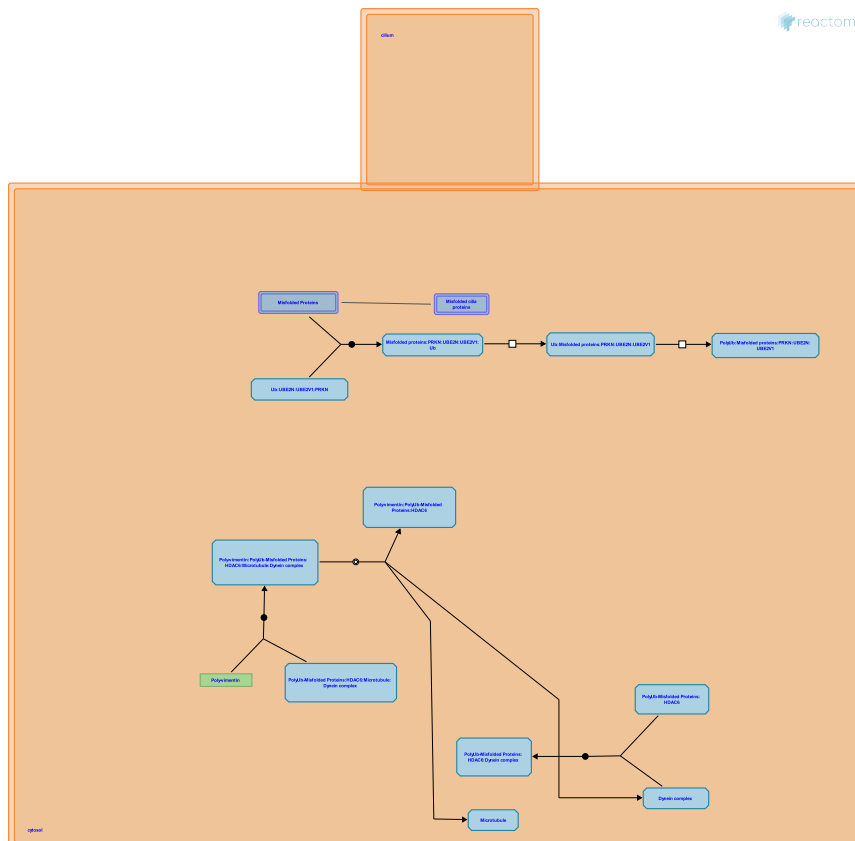


Aggrephagy



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/).

05/05/2024

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

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Reactome database release: 88

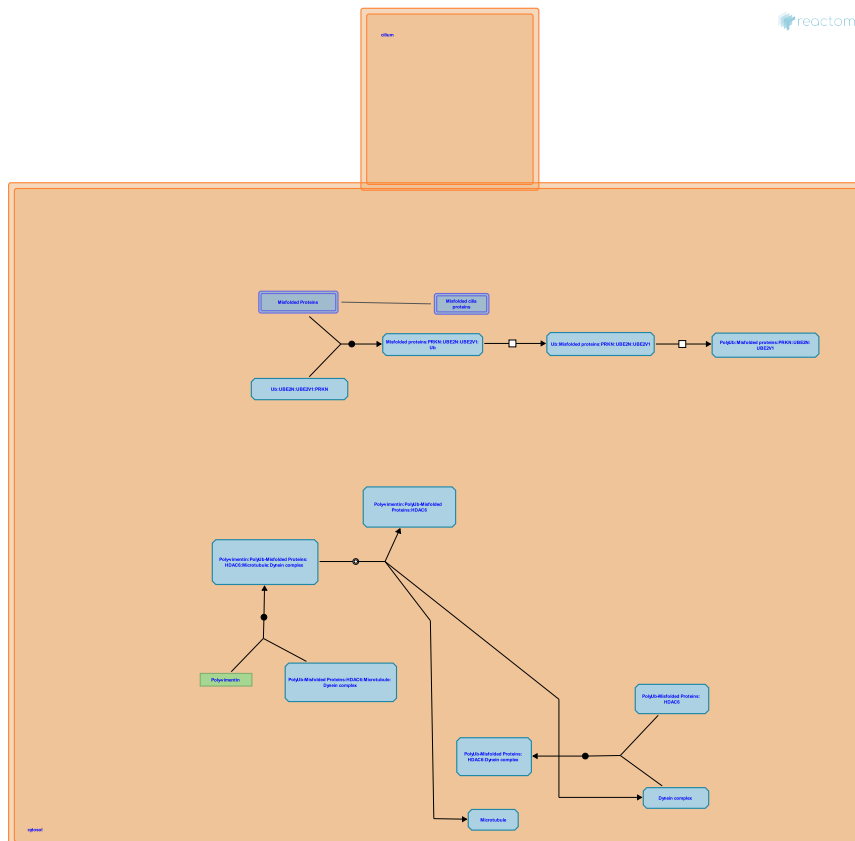
This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

Aggrephagy [↗](#)

