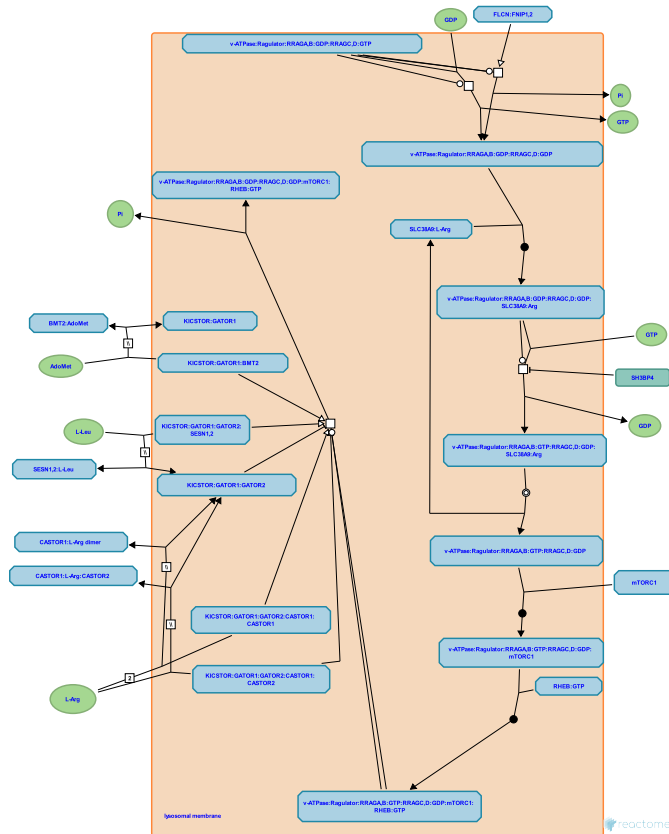


Amino acids regulate mTORC1



European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](https://reactome.org/textbook/).

03/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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 pathway and 12 reactions ([see Table of Contents](#))

SESN1,2 binds L-leucine and dissociates from GATOR2 ↗

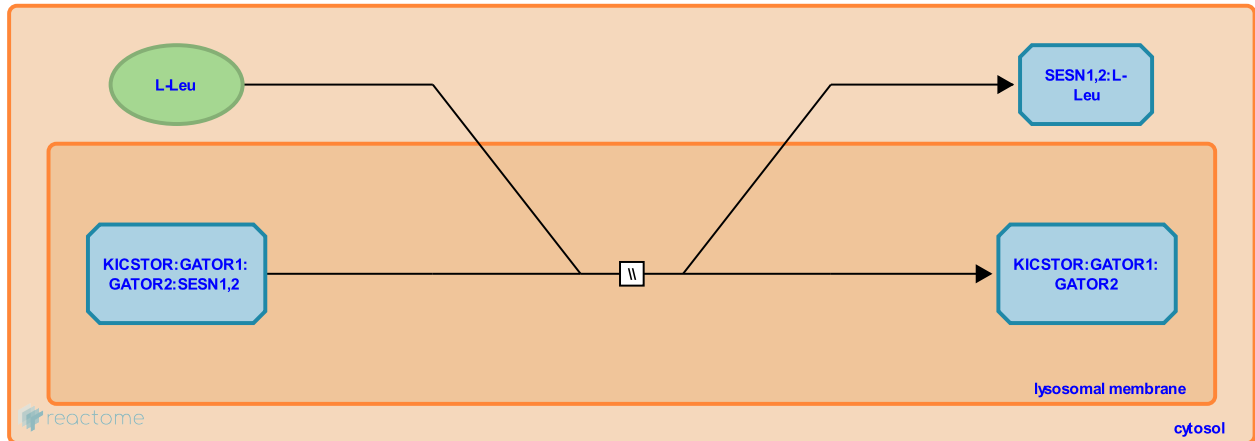
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9639287

