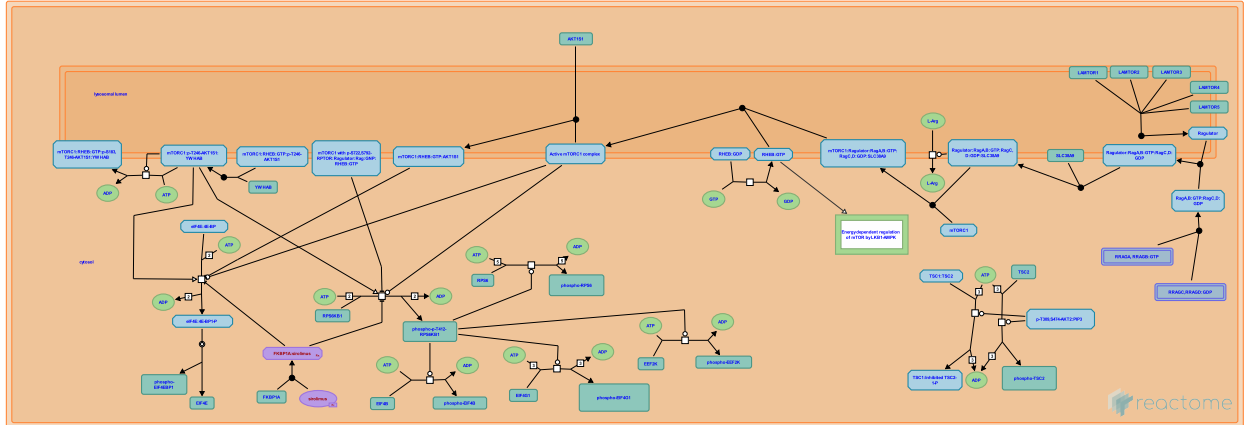# MTOR signalling

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

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.

29/04/2024

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. ↗
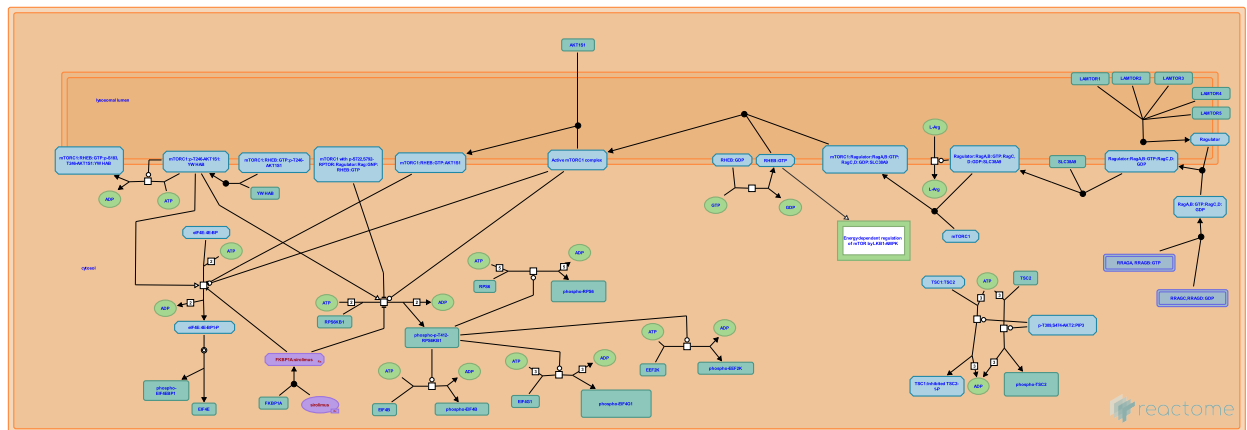
Reactome database release: 88

This document contains 4 pathways and 11 reactions (see Table of Contents)

