RHOBTB3 hydrolyzes ATP

Fort, P., Orlic-Milacic, M., Rivero Crespo, F.
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: 78

This document contains 1 reaction (see Table of Contents)
**RHOBTB3 hydrolyzes ATP**

**Stable identifier:** R-HSA-9706399

**Type:** transition

**Compartments:** trans-Golgi network membrane, cytosol

The GTPase domain of RHOBTB3 is considerably divergent and binds and hydrolyzes ATP instead of GTP by virtue of some critical amino acid replacements in the G4 and G5 motifs (Espinosa et al. 2009). Binding of Rab9 increases the ATPase activity (Espinosa et al. 2009).

**Literature references**


**Editions**

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