Type: omitted

Compartments: lysosomal membrane

Inferred from: [SESN1,2 binds L-leucine and dissociates from GATOR2 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [RRAGC,D hydrolyzes GTP, RRAGC,D exchanges GTP for GDP](#)

CASTOR1 in CASTOR1:CASTOR2 binds L-arginine and dissociates from GATOR2 ↗

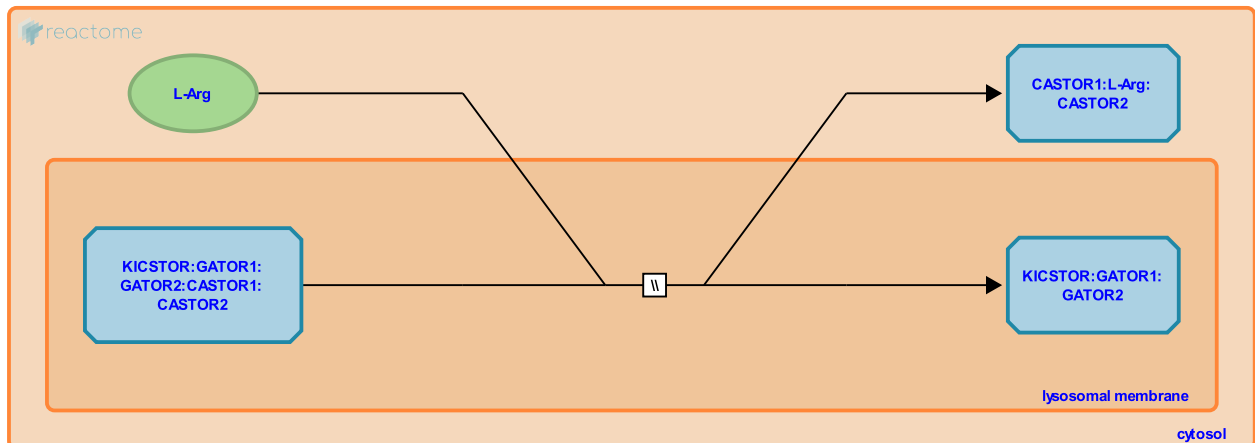
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9640237

Type: omitted

Compartments: lysosomal membrane

Inferred from: [CASTOR1 in CASTOR1:CASTOR2 binds L-arginine and dissociates from GATOR2 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

CASTOR1 homodimer binds L-arginine and dissociates from GATOR2 ↗

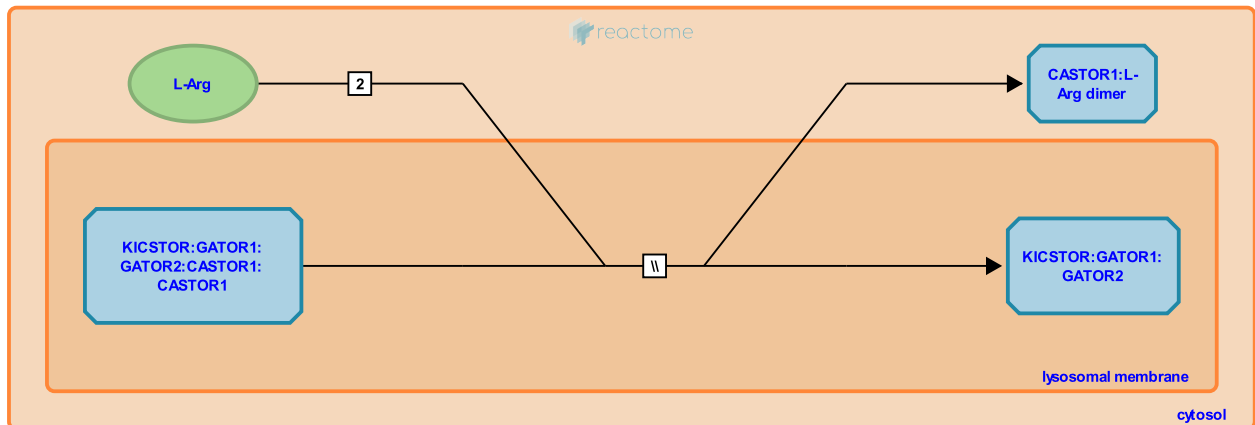
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9657619