MTOR signalling ↗

Stable identifier: R-SSC-165159

Inferred from: MTOR signalling (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.
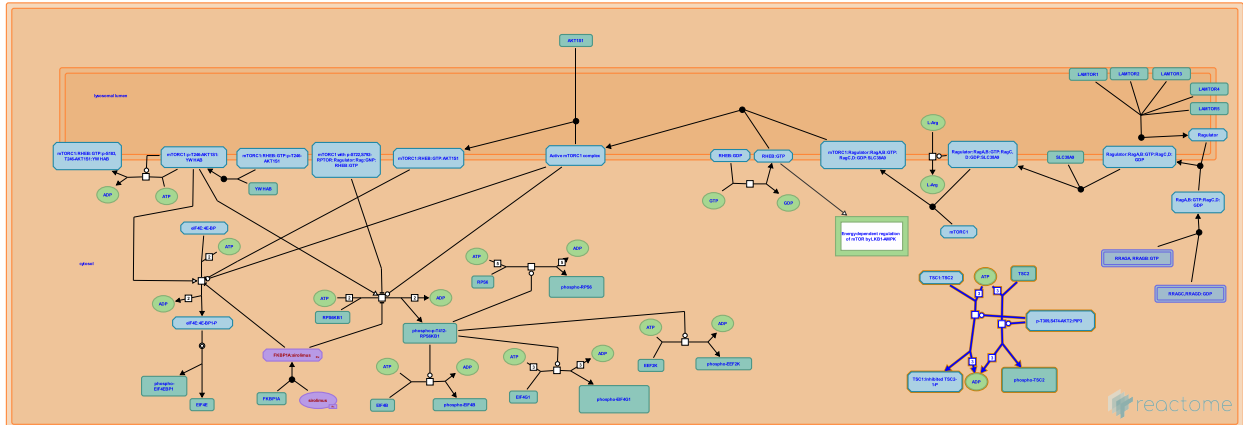
More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Inhibition of TSC complex formation by PKB ↗

Location: MTOR signalling

Stable identifier: R-SSC-165181

Inferred from: Inhibition of TSC complex formation by PKB (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
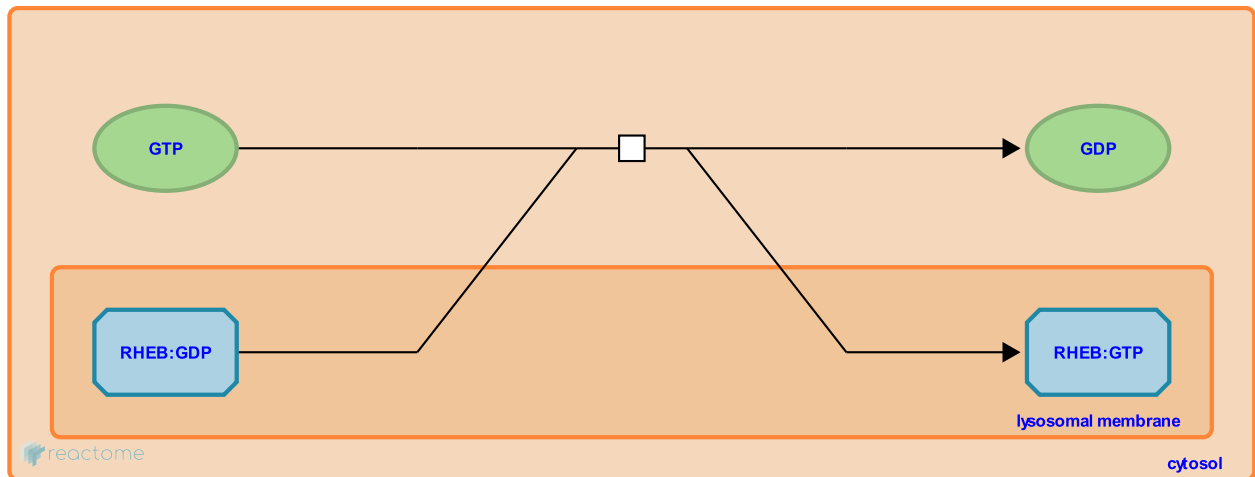
GTP loading by Rheb ↗

Location: MTOR signalling

Stable identifier: R-SSC-165195

Type: transition

Compartments: cytosol, lysosomal membrane

Inferred from: GTP loading by Rheb (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: Formation of active mTORC1 complex
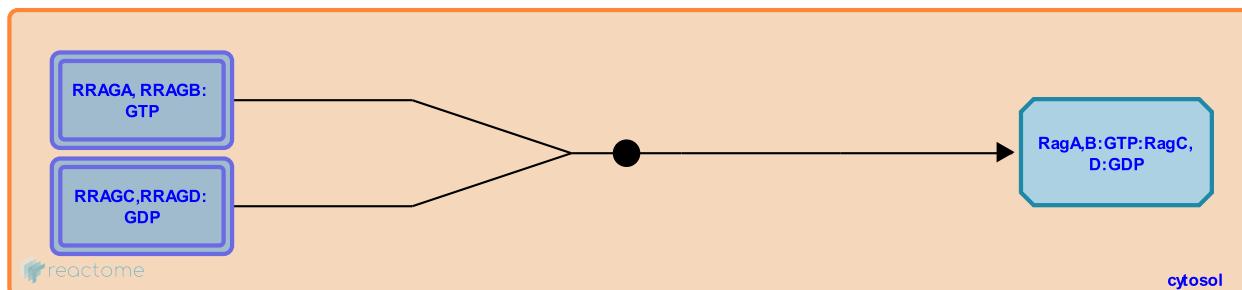
Rag dimer formation ↗

