RNA polymerase II polymerizes primary piRNA transcript

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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


Reactome database release: 83

This document contains 1 reaction (see Table of Contents)
RNA polymerase II polymerizes primary piRNA transcript

Stable identifier: R-MMU-5605301

Type: omitted

Compartments: nucleoplasm

Primary piRNA transcripts originate from multiple copy transposable elements and unique copy non-coding RNAs and mRNAs. As male germ cells progress from fetus to adult, the composition of piRNAs shifts from transposons to unique copy sequences (reviewed in Bortvin 2013). Using computational analyses 161 to 242 piRNA clusters and many other smaller piRNA hotspots have been identified in the mouse genome (Aravin et al. 2008, Rosenkranz and Zischler 2012, Jung et al. 2014).

The A-Myb (Mybl1) transcription factor drives transcription of both piRNA precursors and mRNAs encoding PIWI family proteins (Li et al. 2013).

Literature references


Editions

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