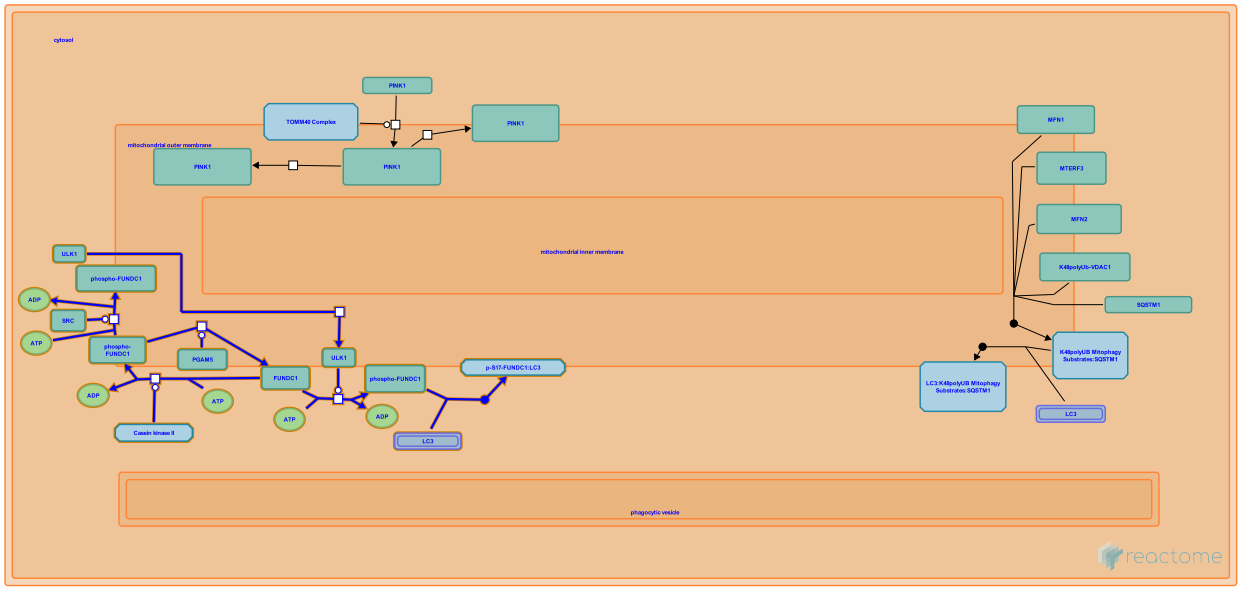
Receptor Mediated Mitophagy



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

02/03/2021

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

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. ↗

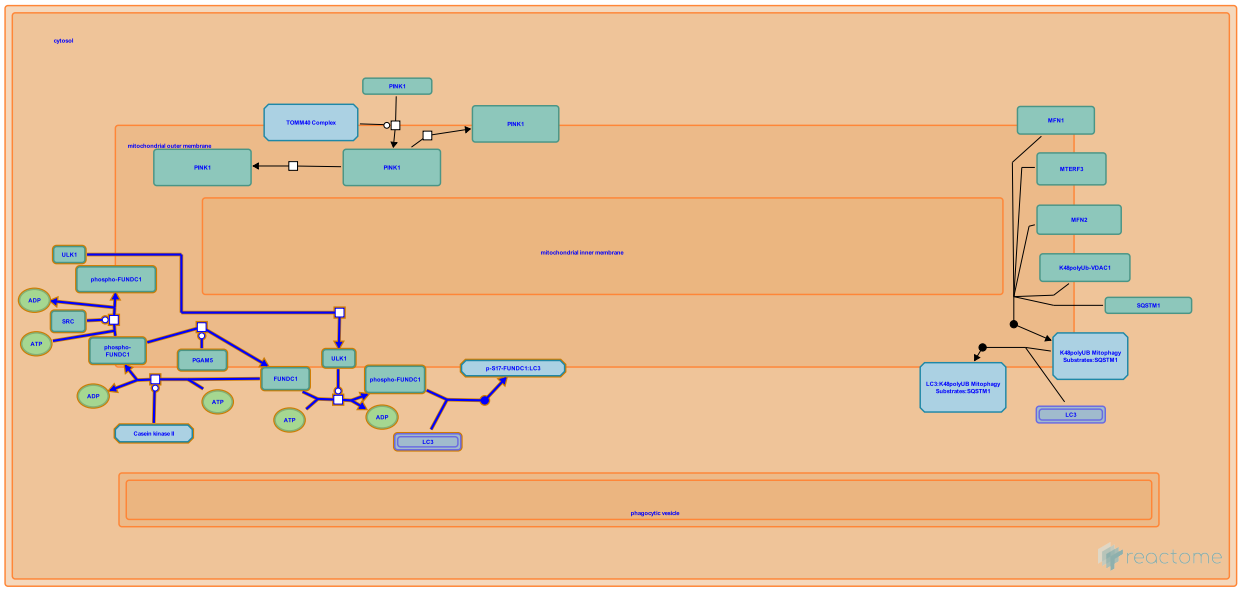
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Receptor Mediated Mitophagy ↗