Location: MTOR signalling

Stable identifier: R-SSC-5653957

Type: binding

Compartments: cytosol

Inferred from: Rag dimer formation (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: Ragulator binds Rag dimers

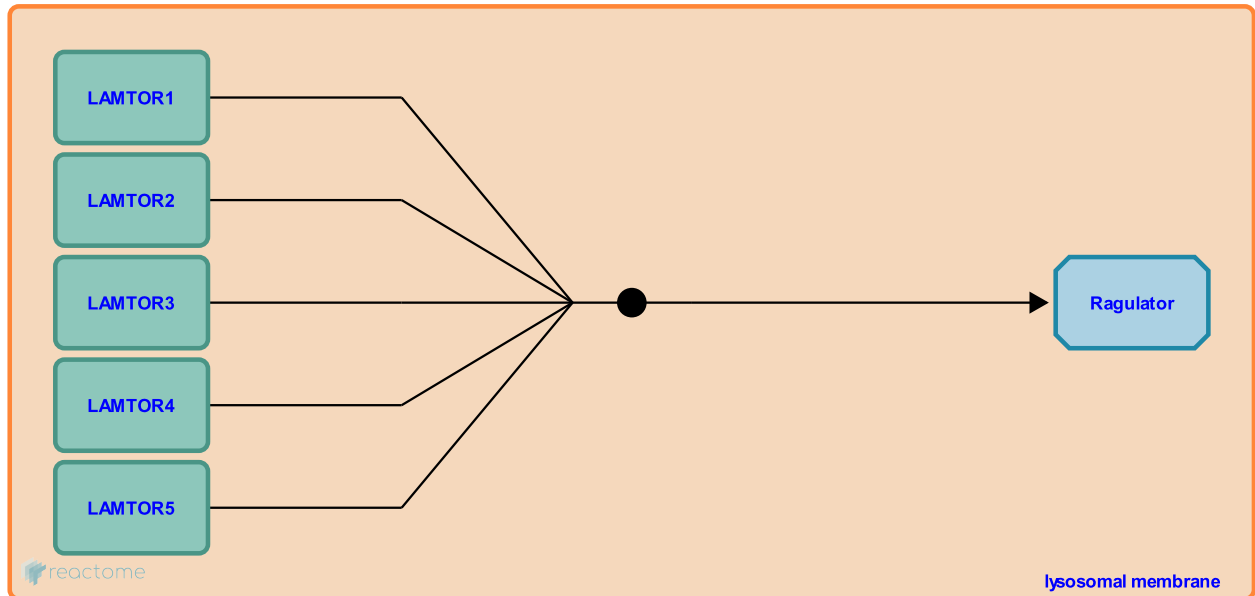## Formation of Ragulator complex ↗

Location: MTOR signalling

Stable identifier: R-SSC-5653936

Type: binding

Compartments: lysosomal membrane

Inferred from: Formation of Ragulator complex (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: Ragulator binds Rag dimers

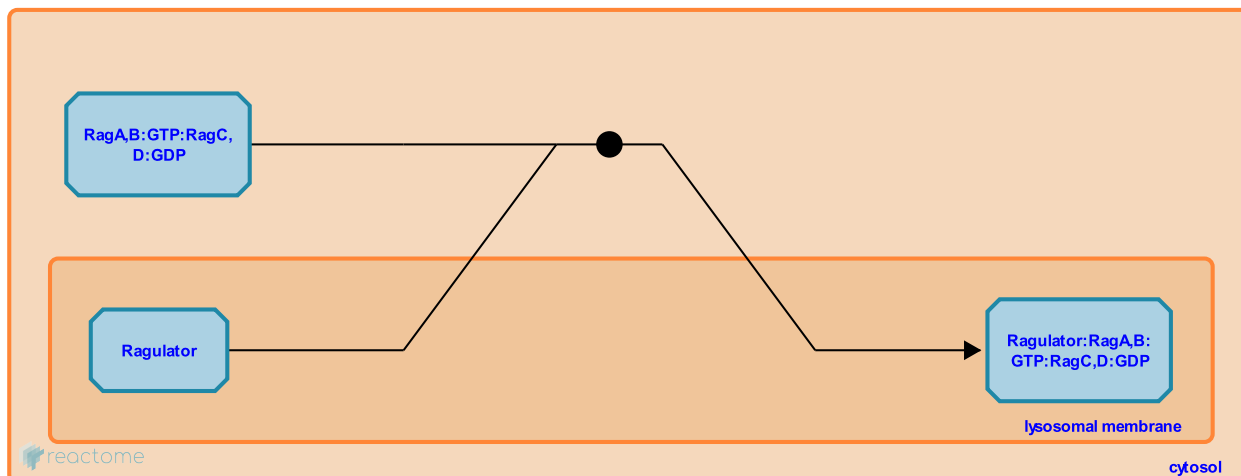# Ragulator binds Rag dimers ↗

Location: MTOR signalling

Stable identifier: R-SSC-5653974

Type: binding

Compartments: cytosol, lysosomal membrane

Inferred from: Ragulator binds Rag dimers (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: Formation of Ragulator complex, Rag dimer formation