Type: omitted

Compartments: lysosomal membrane

Inferred from: [CASTOR1 homodimer binds L-arginine and dissociates from GATOR2 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

BMT2 (SAMTOR) binds S-adenosylmethionine and dissociates from KICSTOR:GATOR1 ↗

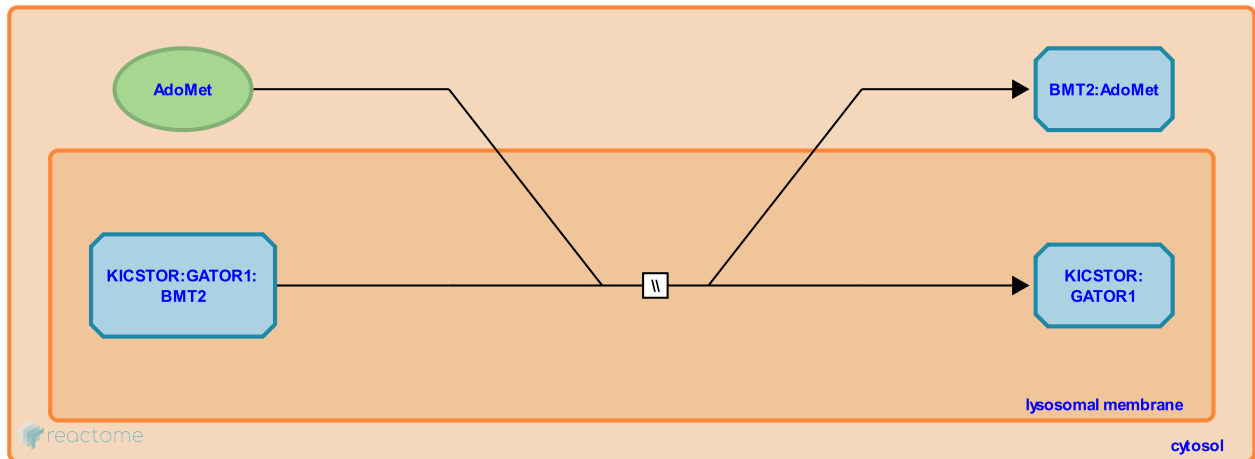
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9640254

Type: omitted

Compartments: lysosomal membrane

Inferred from: [BMT2 \(SAMTOR\) binds S-adenosylmethionine and dissociates from KICSTOR:GATOR1 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

RRAGC,D exchanges GTP for GDP ↗

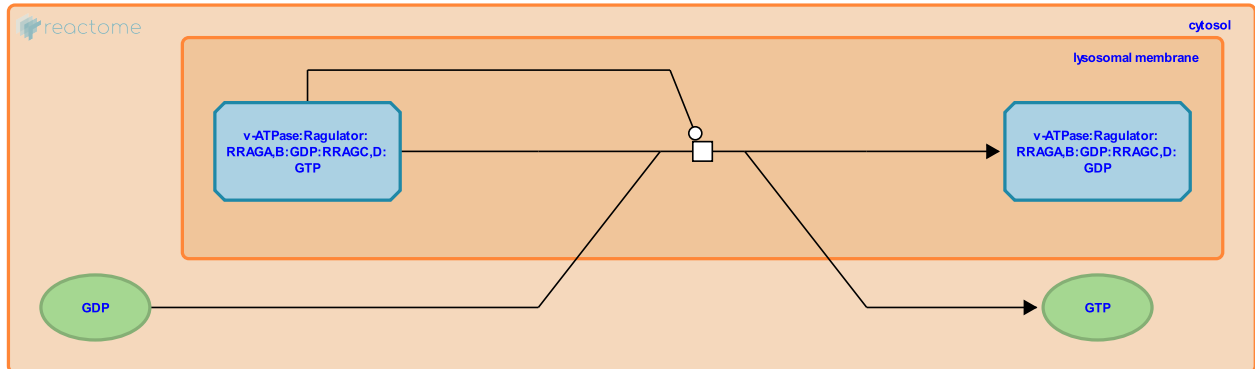
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9639286