Stable identifier: R-SSC-9646399

Compartments: cytosol

Inferred from: [Aggrephagy \(Homo sapiens\)](#)



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>

Misfolded proteins bind PRKN:UBE2N:UBE2V1:Ub ↗

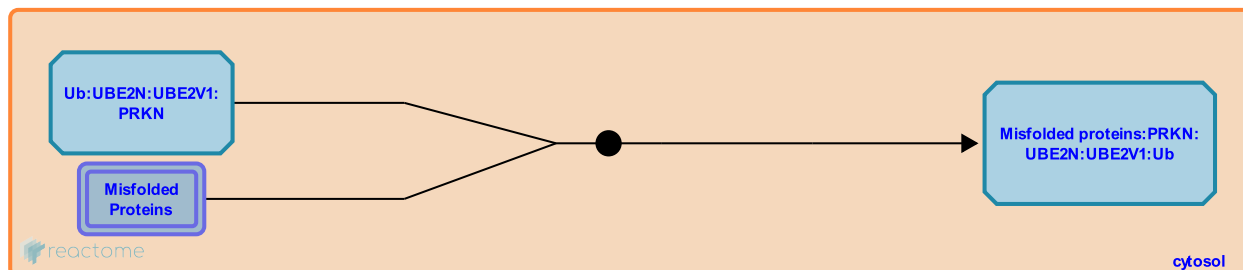
Location: [Aggrephagy](#)

Stable identifier: R-SSC-9641096

Type: binding

Compartments: cytosol

Inferred from: [Misfolded proteins bind PRKN:UBE2N:UBE2V1:Ub \(Homo sapiens\)](#)



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: [Parkin transfers Ub to misfolded proteins](#)

Parkin transfers Ub to misfolded proteins ↗

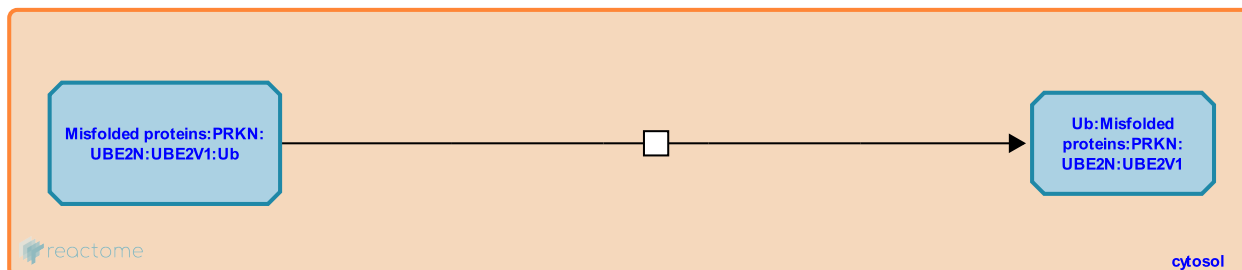
Location: [Aggrephagy](#)

Stable identifier: R-SSC-9641111

Type: transition

Compartments: cytosol

Inferred from: [Parkin transfers Ub to misfolded proteins \(Homo sapiens\)](#)



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: [Misfolded proteins bind PRKN:UBE2N:UBE2V1:Ub](#)

Followed by: [Ub:misfolded proteins polymerize to PolyUb:misfolded proteins](#)

Ub:misfolded proteins polymerize to PolyUb:misfolded proteins ↗

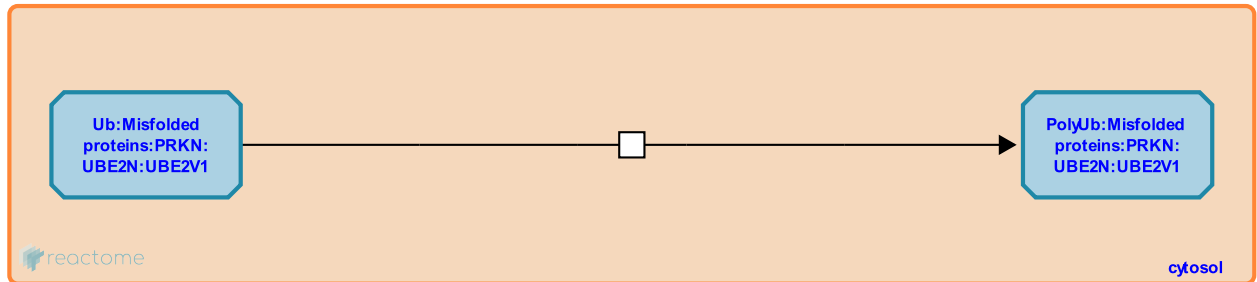
Location: [Aggrephagy](#)

Stable identifier: R-SSC-9641127

Type: transition

Compartments: cytosol

Inferred from: [Ub:misfolded proteins polymerize to PolyUb:misfolded proteins \(Homo sapiens\)](#)



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: [Parkin transfers Ub to misfolded proteins](#)

