ATM binds PEX5

Metzakopian, E., Varusai, TM.

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

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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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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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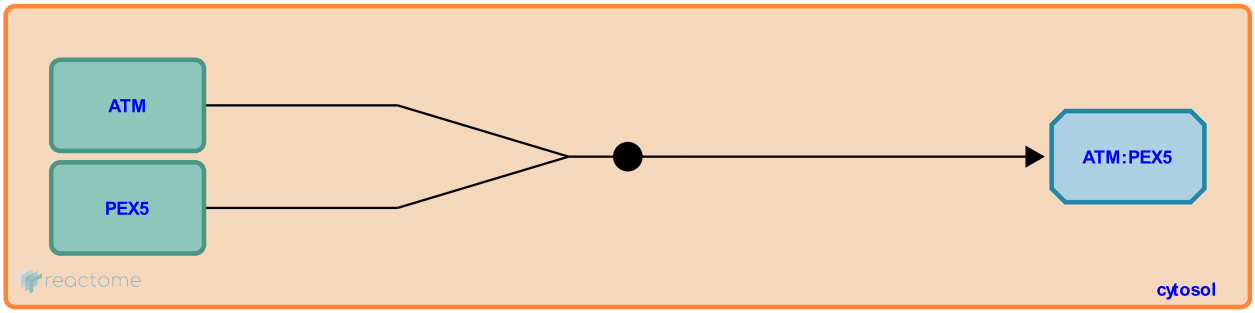
Stable identifier: R-HSA-9664850

Type: binding

Compartments: cytosol



The first step in pexophagy is the initiation by a signal that triggers downstream events to eventually degrade the peroxisome. Ataxia-telangiectasia mutated protein (ATM) is a serine/threonine protein kinase that is involve in DNA damage response. ATM is known to be involved in pexophagy (Katarzyna ZR et al. 2016). ATM binds with Peroxisomal targeting signal 1 receptor (PEX5) with the help of a SRL binding sequence in ATM (Zhang J et al. 2015).

Literature references

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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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