

Proteasome-mediated degradation of Poly- Ub-FBXL7

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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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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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- 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

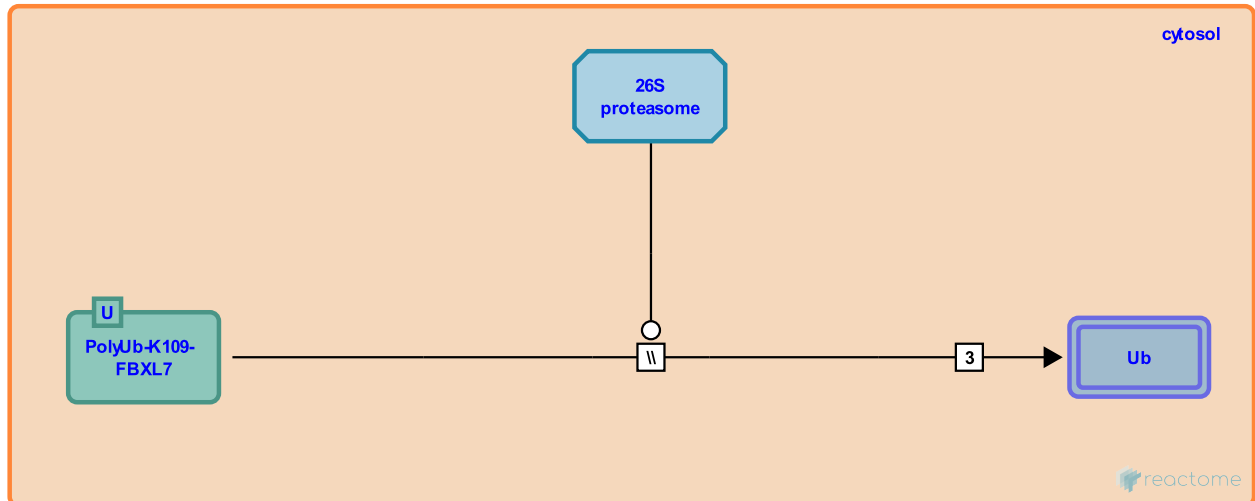
This document contains 1 reaction ([see Table of Contents](#))

Proteasome-mediated degradation of PolyUb-FBXL7 [↗](#)

Stable identifier: R-HSA-8854071

Type: omitted

Compartments: cytosol



FBXL7, polyubiquitinated by the FBXL18-containing SCF complex, is degraded by the proteasome (Liu et al. 2015).

Literature references

Zou, C., Liu, Y., Chen, BB., Lear, T., Mallampalli, RK., Zhao, Y. et al. (2015). F-box protein Fbxl18 mediates polyubiquitylation and proteasomal degradation of the pro-apoptotic SCF subunit Fbxl7. *Cell Death Dis*, 6, e1630. [↗](#)

Editions

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