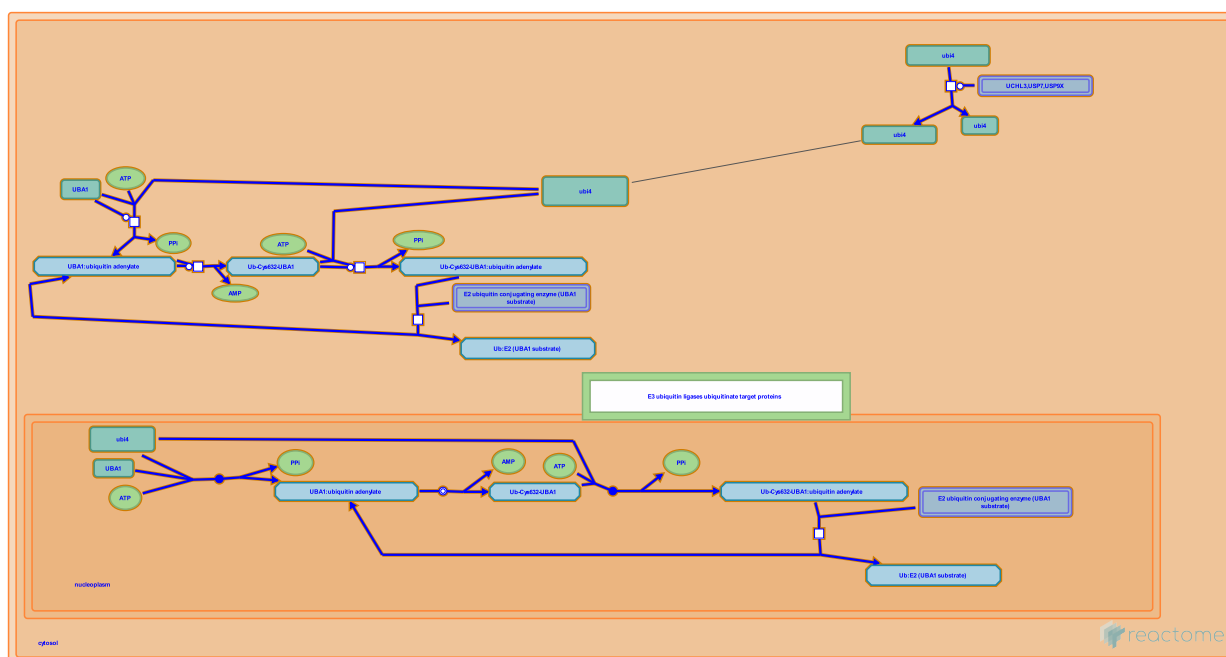


Synthesis of active ubiquitin: roles of E1 and E2 enzymes



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).

19/05/2024

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. [↗](#)

