

Ubiquitination of PAK-2p34

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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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- 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 reaction ([see Table of Contents](#))

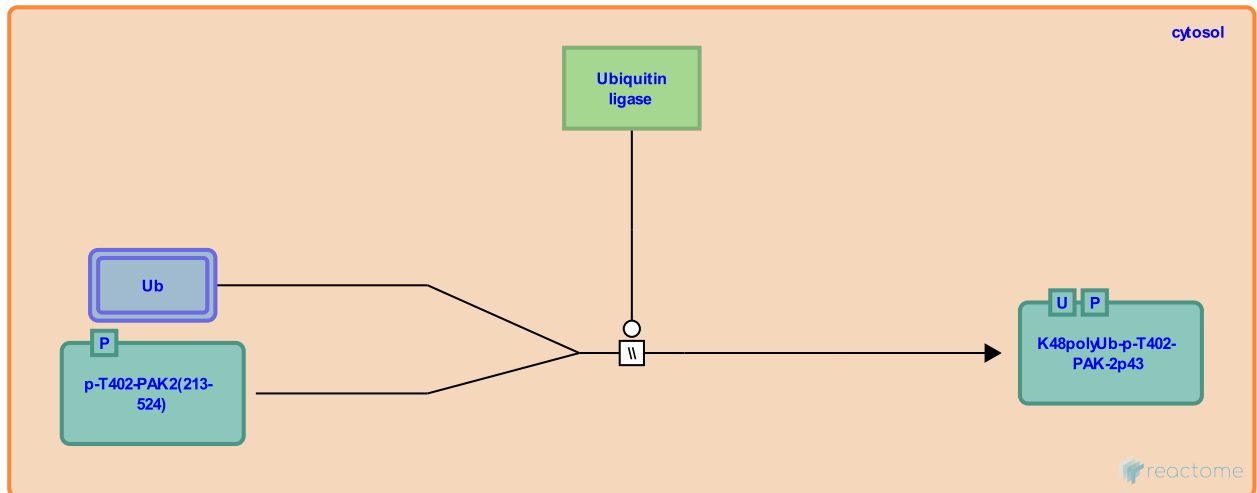
Ubiquitination of PAK-2p34 [↗](#)

Stable identifier: R-HSA-211734

Type: omitted

Compartments: cytosol

Inferred from: [Ubiquitination of PAK-2p34 \(Oryctolagus cuniculus\)](#)



PAK-2p34 is ubiquitinated prior to degradation (Jakobi et al., 2003). Here, ubiquitination of PAK-2p34 is described as occurring in the cytosol. However, to date it is not known whether this occurs in the nucleus or in the cytoplasm. Evidence for this reaction comes from experiments using both human and rabbit proteins. The polyubiquitin synthesized in the reaction is inferred to contain lysine-48 (K48) linkages because the modified protein is targeted to the proteasome (Komander 2009).

Editions

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