

# MAP1LC3B binds ATM dimer:Ub-p- PEX5:SQSTM1

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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

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

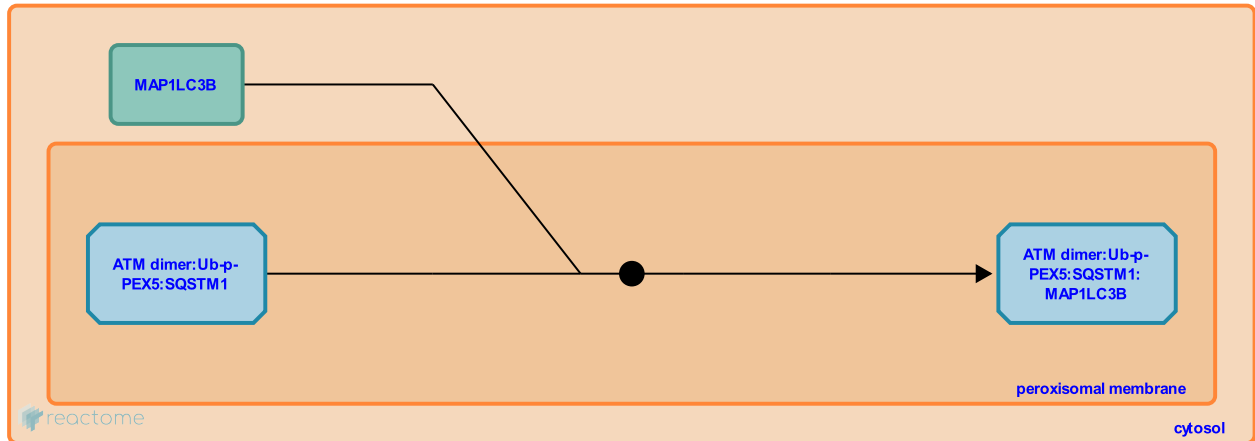
This document contains 1 reaction ([see Table of Contents](#))

## MAP1LC3B binds ATM dimer:Ub-p-PEX5:SQSTM1 [↗](#)

**Stable identifier:** R-HSA-9664855

**Type:** binding

**Compartments:** peroxisomal membrane



Sequestosome 1 (SQSTM1) is an autophagic receptor that recruits ubiquitinated cargo to the autophagosome. SQSTM1 contains a ubiquitin associated (UBA) domain that binds to monoubiquitinated Peroxisomal targeting signal 1 receptor (PEX5) in the peroxisome and an LC3 interacting region (LIR) that binds to Microtubule associated proteins 1A/1B light chain 3B (MAP1LC3B)/LC3 associated with the nascent autophagosome (Pankiv S et al. 2007). Subsequently, the peroxisome is degraded by the autophagy machinery.

### Literature references

Bruun, JA., Clausen, TH., Pankiv, S., Lamark, T., Brech, A., Johansen, T. et al. (2007). p62/SQSTM1 binds directly to Atg8/LC3 to facilitate degradation of ubiquitinated protein aggregates by autophagy. *J. Biol. Chem.*, 282, 24131-45.

[↗](#)

### Editions

2019-10-29	Authored	Varusai, TM.
2019-10-30	Reviewed	Metzakopian, E.
2020-01-13	Edited	Varusai, TM.