Stable identifier: R-SSC-8934903

Compartments: cytosol

Inferred from: Receptor Mediated Mitophagy (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

FUNDC1 is phosphorylated by CK2 ↗

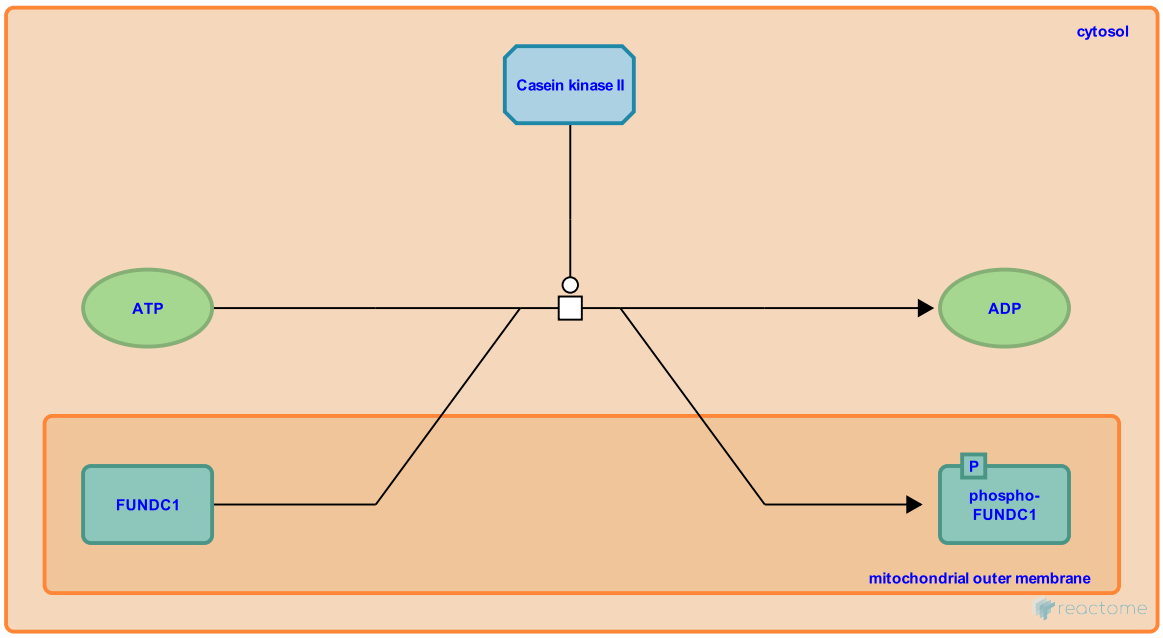
Location: Receptor Mediated Mitophagy

Stable identifier: R-SSC-8948039

Type: transition

Compartments: cytosol

Inferred from: FUNDC1 is phosphorylated by CK2 (Homo sapiens)



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Preceded by: p-S13-FUNDC1 is dephosphorylated by PGAM5

