RRAGC,D 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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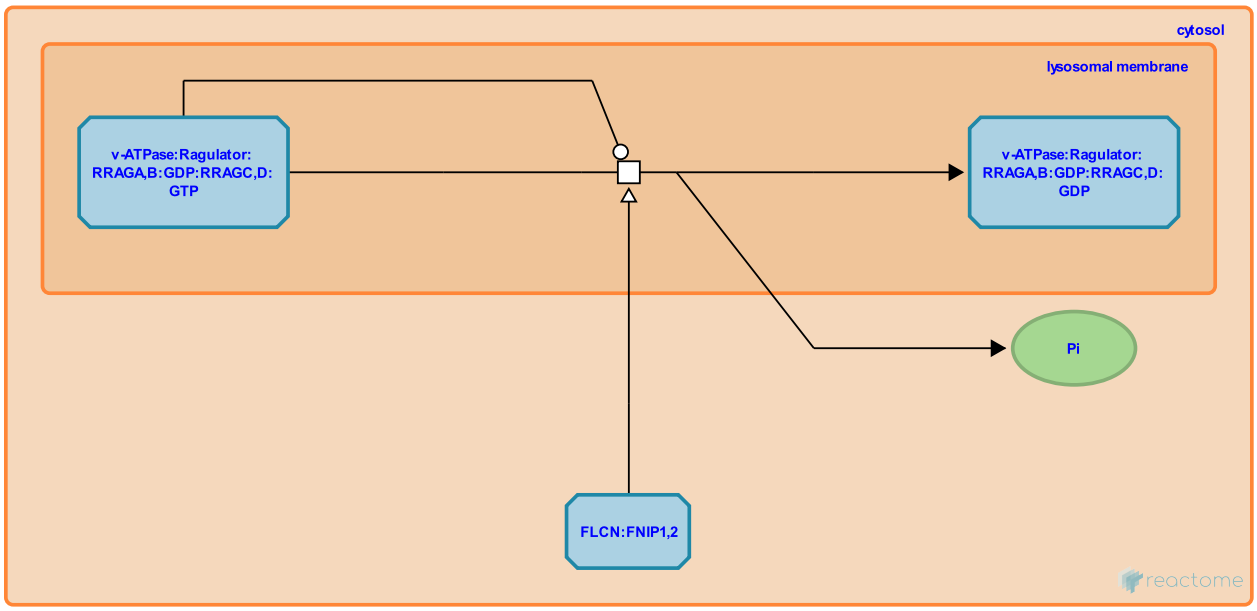
Stable identifier: R-HSA-9645598

Type: transition

Compartments: lysosomal membrane



RRAGC (RagC) and RRAGD (RagD) are guanyl nucleotide-binding proteins that hydrolyze GTP (Tsun et al. 2013, Shen et al. 2017). The GDP-bound form of RRAGC,D is the active form that recruits mTORC1 to the lysosomal membrane (Tsun et al. 2013). RRAGC,D forms a heterodimer with RRAGA,B that has two stable conformations: RRAGA,B:GTP:RRAGC,D:GDP (active) or RRAGA,B:GDP:RRAGC,D:GTP (inactive) (Shen et al. 2017). Folliculin (FLCN) complexed with FNIP1 or FNIP2 interacts with RRAGA (Petit et al. 2013) and acts as a GTPase activator (GAP) for RRAGC:GTP and RRAGD:GTP (Tsun et al. 2013). FLCN is located at the lysosomal membrane during amino acid starvation and in the cytosol during amino acid stimulation (Tsun et al. 2013).

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Editions

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