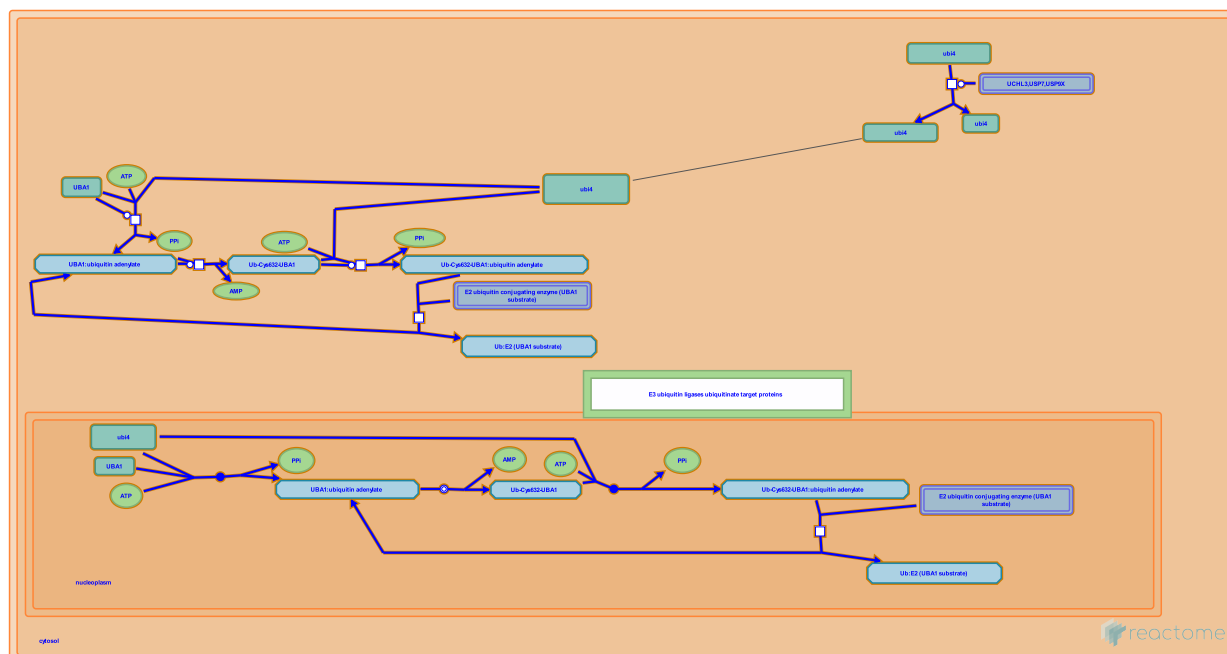
Reactome database release: 88

This document contains 1 pathway and 9 reactions ([see Table of Contents](#))

Synthesis of active ubiquitin: roles of E1 and E2 enzymes ↗

Stable identifier: R-SPO-8866652

Inferred from: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes \(Homo sapiens\)](#)



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>

UHL3,USP7,USP9X cleaves UBA52 yielding ubiquitin ↗

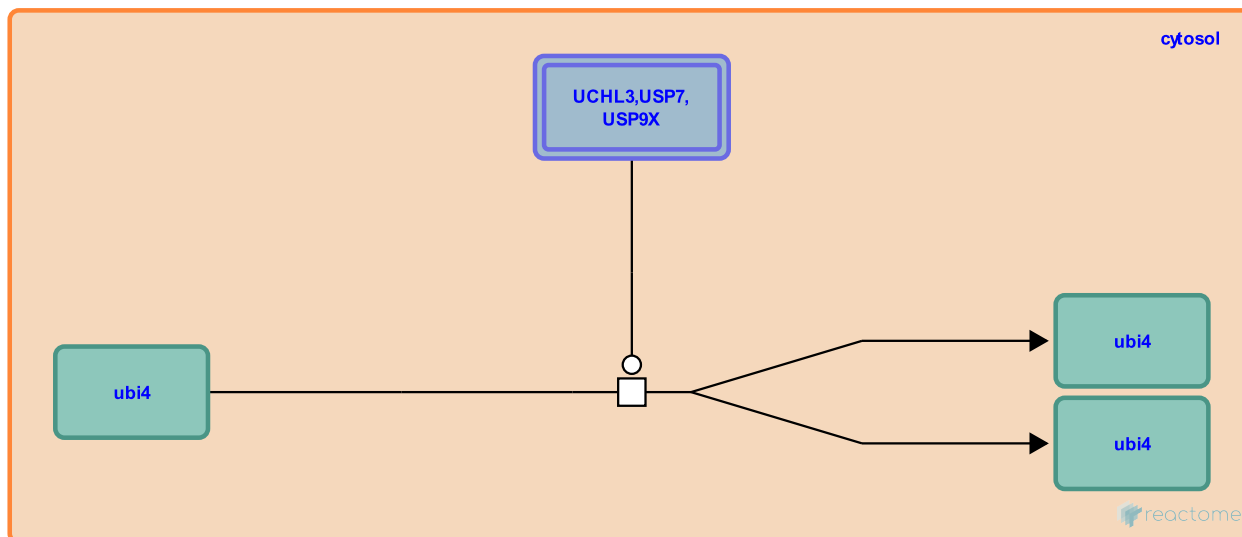
Location: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes](#)

Stable identifier: R-SPO-8853514

Type: transition

Compartments: cytosol

Inferred from: [UHL3,USP7,USP9X cleaves UBA52 yielding ubiquitin \(Homo sapiens\)](#)



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.

