Removal of miRNA passenger strand

Gopinathrao, G., May, B., Tomari, Y.
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: 73

This document contains 1 reaction (see Table of Contents)

https://reactome.org
Removal of miRNA passenger strand

Stable identifier: R-HSA-210805

Type: omitted

Compartments: cytosol

A short double-stranded RNA is passed from DICER1 to an Argonaute protein and rendered single-stranded by removal and loss of the passenger strand. All Argonautes (AGO1 (EIF2C1), AGO2 (EIF2C2), AGO3 (EIF2C3), AGO4 (EIF2C4)) can remove the passenger strand without cleaving it and most miRNAs are processed in this way. AGO2 (EIF2C2) can cleave the passenger strand of a subset of miRNAs that have no mismatches in the central region (Shin et al. 2008).

RNA helicase A associated with the RISC loading complex can facilitate removal of the passenger strand.

The mechanism that selects which strand is retained as the guide RNA is not well understood in humans. Overhanging nucleotides and strength of base-pairing at each end of the input duplex are observed to influence strand selection.

In cultured cells Argonaute proteins loaded with miRNAs or siRNAs are predominantly located in association with TARBP2 or PRKRA at the cytosolic face of the rough endoplasmic reticulum. In adult non-dividing cells most Argonaute-bound miRNAs are located in low molecular weight complexes but shift to larger complexes containing GW182 in response to phosphoinositide-3-kinase/mTOR signaling.

Literature references


Editions

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