

# RHOBTB3 hydrolyzes ATP

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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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- 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. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

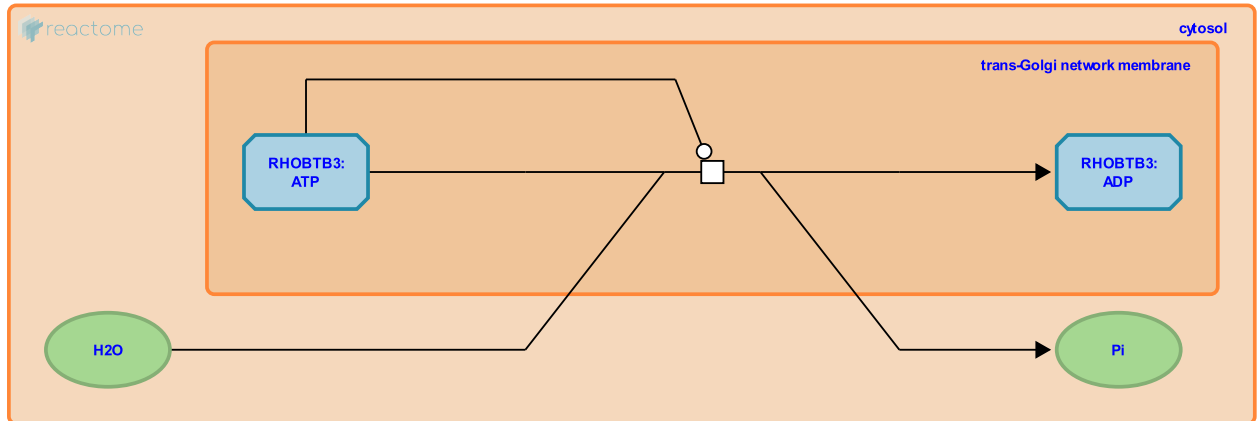
This document contains 1 reaction ([see Table of Contents](#))

## 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

Espinosa, EJ., Calero, M., Sridevi, K., Pfeffer, SR. (2009). RhoBTB3: a Rho GTPase-family ATPase required for endosome to Golgi transport. *Cell*, 137, 938-48. [↗](#)

### Editions

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