Followed by: p-S13, FUNDC1 is phosphorylated by CK2 at Tyr18, p-S13-FUNDC1 is dephosphorylated by PGAM5

p-S13, FUNDC1 is phosphorylated by CK2 at Tyr18 ↗

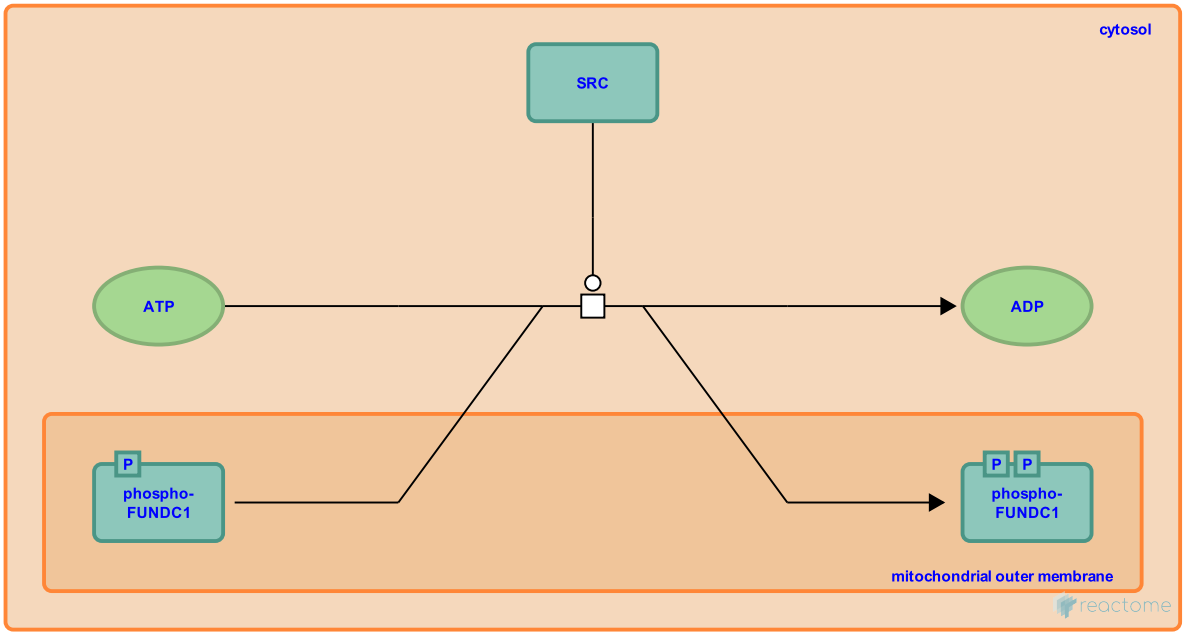
Location: Receptor Mediated Mitophagy

Stable identifier: R-SSC-8948143

Type: transition

Compartments: cytosol

Inferred from: p-S13, FUNDC1 is phosphorylated by CK2 at Tyr18 (Homo sapiens)



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Preceded by: FUNDC1 is phosphorylated by CK2

