# Dicer cleaves double-stranded RNA to yield double-stranded siRNA

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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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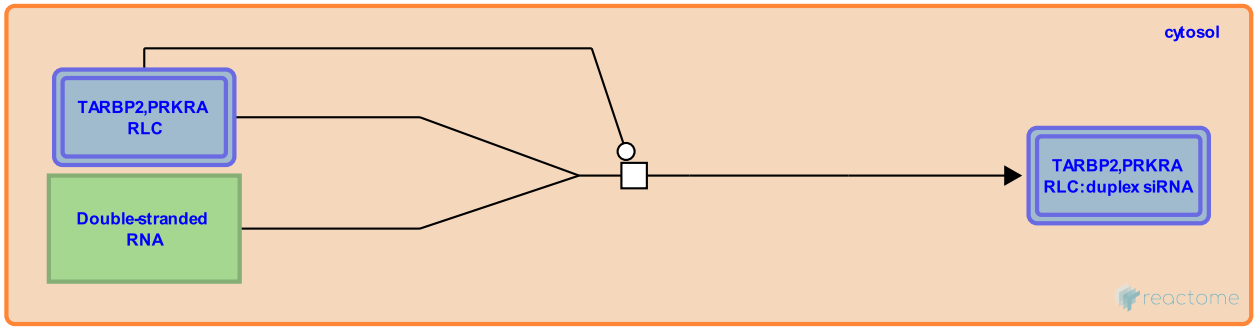
**Stable identifier:** R-HSA-426464

**Type:** transition

**Compartments:** cytosol




Double stranded RNA binds the RISC loading complex and DICER1, an RNase III component of the complex, cleaves double-stranded RNAs to yield short double-stranded RNAs of 21-25 nucleotides, duplex siRNAs (small interfering RNAs). SiRNAs are similar to microRNAs (miRNAs) in their final structure but differ from miRNAs in their source: siRNAs are produced from long double stranded RNAs that originate from viruses, transposable elements, centromeric repeats and other repetitive structures.
The RLC as originally characterized contains DICER1, AGO2, and TARBP2 (TRBP). Alternative RLCs appear to contain other Argonaute proteins (AGO1, AGO3, AGO4) rather than AGO2 and PRKRA rather than TARBP2. 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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| 2009-06-10 | Authored, Edited | May, B. |
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