

ATM dimer:p-PEX5 ubiquitinates to form ATM dimer:Ub-p-PEX5

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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

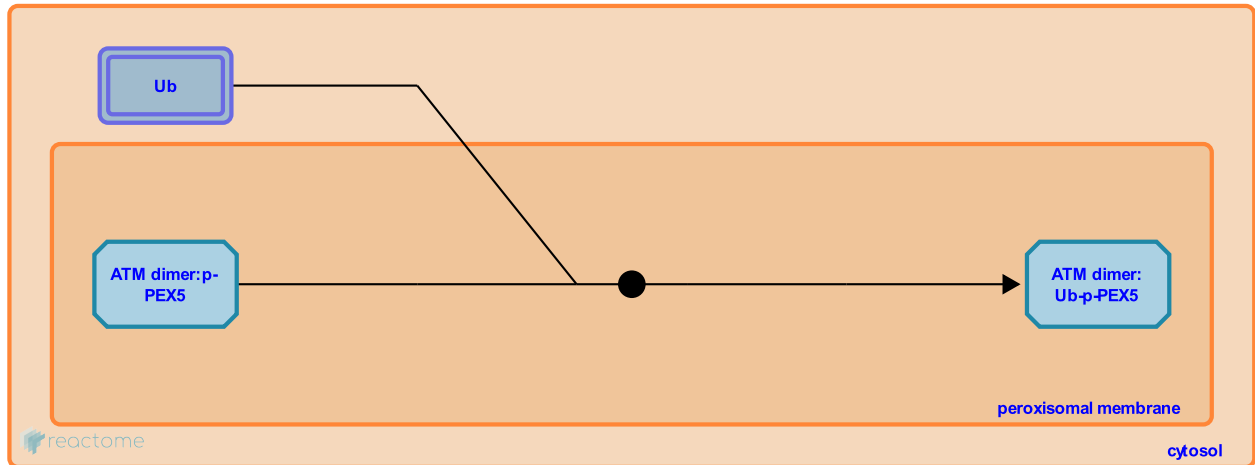
This document contains 1 reaction ([see Table of Contents](#))

ATM dimer:p-PEX5 ubiquitinates to form ATM dimer:Ub-p-PEX5 [↗](#)

Stable identifier: R-HSA-9664888

Type: binding

Compartments: peroxisomal membrane



Phosphorylation of Peroxisomal targeting signal 1 receptor protein (PEX5) at Ser141 promotes the ubiquitination of PEX5. The RING peroxins complex composed of: Peroxisome biogenesis factor 2 (PEX2), Peroxisome biogenesis factor 10 (PEX10), and Peroxisome assembly protein 12 (PEX12) form part of a peroxisome localized E3 ligase that ubiquitinates PEX5 at Lys209 (Zhang J et al. 2015). This mono ubiquitination of PEX5 helps to recruit the autophagy machinery to the peroxisome.

Literature references

Kim, J., Walker, CL., Pandita, TK., Charaka, VK., Jing, J., Dere, R. et al. (2015). ATM functions at the peroxisome to induce pexophagy in response to ROS. *Nat. Cell Biol.*, 17, 1259-69. [↗](#)

Editions

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