p-S13-FUNDC1 is dephosphorylated by PGAM5 ↗

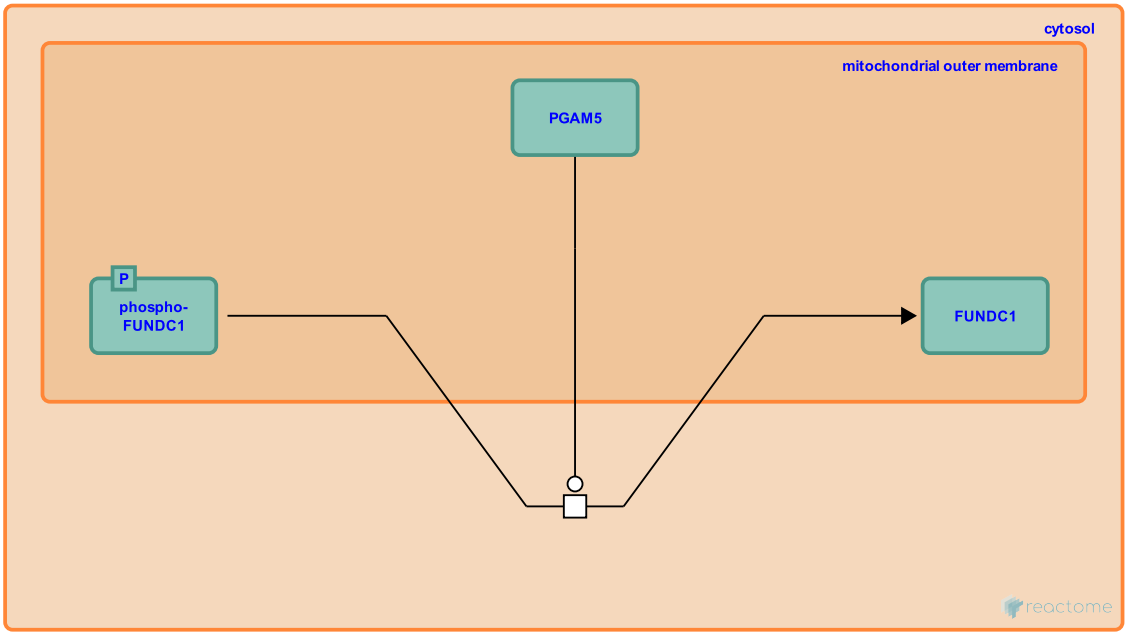
Location: Receptor Mediated Mitophagy

Stable identifier: R-SSC-8948139

Type: transition

Compartments: cytosol

Inferred from: p-S13-FUNDC1 is dephosphorylated by PGAM5 (Homo sapiens)



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Preceded by: FUNDC1 is phosphorylated by CK2

Followed by: FUNDC1 is phosphorylated by CK2, FUNDC1 is phosphorylated by ULK1 at Ser17

ULK1 Translocates to the mitochondria ↗

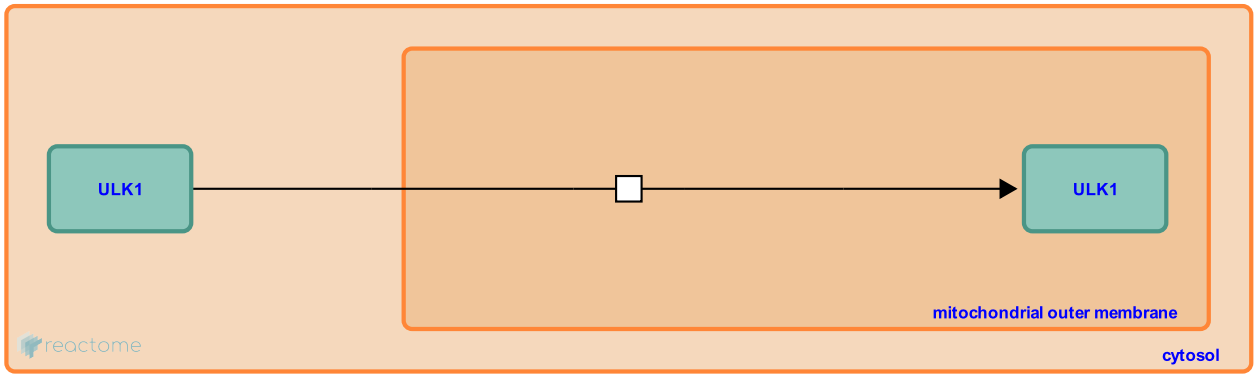
Location: Receptor Mediated Mitophagy

Stable identifier: R-SSC-8948136

Type: transition

Compartments: mitochondrial outer membrane

Inferred from: ULK1 Translocates to the mitochondria (Homo sapiens)



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Followed by: FUNDC1 is phosphorylated by ULK1 at Ser17

