifier:** R-HSA-2318752

**Type:** binding

**Compartments:** cytosol

MIR26A microRNAs, miR-26A1 and miR-26A2, transcribed from genes on chromosome 3 and 12, respectively, bind PTEN mRNA (Huse et al. 2009).

The MIR26A2 locus is frequently amplified in glioma tumors that retain one wild-type PTEN allele. The resulting miR-26A2 overexpression leads to down-regulation of PTEN protein level. Overexpression of miR-26A2 was shown to enhance tumorigenesis and negatively correlates with the loss of heterozygosity at the PTEN locus in a mouse PTEN +/- glioma model, based on monoallelic PTEN loss (Huse et al. 2009, Kim et al. 2010).

**Literature references**


**Editions**

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