

RHOT2 hydrolyzes GTP

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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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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 88

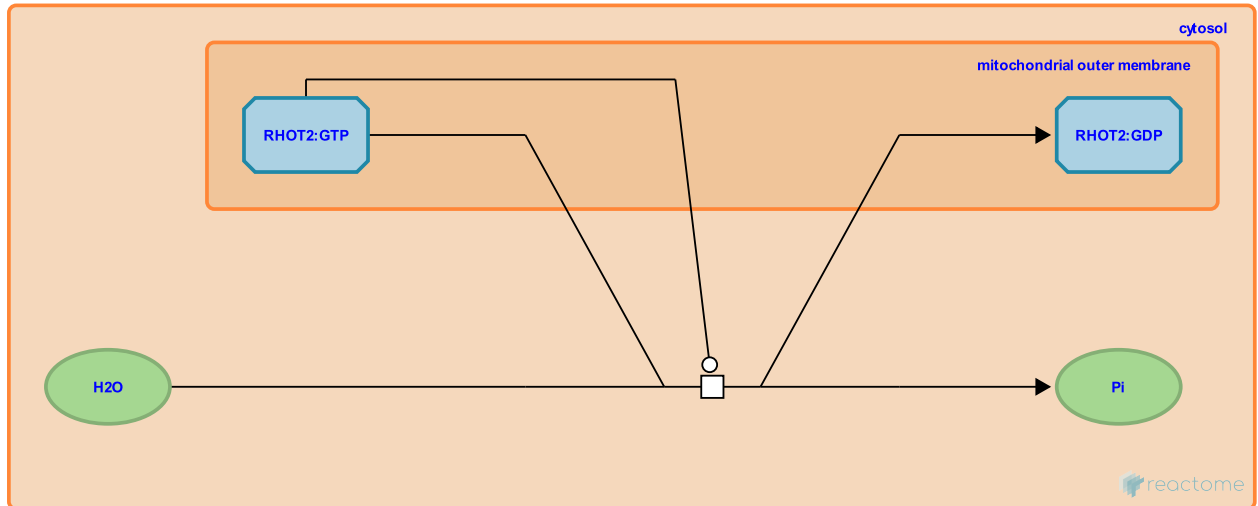
This document contains 1 reaction ([see Table of Contents](#))

RHOT2 hydrolyzes GTP [↗](#)

Stable identifier: R-HSA-9018826

Type: transition

Compartments: cytosol, mitochondrial outer membrane



RHOT2 (Miro2) possesses a high intrinsic GTPase activity and does not require a GTPase activator protein (GAP) to hydrolyze GTP (Peters et al. 2018).

Literature references

Lakey, JH., Kay, L., Soundararajan, M., Eswaran, J., Peters, DT. (2018). Human Miro Proteins Act as NTP Hydrolases through a Novel, Non-Canonical Catalytic Mechanism. *Int J Mol Sci*, 19. [↗](#)

Editions

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