FUNDC1 is phosphorylated by ULK1 at Ser17 ↗

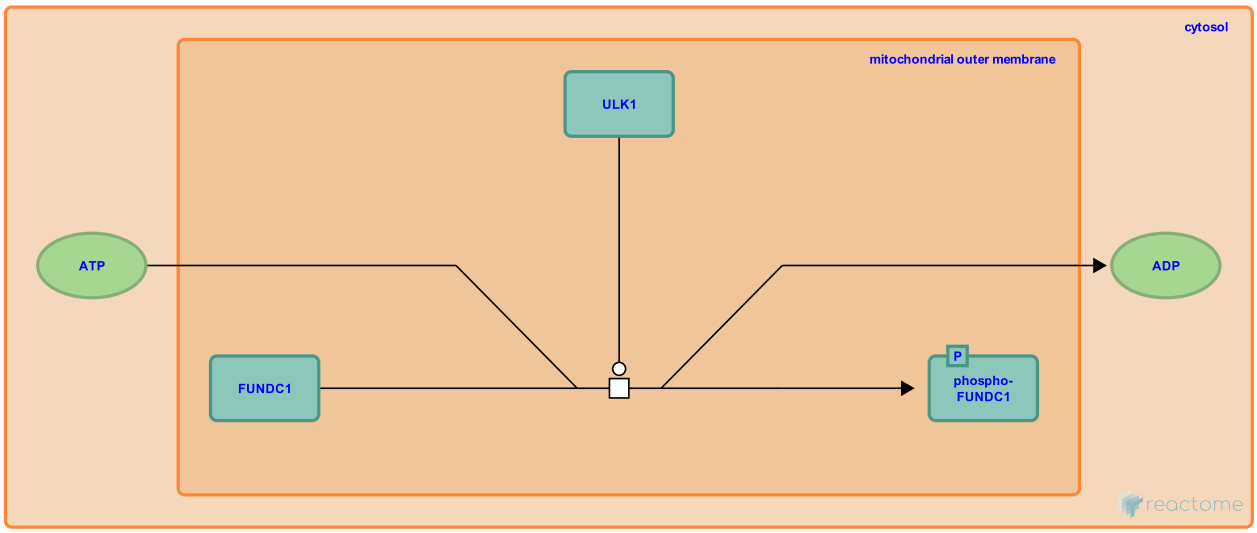
Location: Receptor Mediated Mitophagy

Stable identifier: R-SSC-8948146

Type: transition

Compartments: mitochondrial outer membrane

Inferred from: FUNDC1 is phosphorylated by ULK1 at Ser17 (Homo sapiens)



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Preceded by: ULK1 Translocates to the mitochondria, p-S13-FUNDC1 is dephosphorylated by PGAM5

Followed by: Phosphorylated FUNDC1 links damaged mitochondria to LC3

Phosphorylated FUNDC1 links damaged mitochondria to LC3 ↗

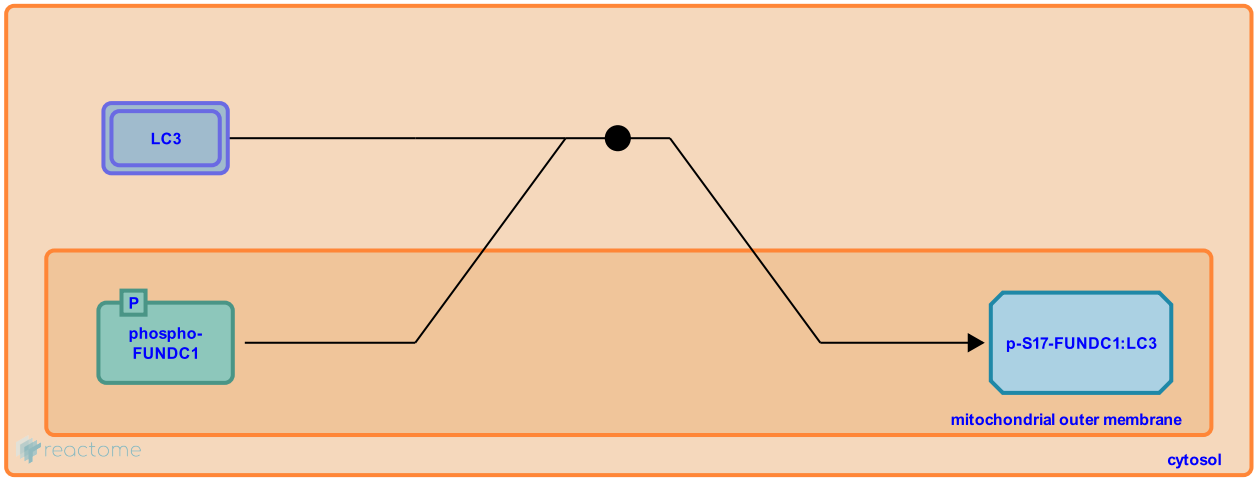
Location: Receptor Mediated Mitophagy

Stable identifier: R-SSC-8959573

Type: binding

Compartments: cytosol

Inferred from: Phosphorylated FUNDC1 links damaged mitochondria to LC3 (Homo sapiens)



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Preceded by: FUNDC1 is phosphorylated by ULK1 at Ser17

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