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Followed by: [UBA1 adenylates ubiquitin in the cytosol](#)

UBA1 adenylates ubiquitin in the cytosol ↗

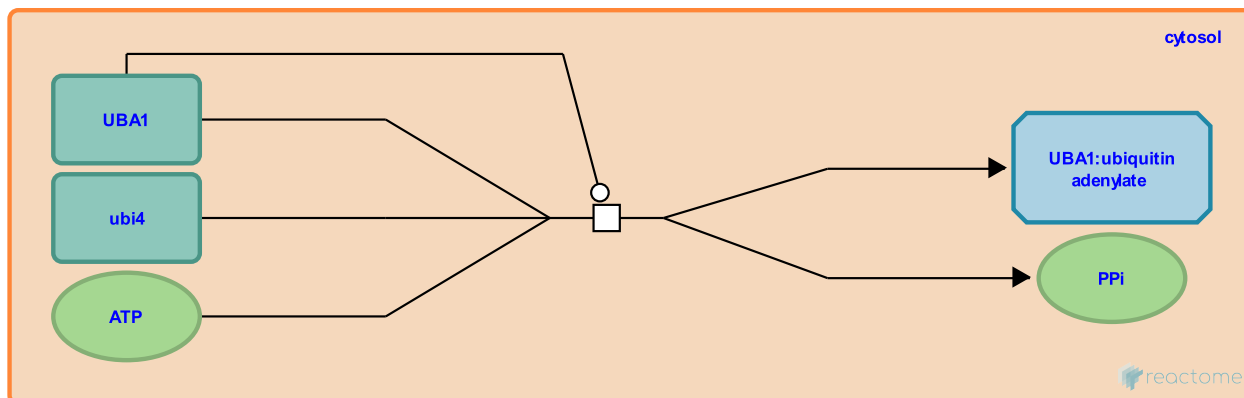
Location: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes](#)

Stable identifier: R-SPO-8852134

Type: transition

Compartments: cytosol

Inferred from: [UBA1 adenylates ubiquitin in the 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: [UCHL3,USP7,USP9X cleaves UBA52 yielding ubiquitin](#)

Followed by: [UBA1 conjugates ubiquitin to UBA1 in the cytosol](#)

UBA1 conjugates ubiquitin to UBA1 in the cytosol ↗

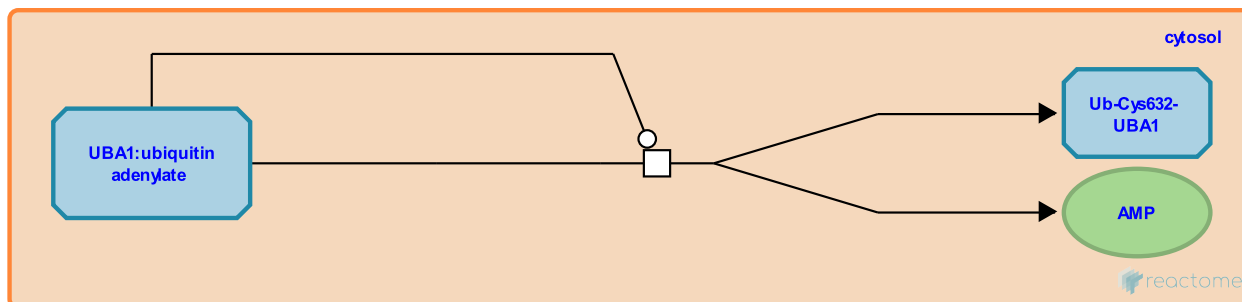
Location: Synthesis of active ubiquitin: roles of E1 and E2 enzymes

