reactome

Dicer cleaves pre-miRNA to yield duplex miRNA

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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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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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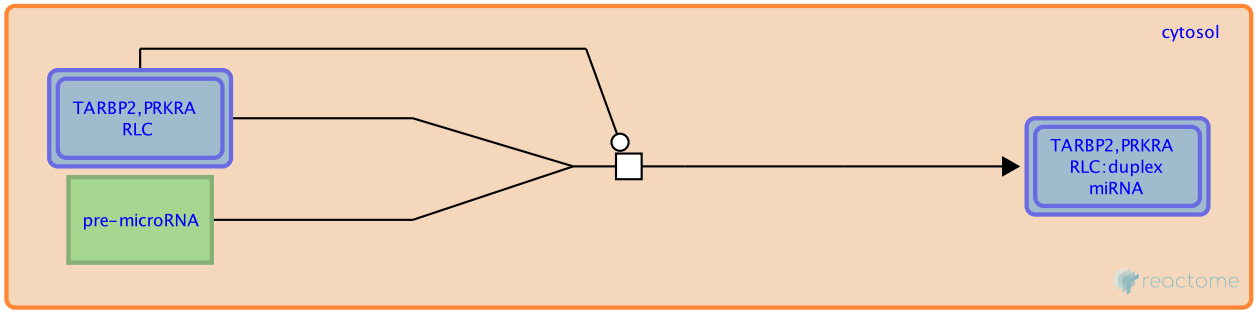
Stable identifier: R-HSA-203862

Type: transition

Compartments: cytosol



Pre-miRNA binds the RISC loading complex (RLC), a complex containing DICER1, AGO2, and TARBP2 (TRBP). Alternative loading complexes contain AGO1, AGO3, or AGO4 rather than AGO2 and PRKRA (PACT) rather than TARBP2. The pre-miRNA substrate has an internal loop and a protruding 3' end created by cleavage by DROSHA:DGCR8. The DICER1:TARBP2 subcomplex or DICER1:PRKRA subcomplex recognizes this structure and the DICER1 component cleaves the pre-miRNA near the loop. The product is a double-stranded RNA of 21-25 nucleotides having 2-nucleotide protrusions at each 3' end. The products have 5' phosphates and 3' hydroxyl groups. Diffusion activity of TARBP2 and PRKRA along duplex RNA may enhance processing by DICER1.

Literature references

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Editions

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