PolyUb-Misfolded Proteins:HDAC6 bind dynein motor ↗

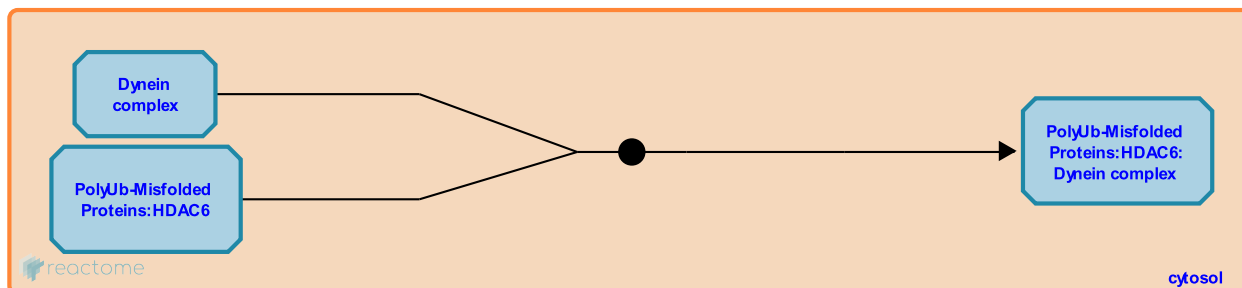
Location: [Aggrephagy](#)

Stable identifier: R-SSC-9646348

Type: binding

Compartments: cytosol

Inferred from: [PolyUb-Misfolded Proteins:HDAC6 bind dynein motor \(Homo sapiens\)](#)



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: [Aggresome dissociates from dynein and microtubule](#)

PolyUb-Misfolded proteins bind vimentin to form aggresome ↗

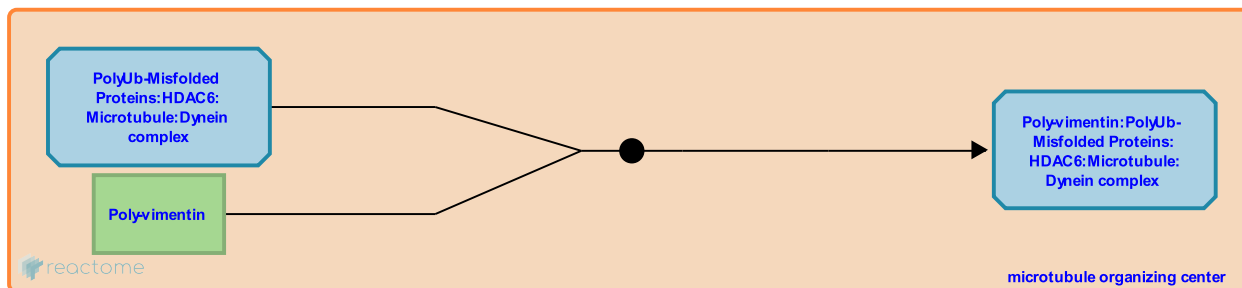
Location: Aggrephagy

Stable identifier: R-SSC-9646679

Type: binding

Compartments: microtubule organizing center

Inferred from: PolyUb-Misfolded proteins bind vimentin to form aggresome (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: Aggresome dissociates from dynein and microtubule

Aggresome dissociates from dynein and microtubule ↗

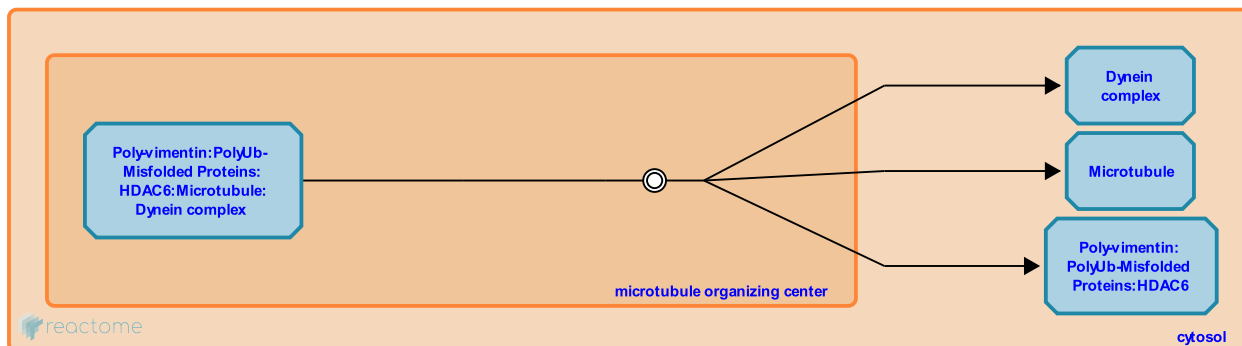
Location: Aggrephagy

Stable identifier: R-SSC-9646685

Type: dissociation

Compartments: microtubule organizing center

Inferred from: Aggresome dissociates from dynein and microtubule (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: PolyUb-Misfolded proteins bind vimentin to form aggresome

Followed by: PolyUb-Misfolded Proteins:HDAC6 bind dynein motor

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