Ubiquitination of PAK-2p34

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20/04/2021

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. ↗

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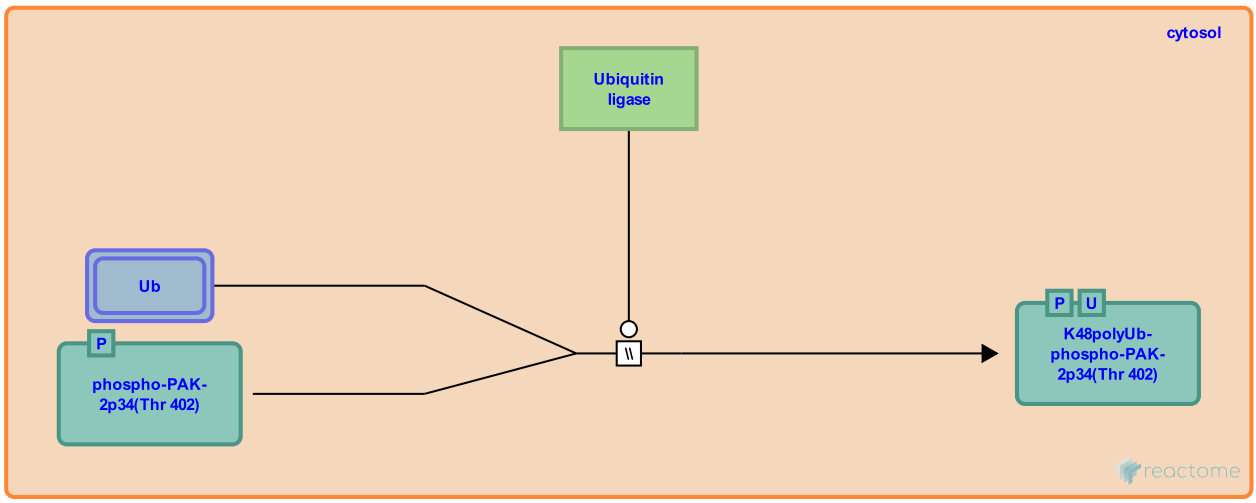
Stable identifier: R-NUL-212920

Type: omitted

Compartments: cytosol



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).

Literature references

Jakobi, R., McCarthy, CC., Koeppel, MA., Stringer, DK. (2003). Caspase-activated PAK-2 is regulated by subcellular targeting and proteasomal degradation. *J Biol Chem, 278*, 38675-85.

Editions

2008-02-04	Edited	Matthews, L.
2008-02-05	Authored	Jakobi, R.
2008-05-21	Reviewed	Chang, E.
2008-05-23	Edited	Matthews, L.