reactome

RUNX1 mRNA translation is inhibited by miR-17, miR-18a, miR-20a, miR-27a, miR-106a, miR-215, miR-302b, miR-378 and miR-675

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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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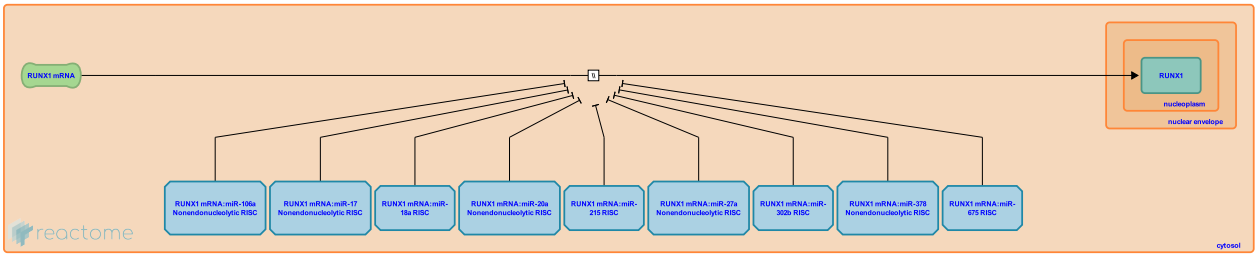
Stable identifier: R-HSA-8935785

Type: omitted

Compartments: cytosol, nucleoplasm



Several microRNAs inhibit RUNX1 mRNA translation without affecting RUNX1 mRNA levels and are thus assumed to function as components of the nonendonucleolytic RISC. These microRNAs include miR 17, miR 20a and miR 106a (Fontana et al. 2007), miR 27a (Ben-Ami et al. 2009), miR 378a (Browne et al. 2016). As RUNX1 directly regulates transcription of the MIR27A gene, RUNX1 and MIR27A constitute a negative feedback loop involved in megakaryocyte differentiation and may regulate the switch between megakaryocytic and erythroid lineages (Ben Ami et al. 2009).

Inhibition of RUNX1 mRNA translation by other microRNAs results in decreased RUNX1 mRNA levels and these microRNAs are therefore assumed to function as components of the endonucleolytic RISC but it is possible that they additionally function as components of nonendonucleolytic RISC. MicroRNAs in this group include miR-18a (Miao et al. 2015), miR-215 (Li et al. 2016), miR-302b (Ge et al. 2014) and miR 675 (Zhuang et al. 2014).

MicroRNA miR 215 binding to the 3'UTR of RUNX1 mRNA inhibits RUNX1 mRNA translation and reduces RUNX1 mRNA levels (Li et al. 2016).

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Editions

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