Stable identifier: R-SPO-8852133

Type: transition

Compartments: cytosol

Inferred from: UBA1 conjugates ubiquitin to UBA1 in the 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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: UBA1 adenylates ubiquitin in the cytosol

Followed by: Ub-Cys632-UBA1 adenylates ubiquitin in the cytosol

Ub-Cys632-UBA1 adenylates ubiquitin in the cytosol ↗

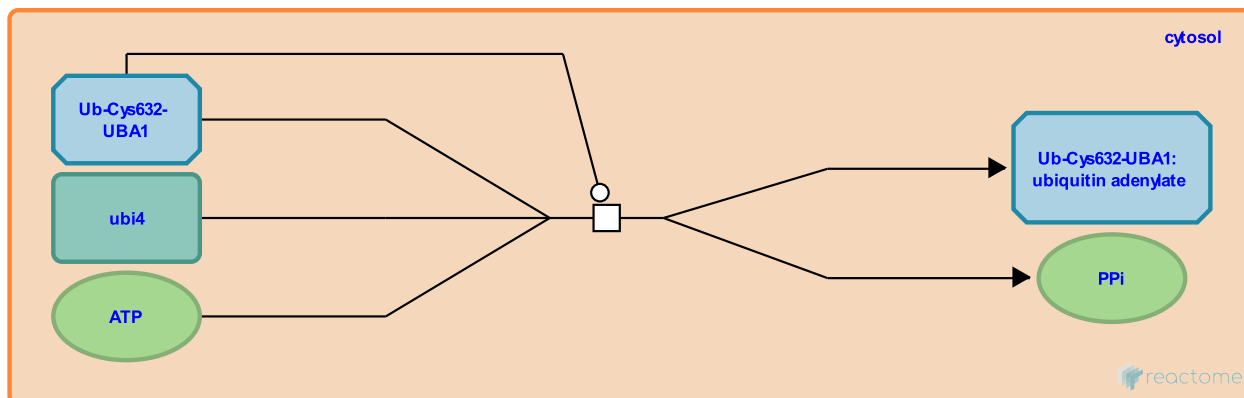
Location: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes](#)

Stable identifier: R-SPO-8852132

Type: transition

Compartments: cytosol

Inferred from: [Ub-Cys632-UBA1 adenylates ubiquitin in the 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: [UBA1 conjugates ubiquitin to UBA1 in the cytosol](#)

Followed by: [UBA1 conjugates ubiquitin to cytosolic E2 enzymes](#)

UBA1 conjugates ubiquitin to cytosolic E2 enzymes ↗

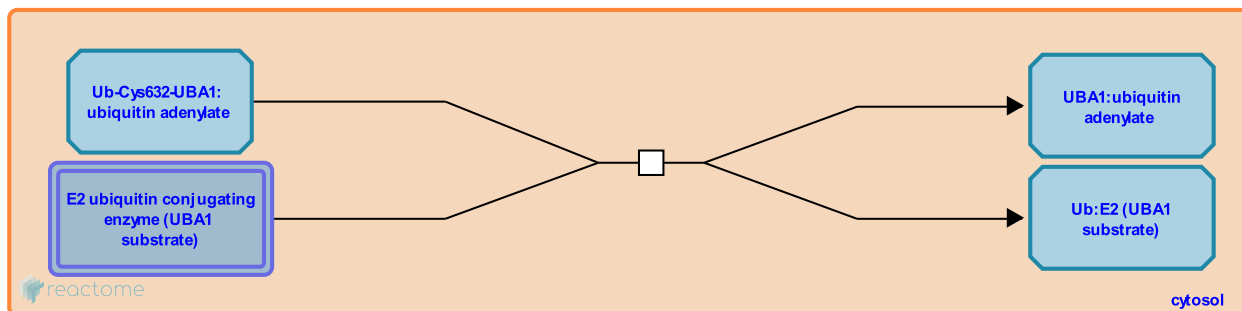
Location: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes](#)