Type: transition

Compartments: lysosomal membrane

Inferred from: [RRAGC,D exchanges GTP for GDP \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [SESN1,2 binds L-leucine and dissociates from GATOR2](#)

Followed by: [v-ATPase:Ragulator:RagA,B:GDP:RagC,D:GDP binds SLC38A9:Arginine](#)

RRAGC,D hydrolyzes GTP ↗

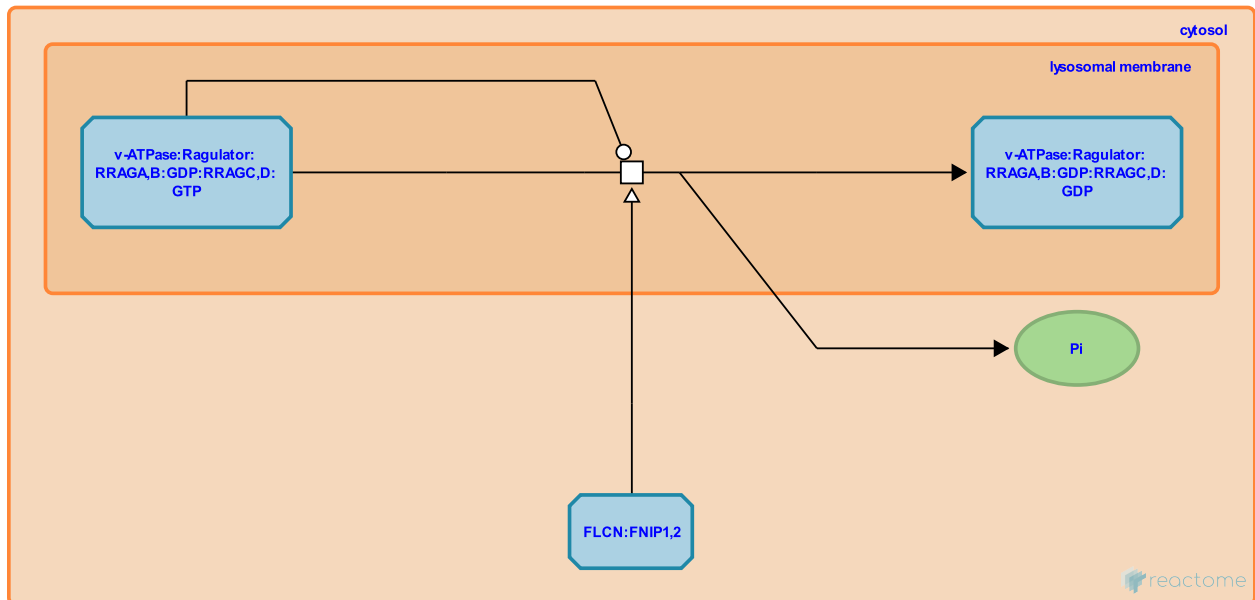
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9645598