Followed by: SLC38A9 binds Ragulator:Rag dimers
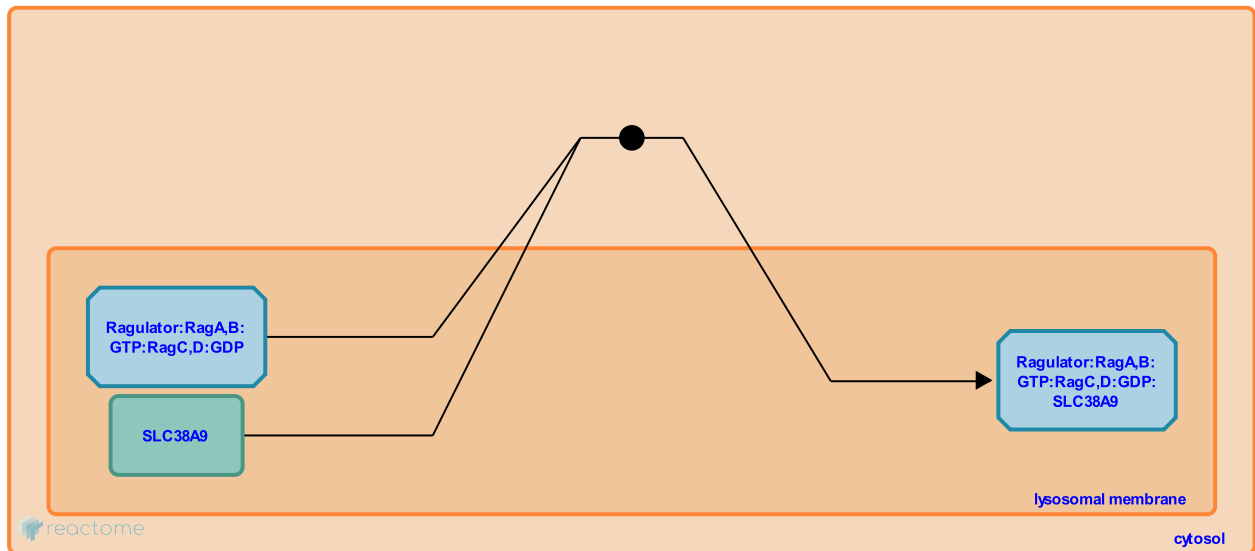
SLC38A9 binds Ragulator:Rag dimers ↗

Location: MTOR signalling

Stable identifier: R-SSC-8952716

Type: binding

Compartments: cytosol, lysosomal membrane

Inferred from: SLC38A9 binds Ragulator:Rag dimers (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: Ragulator binds Rag dimers

Followed by: Ragulator:Rag dimers:SLC38A9 bind mTORC1, SLC38A9 transports L-Arg from lysosomal lumen to cytosol