Stable identifier: R-SPO-8852129

Type: transition

Compartments: cytosol

Inferred from: [UBA1 conjugates ubiquitin to cytosolic E2 enzymes \(Homo sapiens\)](#)



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: [Ub-Cys632-UBA1 adenylates ubiquitin in the cytosol](#)

UBA1 adenylates ubiquitin in the nucleoplasm ↗

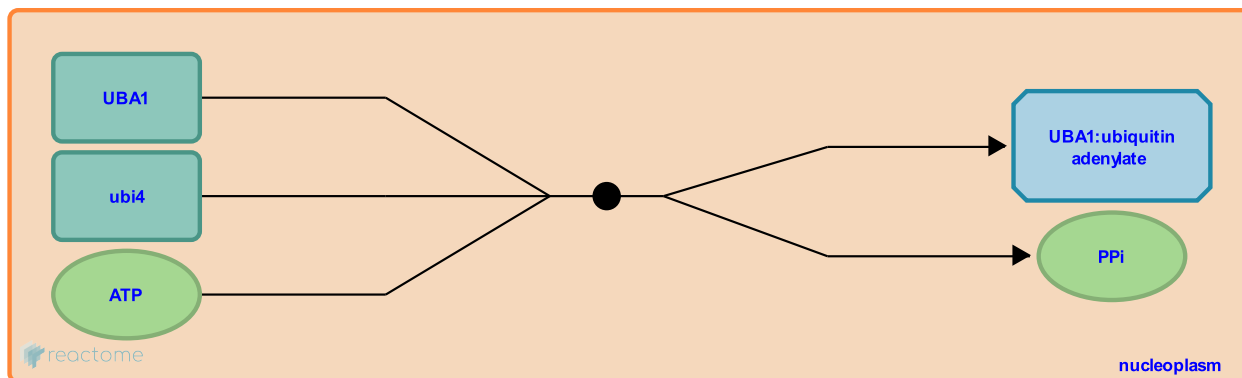
Location: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes](#)

Stable identifier: R-SPO-8852128

Type: binding

Compartments: nucleoplasm

Inferred from: [UBA1 adenylates ubiquitin in the nucleoplasm \(Homo sapiens\)](#)



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: [UBA1 conjugates ubiquitin to UBA1 in the nucleus](#)

UBA1 conjugates ubiquitin to UBA1 in the nucleus ↗

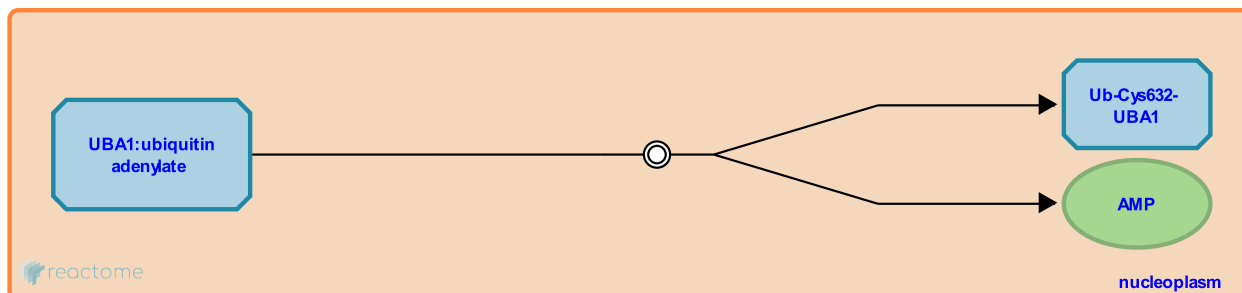
Location: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes](#)

Stable identifier: R-SPO-8852136

Type: dissociation

Compartments: nucleoplasm

Inferred from: [UBA1 conjugates ubiquitin to UBA1 in the nucleus \(Homo sapiens\)](#)



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: [UBA1 adenylates ubiquitin in the nucleoplasm](#)

Followed by: [Ub-Cys632-UBA1 adenylates ubiquitin in the nucleus](#)