Type: transition

Compartments: lysosomal membrane

Inferred from: [RRAGC,D hydrolyzes GTP \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [SESN1,2 binds L-leucine and dissociates from GATOR2](#)

v-ATPase:Ragulator:RagA,B:GDP:RagC,D:GDP binds SLC38A9:Arginine ↗

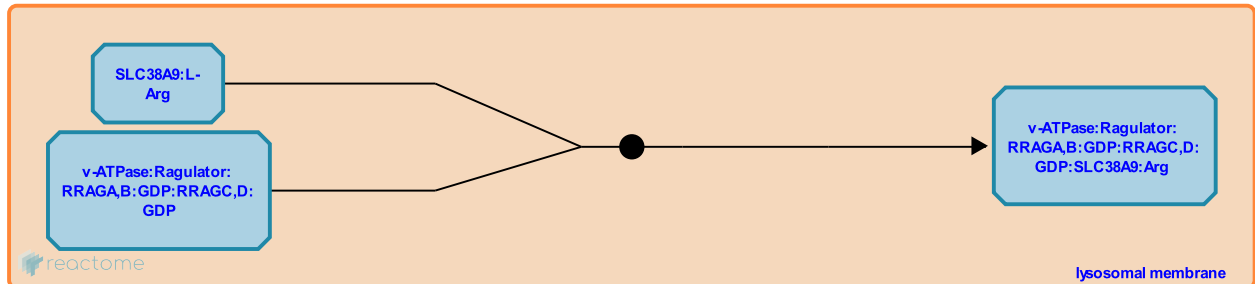
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9640175

Type: binding

Compartments: lysosomal membrane

Inferred from: [v-ATPase:Ragulator:RagA,B:GDP:RagC,D:GDP binds SLC38A9:Arginine \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [RRAGC,D exchanges GTP for GDP](#)

Followed by: [RRAGA,B exchanges GDP for GTP](#)

RRAGA,B exchanges GDP for GTP ↗

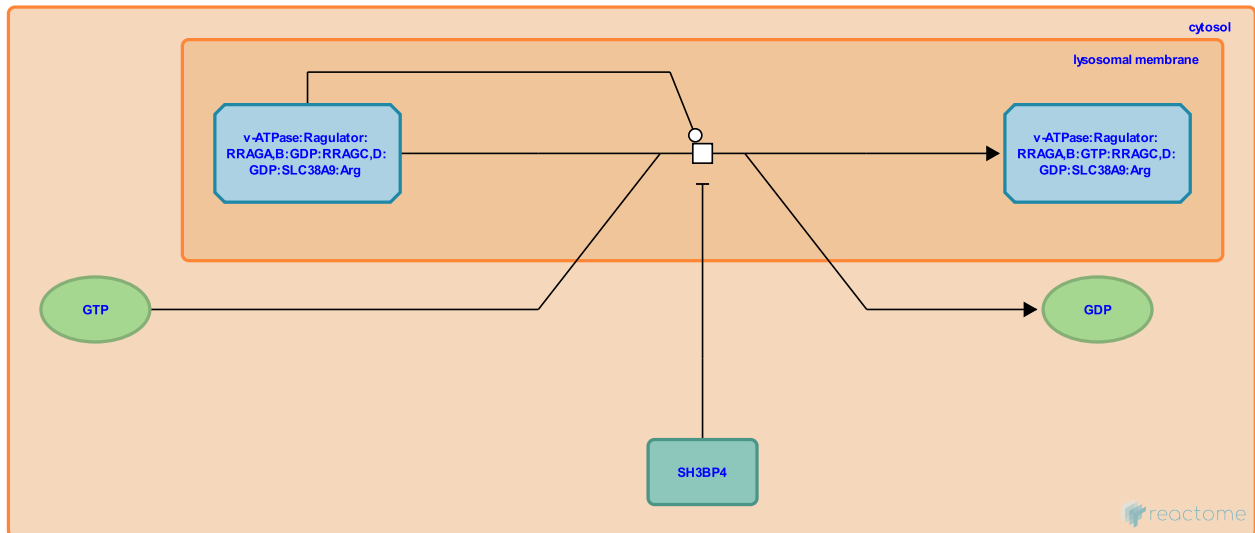
Location: Amino acids regulate mTORC1

Stable identifier: R-CFA-9640167

Type: transition

Compartments: lysosomal membrane

Inferred from: RRAGA,B exchanges GDP for GTP (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: v-ATPase:Ragulator:RagA,B:GDP:RagC,D:GDP binds SLC38A9:Arginine

