Formation of Ragulator complex

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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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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. ↗

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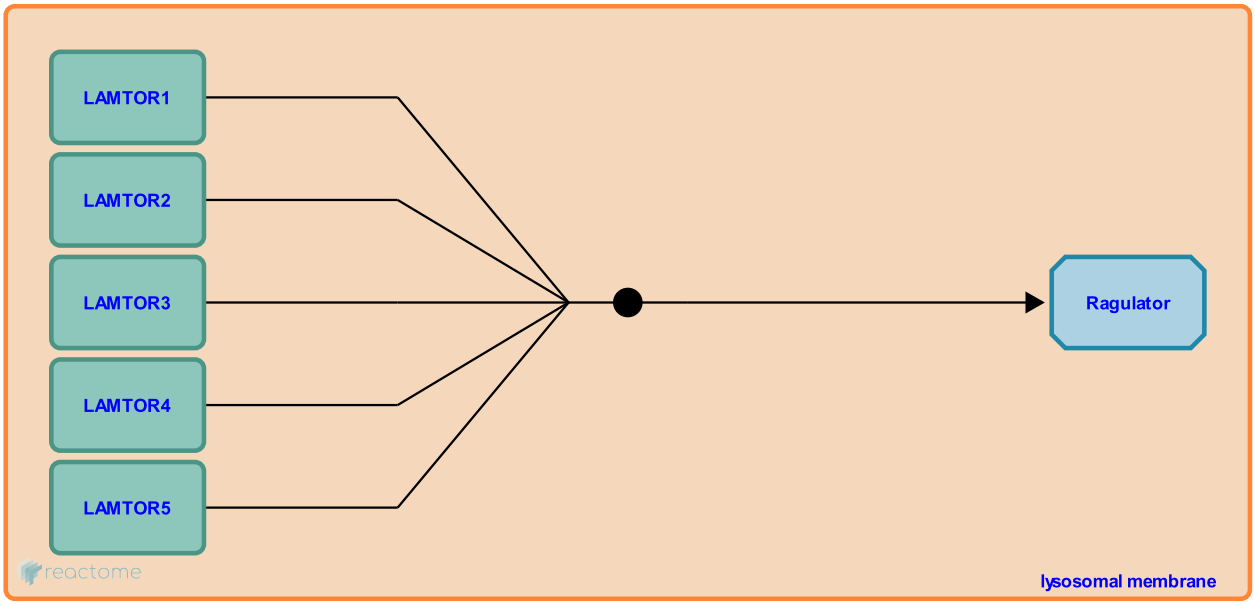
Stable identifier: R-HSA-5653936

Type: binding

Compartments: lysosomal membrane



A complex of LAMTOR1 to 5, known as Ragulator, interacts with Rag GTPases recruiting them to lysosomes, an essential step in mTORC1 activation (Sancak et al. 2010). LAMTOR1 is probably myristoylated and/or palmitoylated to enhance its assocation with the lysosomal surface, acting as a platform for the other members of the compex. Lamtor1 (Nada et al. 2009) and Lamtor2 (Teis et al. 2006) knockout mice exhibit severe growth retardation, severe defects in intracellular organelle organization and embryonic lethality. Partial reduction of LAMTOR2 in humans leads to reduced height (Bohn et al. 2007).

Literature references

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Editions

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