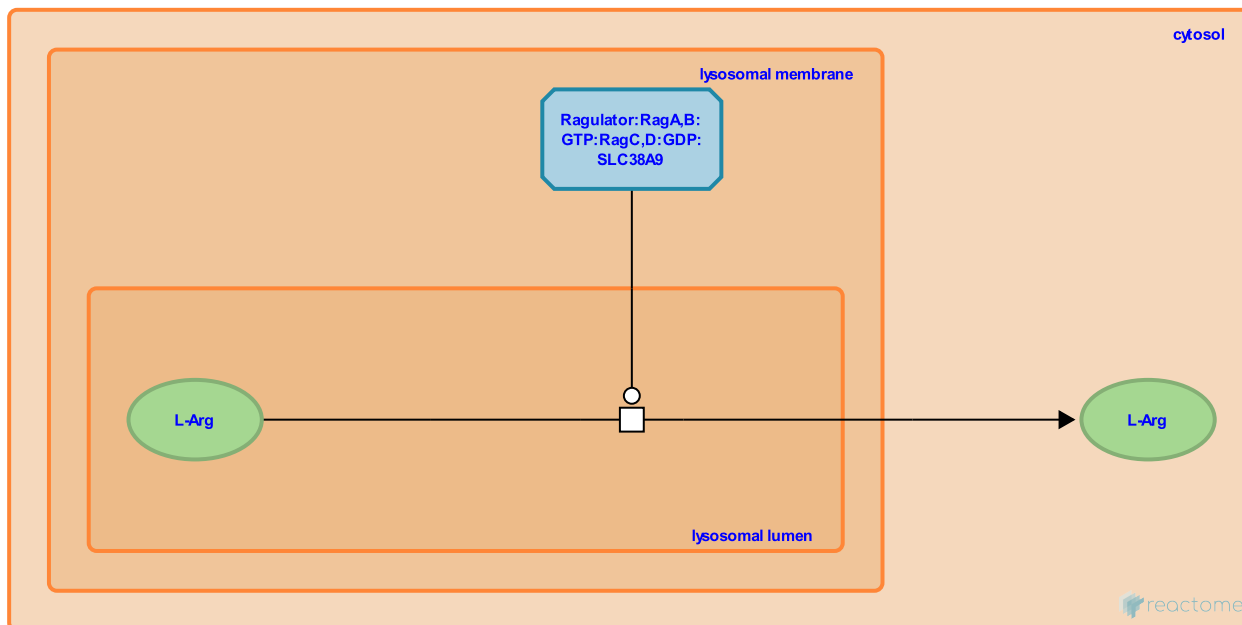# SLC38A9 transports L-Arg from lysosomal lumen to cytosol ↗

Location: MTOR signalling

Stable identifier: R-SSC-8952726

Type: transition

Compartments: lysosomal lumen, cytosol, lysosomal membrane

Inferred from: SLC38A9 transports L-Arg from lysosomal lumen to cytosol (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: SLC38A9 binds Ragulator:Rag dimers

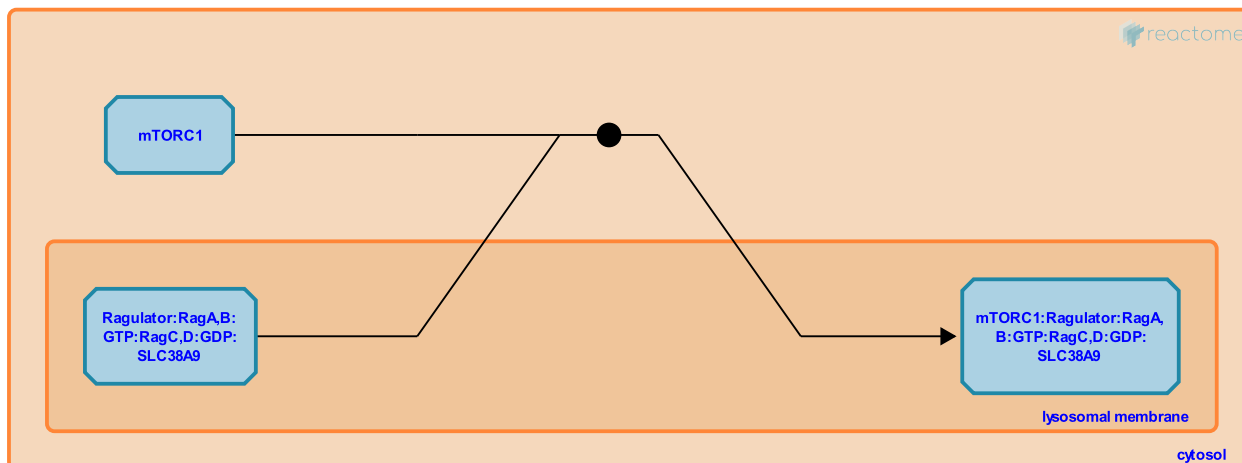# Ragulator:Rag dimers:SLC38A9 bind mTORC1 ↗

Location: MTOR signalling

Stable identifier: R-SSC-5653968

Type: binding

Compartments: cytosol, lysosomal membrane

Inferred from: Ragulator:Rag dimers:SLC38A9 bind 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: SLC38A9 binds Ragulator:Rag dimers