Followed by: v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP:SLC38A9:Arginine dissociates yielding v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP and SLC38A9:Arginine

v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP:SLC38A9:Arginine dissociates yielding v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP and SLC38A9:Arginine ↗

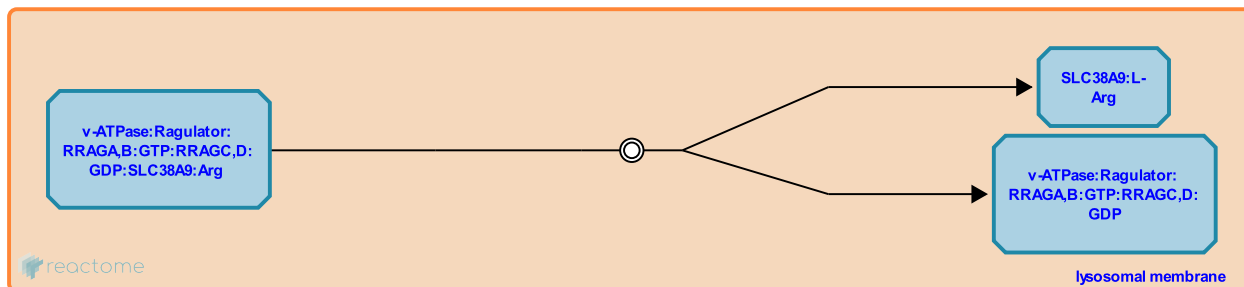
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9640168

Type: dissociation

Compartments: lysosomal membrane

Inferred from: [v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP:SLC38A9:Arginine dissociates yielding v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP and SLC38A9:Arginine \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [RRAGA,B exchanges GDP for GTP](#)

Followed by: [v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP binds mTORC1](#)

v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP binds mTORC1 ↗

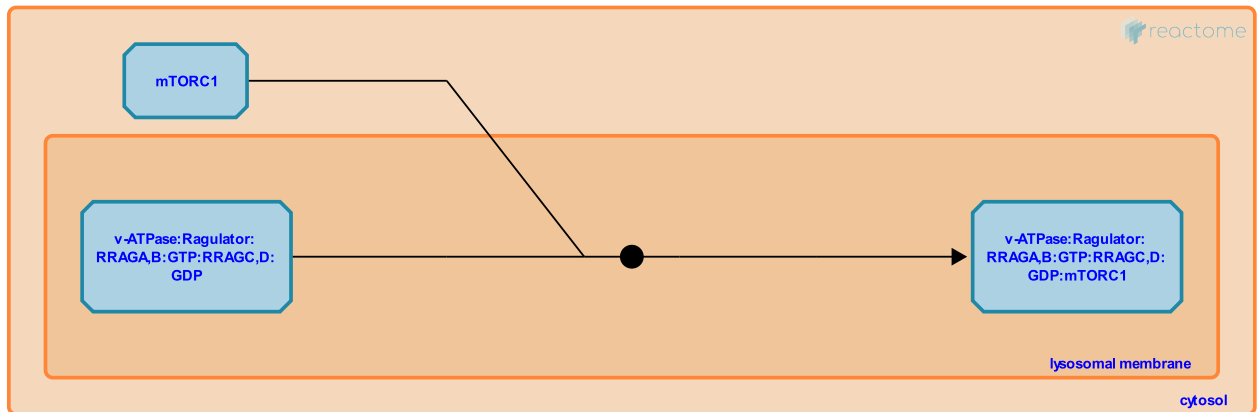
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9645608

