

miR-19b microRNA binds PTEN mRNA

Kriplani, N., Leslie, N., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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

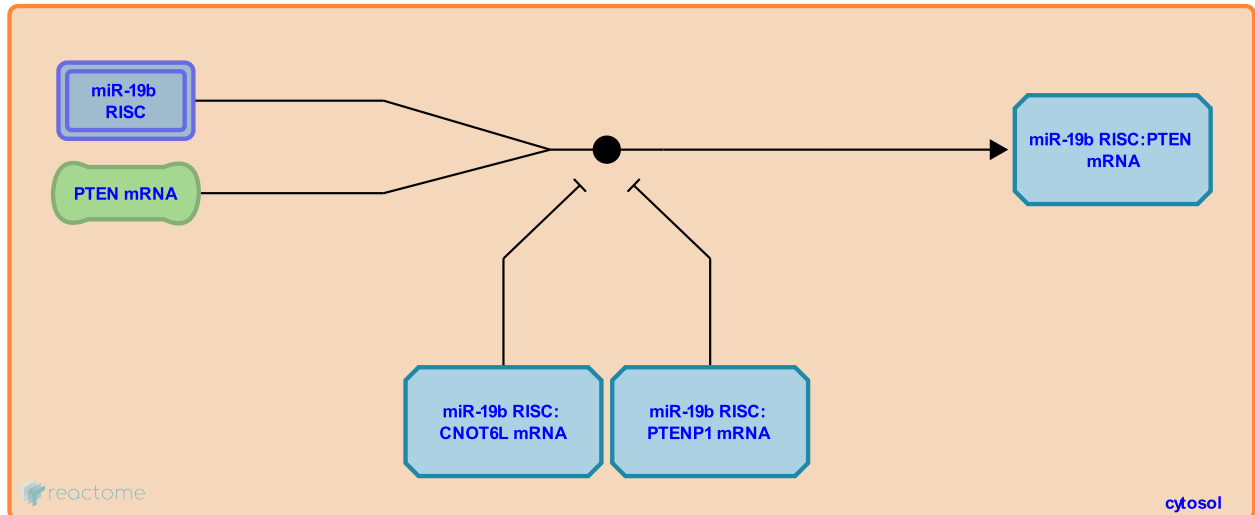
This document contains 1 reaction ([see Table of Contents](#))

miR-19b microRNA binds PTEN mRNA [↗](#)

Stable identifier: R-HSA-8948569

Type: binding

Compartments: cytosol



MicroRNA miR-19b, encoded by two genomic loci, MIR19B1 and MIR19B2, is homologous to miR-19a and also binds to the 3'UTR of PTEN mRNA (Poliseno, Salmena, Zhang et al. 2010). miR-19b microRNA 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-19b microRNA also functions as a part of the nonendonucleolytic RISC.

Literature references

Pandolfi, PP., Carver, B., Haveman, WJ., Poliseno, L., Zhang, J., Salmena, L. (2010). A coding-independent function of gene and pseudogene mRNAs regulates tumour biology. *Nature*, 465, 1033-8. [↗](#)

Editions

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