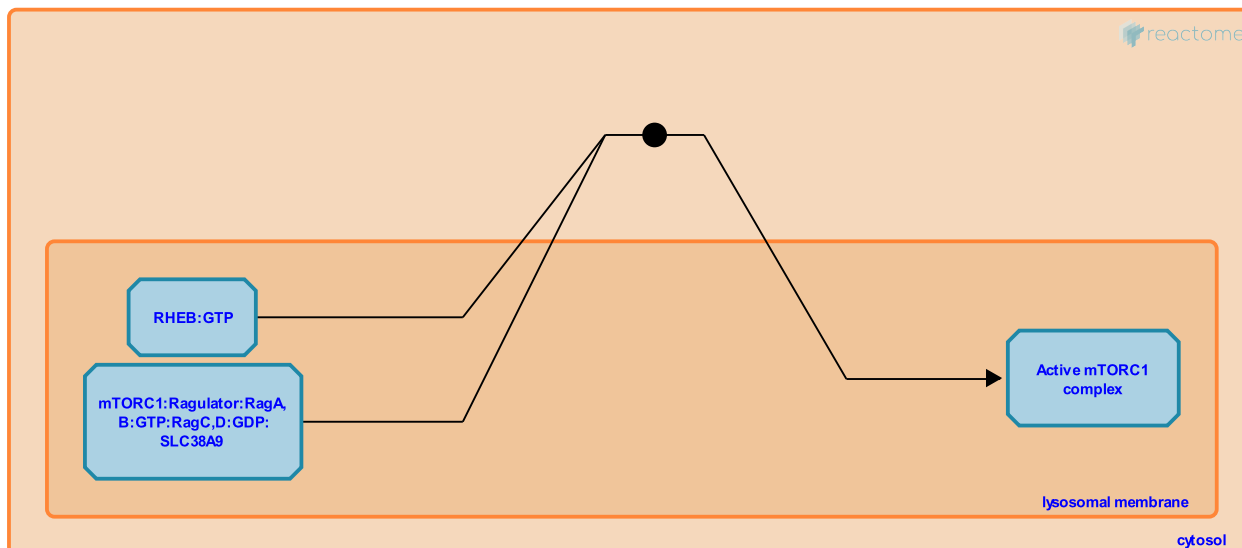# Formation of active mTORC1 complex ↗

Location: MTOR signalling

Stable identifier: R-SSC-165680

Type: binding

Compartments: cytosol, lysosomal membrane

Inferred from: Formation of active mTORC1 complex (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: GTP loading by Rheb

Followed by: AKT1S1 (PRAS40) binds mTORC1

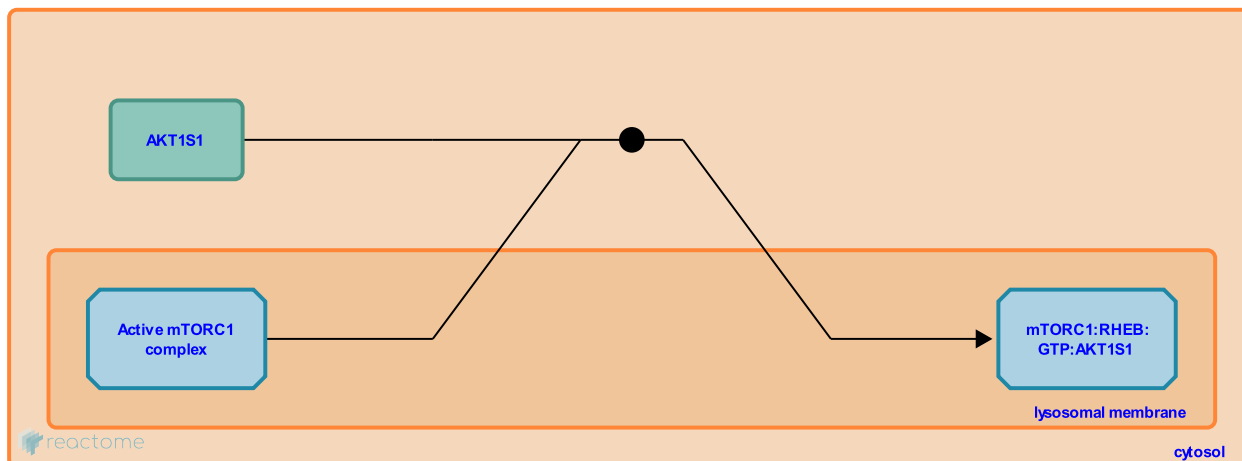# AKT1S1 (PRAS40) binds mTORC1 ↗

Location: MTOR signalling

Stable identifier: R-SSC-5672843

Type: binding

Compartments: cytosol, lysosomal membrane

Inferred from: AKT1S1 (PRAS40) 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: Formation of active mTORC1 complex

