

Ub:misfolded proteins polymerize to Poly- Ub:misfolded proteins

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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

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Reactome database release: 88

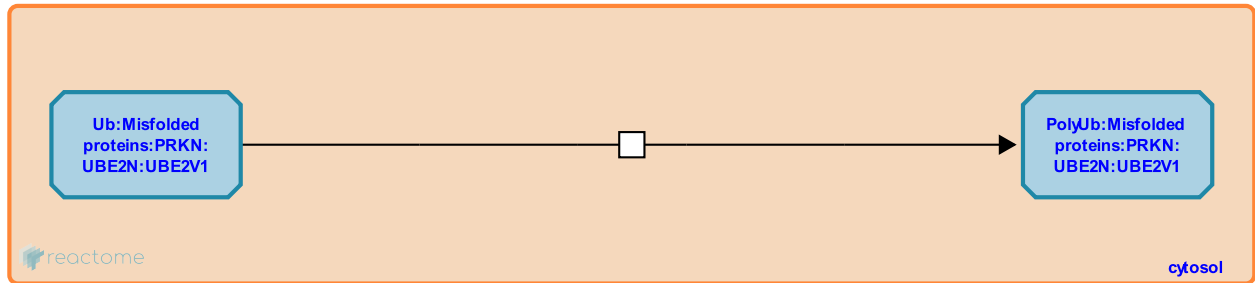
This document contains 1 reaction ([see Table of Contents](#))

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

Stable identifier: R-HSA-9641127

Type: transition

Compartments: cytosol



Misfolded proteins in the cytosol are targeted to degradation via ubiquitination. The E2 UBE2N/UBE2V1 and E3 ligase ubiquitination system recruits and transfers ubiquitin molecules to misfolded proteins. The E3 ligase Parkin tags the proteins with multiple K63-linked ubiquitin molecules (Olzmann JA et al. 2007).

Literature references

Chin, LS., Palmiter, RD., Chudaev, MV., Perez, FA., Olzmann, JA., Chen, J. et al. (2007). Parkin-mediated K63-linked polyubiquitination targets misfolded DJ-1 to aggresomes via binding to HDAC6. *J. Cell Biol.*, 178, 1025-38. [↗](#)

Editions

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