

miR-106 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

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Reactome database release: 88

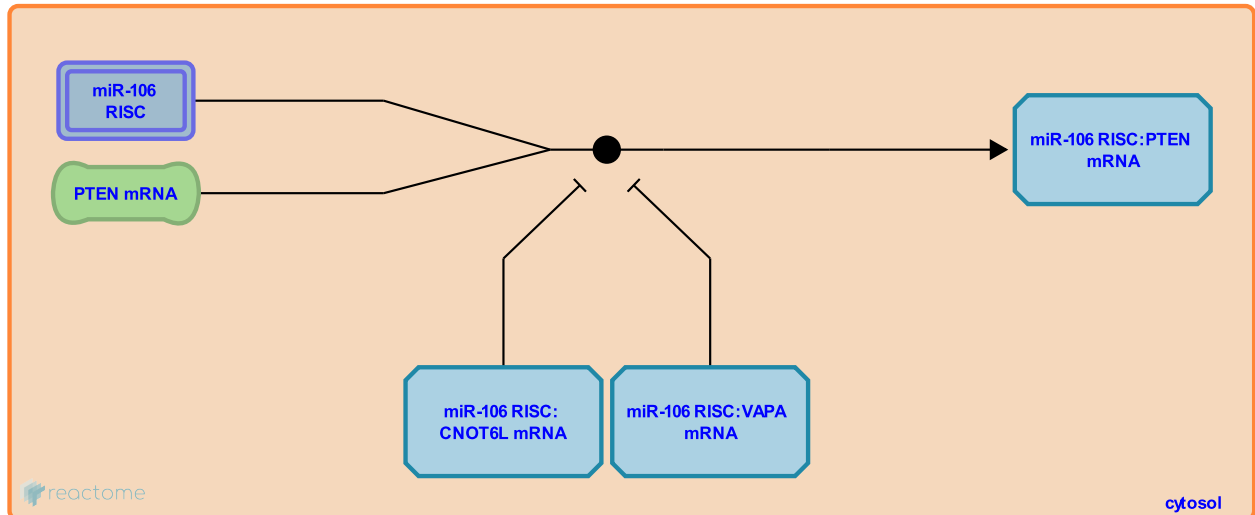
This document contains 1 reaction ([see Table of Contents](#))

miR-106 microRNAs bind PTEN mRNA [↗](#)

Stable identifier: R-HSA-8944632

Type: binding

Compartments: cytosol



MicroRNA miR-106b-5p, one of the two mature products of miR-106b, binds the 3'UTR of PTEN mRNA (Poliseno et al. 2010). miR-106b causes reduction in both PTEN mRNA and protein levels and is thus shown to function as a part of the endonucleolytic RISC. It is possible that miR-106b also functions as a part of the nonendonucleolytic RISC. MicroRNA miR-106a-5p, one of the two mature products of miR-106a, is homologous to miR-106b and binds to the 3'UTR of PTEN mRNA. miR-106a presumably functions in a manner similar to miR-106b (Tay et al. 2011).

Literature references

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Editions

2016-08-11	Authored	Carracedo, A., Salmena, L.
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