Phosphorylated AKT1S1:mTORC1 binds YWHAB ↗
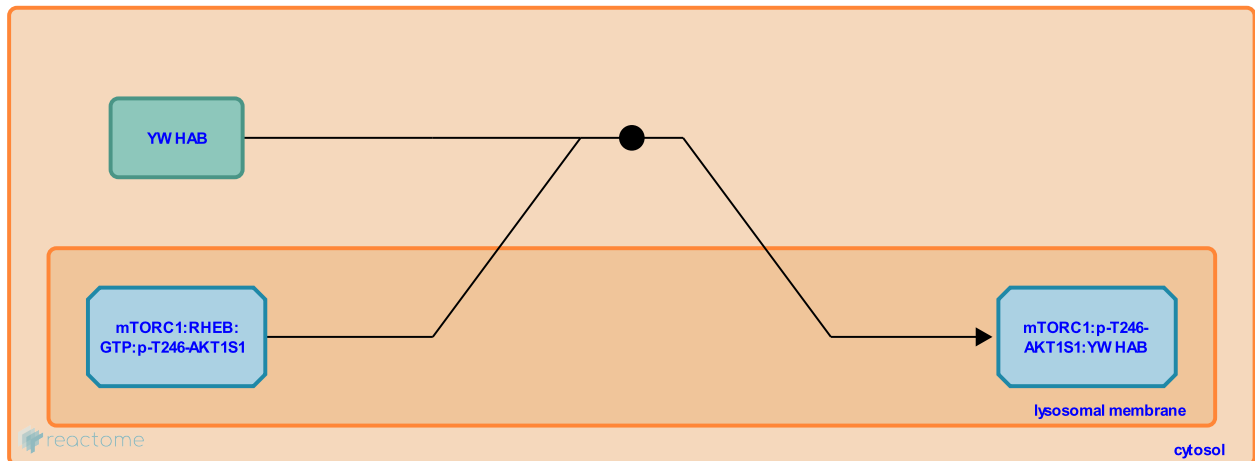
Location: MTOR signalling

Stable identifier: R-SSC-5672824

Type: binding

Compartments: cytosol, lysosomal membrane

Inferred from: Phosphorylated AKT1S1:mTORC1 binds YWHAB (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
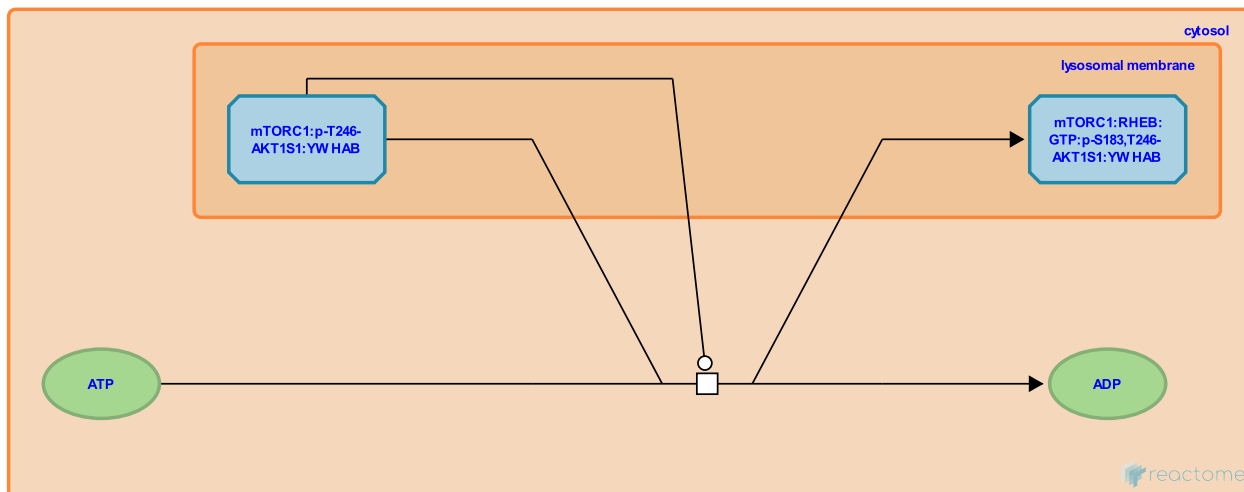
mTORC1 phosphorylates AKT1S1 ↗