Ub-Cys632-UBA1 adenylates ubiquitin in the nucleus ↗

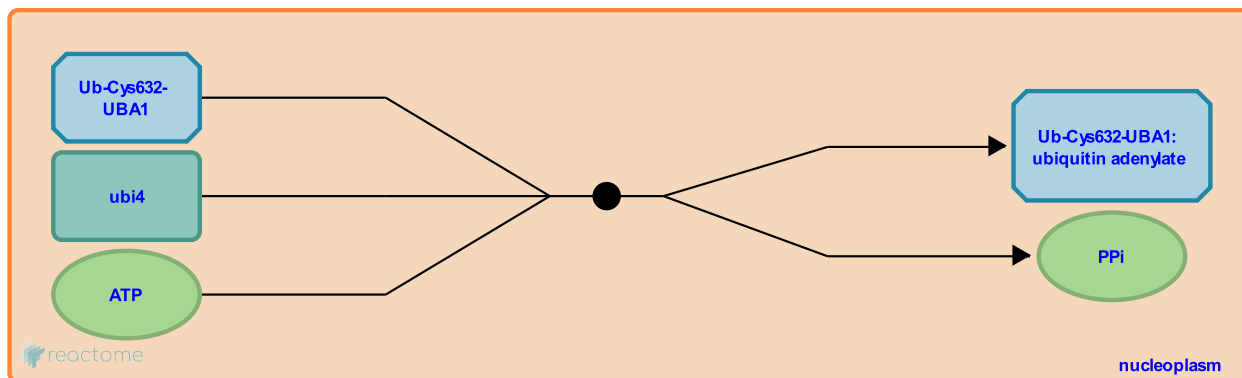
Location: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes](#)

Stable identifier: R-SPO-8852131

Type: binding

Compartments: nucleoplasm

Inferred from: [Ub-Cys632-UBA1 adenylates ubiquitin in the nucleus \(Homo sapiens\)](#)



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: [UBA1 conjugates ubiquitin to UBA1 in the nucleus](#)

Followed by: [UBA1 conjugates ubiquitin to nuclear E2 enzymes](#)

UBA1 conjugates ubiquitin to nuclear E2 enzymes ↗

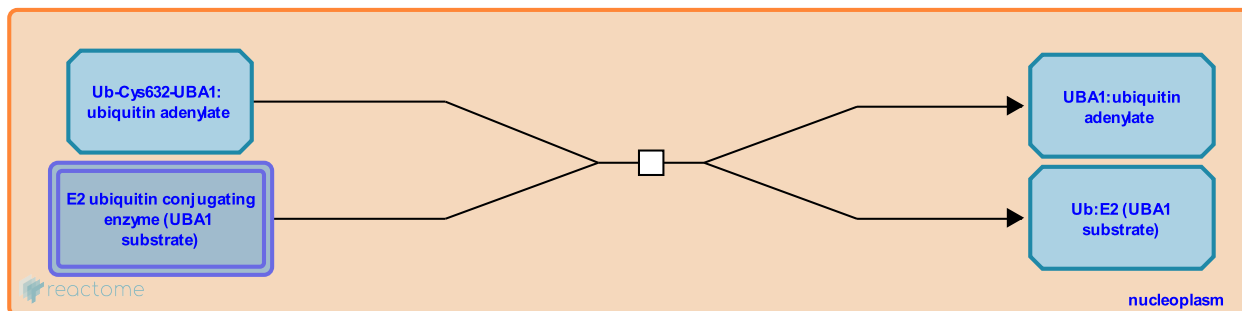
Location: [Synthesis of active ubiquitin: roles of E1 and E2 enzymes](#)

Stable identifier: R-SPO-8852130

Type: transition

Compartments: nucleoplasm

Inferred from: [UBA1 conjugates ubiquitin to nuclear E2 enzymes \(Homo sapiens\)](#)



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: [Ub-Cys632-UBA1 adenylates ubiquitin in the nucleus](#)

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