

# USP30 binds ATM dimer:Ub-p-PEX5

Metzakopian, E., Varusai, TM.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

03/05/2024

## 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. [↗](#)
- 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

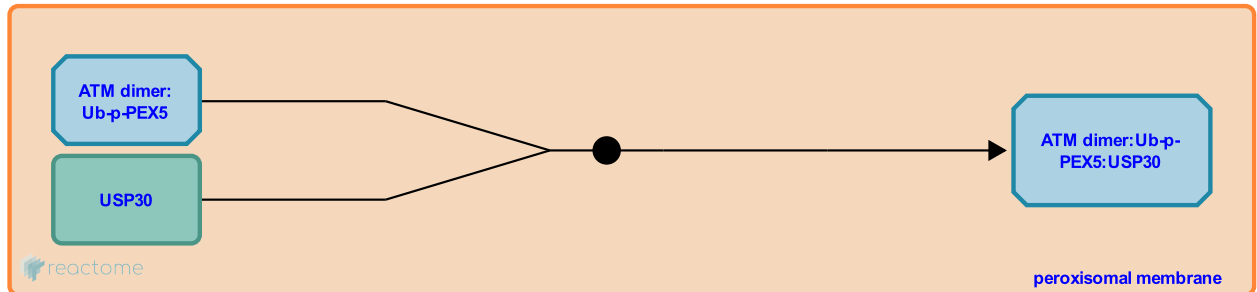
This document contains 1 reaction ([see Table of Contents](#))

## USP30 binds ATM dimer:Ub-p-PEX5 [↗](#)

**Stable identifier:** R-HSA-9674131

**Type:** binding

**Compartments:** peroxisomal membrane



As a deubiquitinase, Ubiquitin carboxyl-terminal hydrolase 30 (USP30) can reverse the action of E3 ligase on peroxisomal membrane proteins. Studies show that USP30 can localise in the peroxisomal membrane and interact with ubiquitinated PEX5 (Riccio V et al. 2019, Marcassa E et al. 2019).

### Literature references

Rusilowicz-Jones, EV., Clague, MJ., Jardine, J., Marcassa, E., Urbé, S., Kallinos, A. (2019). New aspects of USP30 biology in the regulation of pexophagy. *Autophagy*, 15, 1634-1637. [↗](#)

Riccio, V., McQuibban, GA., Kim, PK. (2019). USP30: protector of peroxisomes and mitochondria. *Mol Cell Oncol*, 6, 1600350. [↗](#)

Vissa, M., Strilchuk, AW., Demers, N., Hua, R., Riccio, V., McQuibban, GA. et al. (2019). Deubiquitinating enzyme USP30 maintains basal peroxisome abundance by regulating pexophagy. *J. Cell Biol.*, 218, 798-807. [↗](#)

### Editions

2019-10-30	Reviewed	Metzakopian, E.
2020-01-06	Authored	Varusai, TM.
2020-01-13	Edited	Varusai, TM.