Location: MTOR signalling

Stable identifier: R-SSC-5672828

Type: transition

Compartments: cytosol, lysosomal membrane

Inferred from: mTORC1 phosphorylates AKT1S1 (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.
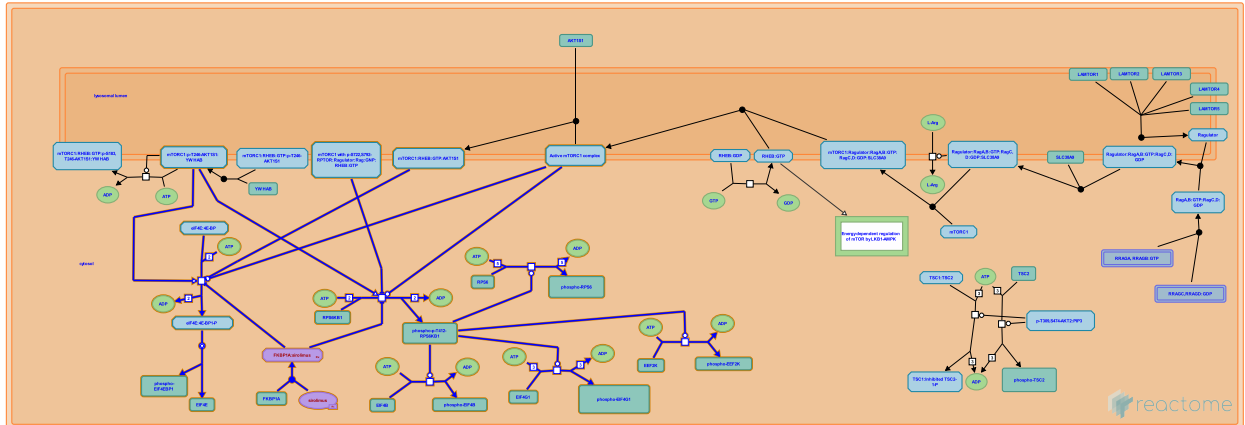
More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

mTORC1-mediated signalling ↗

Location: MTOR signalling

Stable identifier: R-SSC-166208

Inferred from: mTORC1-mediated signalling (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.
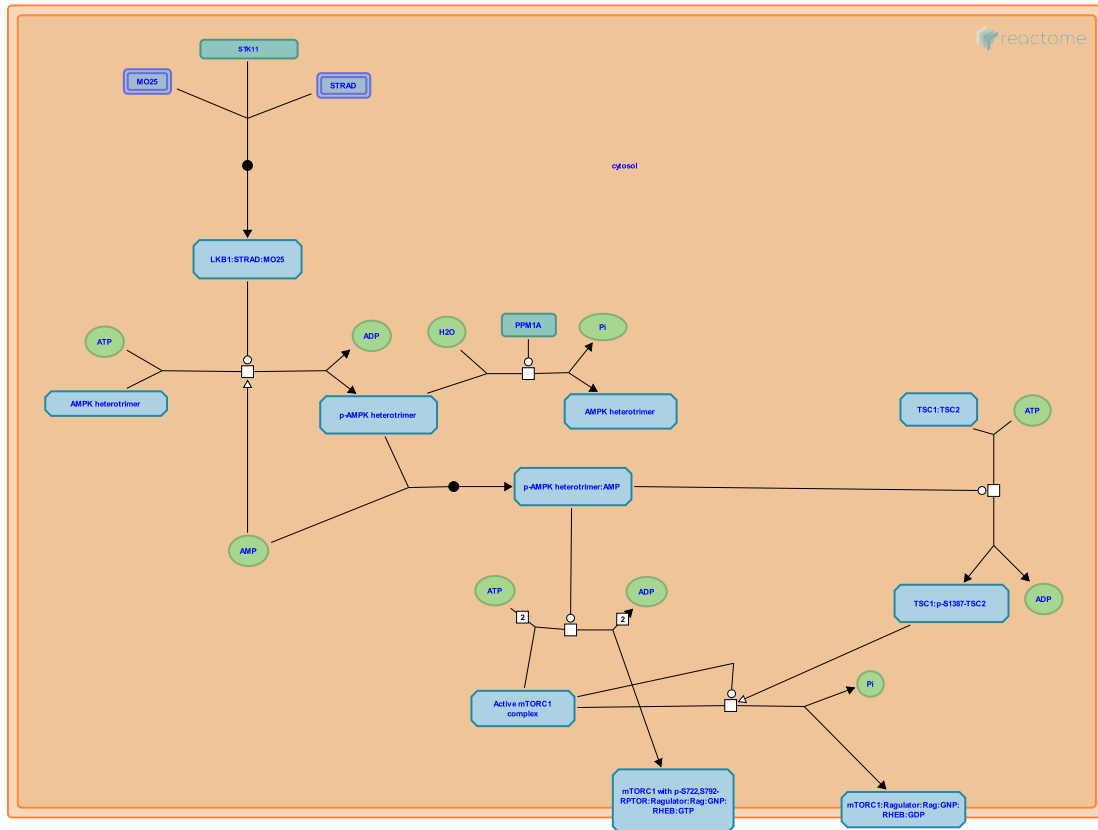
More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Energy dependent regulation of mTOR by LKB1-AMPK ↗

Location: MTOR signalling

Stable identifier: R-SSC-380972

Inferred from: Energy dependent regulation of mTOR by LKB1-AMPK (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

Table of Contents