Type: binding

Compartments: lysosomal membrane

Inferred from: [v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP binds mTORC1 \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP:SLC38A9:Arginine dissociates yielding v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP and SLC38A9:Arginine](#)

Followed by: [mTORC1 binds RHEB:GTP](#)

mTORC1 binds RHEB:GTP ↗

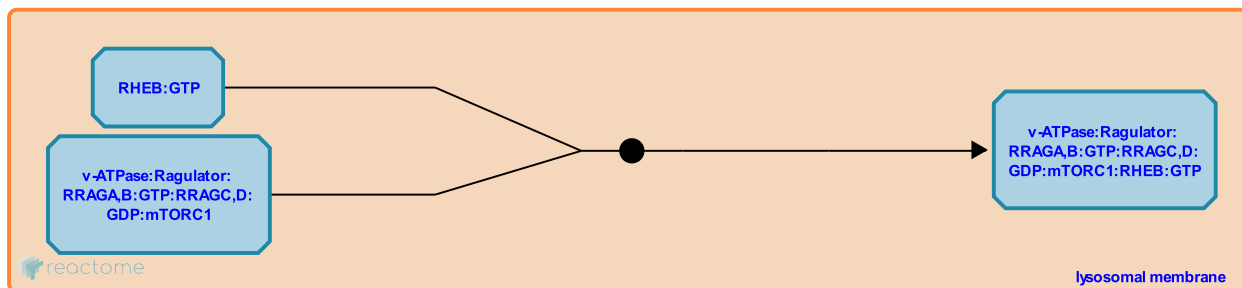
Location: [Amino acids regulate mTORC1](#)

Stable identifier: R-CFA-9646468

Type: binding

Compartments: lysosomal membrane

Inferred from: [mTORC1 binds RHEB:GTP \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](#) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP binds mTORC1](#)

RRAGA,B hydrolyzes GTP ↗

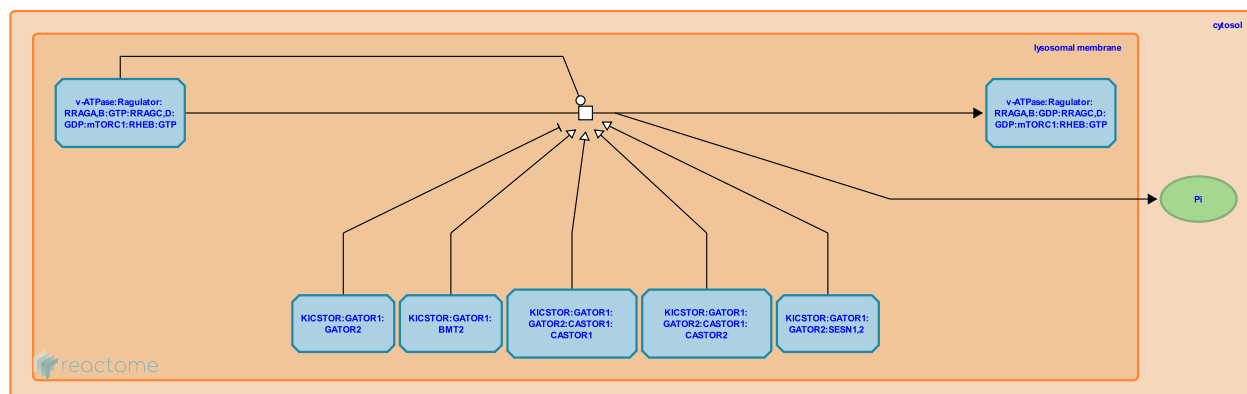
Location: Amino acids regulate mTORC1

Stable identifier: R-CFA-9640195

Type: transition

Compartments: lysosomal membrane

Inferred from: RRAGA,B hydrolyzes GTP (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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↗ v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP:SLC38A9:Arginine dissociates yielding v-ATPase:Ragulator:RRAGA,B:GTP:RRAGC,D:GDP and SLC38A9:Arginine	11
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