

Ragulator binds Rag dimers

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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

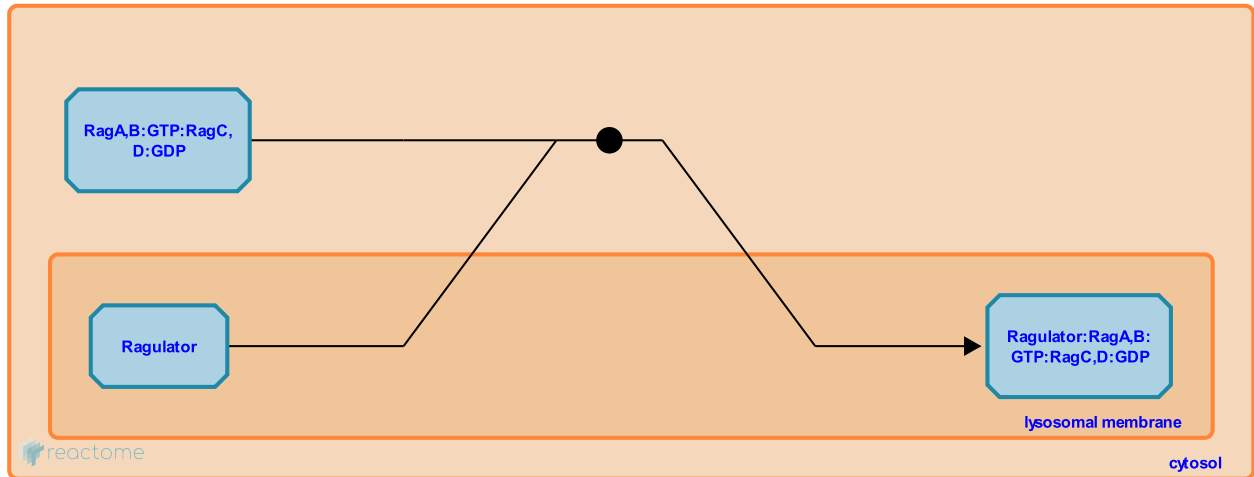
This document contains 1 reaction ([see Table of Contents](#))

Ragulator binds Rag dimers [↗](#)

Stable identifier: R-HSA-5653974

Type: binding

Compartments: cytosol, lysosomal membrane



A complex of LAMTOR1-5, known as Ragulator, interacts with Rag GTPases, recruiting them to lysosomes, an essential step in mTORC1 activation by amino acids (Sancak et al. 2010).

Literature references

Sabatini, DM., Zoncu, R., Sancak, Y., Bar-Peled, L., Nada, S., Markhard, AL. (2010). Ragulator-Rag complex targets mTORC1 to the lysosomal surface and is necessary for its activation by amino acids. *Cell*, 141, 290-303. [↗](#)

Editions

| | | |
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