

SQSTM1 binds 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.

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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 77

This document contains 1 reaction (see Table of Contents)

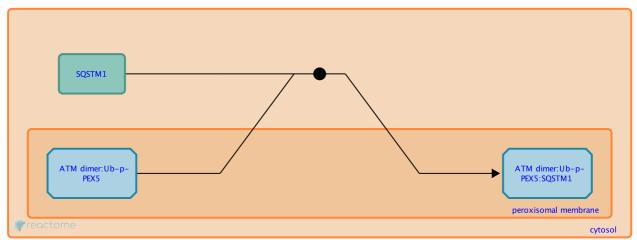
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SQSTM1 binds ATM dimer:Ub-p-PEX5 **↗**

Stable identifier: R-HSA-9664892

Type: binding

Compartments: cytosol, peroxisomal membrane



Sequestosome 1 (SQSTM1) is an autophagy adaptor that serves to bridge ubiquitinated cargo and the autophagosome. It binds ubiquitinated cargo via its UBA domain. SQSTM1 in the cytosol recognizes and binds with ubiquitinated Peroxisomal targeting signal 1 receptor (PEX5) in the peroxisomal membrane (Zhang et al. 2015).

Literature references

Zhang, J., Tripathi, DN., Jing, J., Alexander, A., Kim, J., Powell, RT. et al. (2015). ATM functions at the peroxisome to induce pexophagy in response to ROS. *Nat. Cell Biol.*, 17, 1259-69.

Editions

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

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