miR-205 microRNA binds PTEN mRNA

Carracedo, A., Kriplani, N., Leslie, N., Orlic-Milacic, M., Salmena, L.
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: 78

This document contains 1 reaction (see Table of Contents)

https://reactome.org
miR-205 microRNA binds PTEN mRNA

Stable identifier: R-HSA-8944684

Type: binding

Compartments: cytosol

MicroRNA miR-205-5p, one of the two mature products of miR-205, binds the 3'UTR of the PTEN mRNA, resulting in downregulation of PTEN mRNA and protein levels. miR-205 functions as part of both endonucleolytic and nonendonucleolytic RISCs (Qu et al. 2012, Cai et al. 2013). In addition to PTEN, miR-205 targets another negative regulator of PI3K/AKT signaling - the protein serine/threonine phosphatase PHLPP2 (Cai et al. 2013).

Literature references


Editions

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<td>Carracedo, A., Salmena, L.</td>
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<td>Orlic-Milacic, M.</td>
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