Pexophagy

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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


Reactome database release: 79

This document contains 1 pathway and 13 reactions (see Table of Contents)
Pexophagy

**Stable identifier:** R-HSA-9664873

**Compartments:** peroxisomal membrane, cytosol

Peroxisomes are cytosolic organelles involved in the catabolism of branched and long-chain fatty acids and in the reduction of reactive oxygen species (ROS). Peroxisomes homeostasis is critical to maintain ROS levels. Consequently, it is important to eliminate dysfunctional peroxisomes. The degradation of peroxisomes by autophagy is known as pexophagy (Katarzyna ZR et al. 2016). Pexophagy can be triggered by a shift in nutrient conditions.

**Literature references**


**Editions**

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<th>Date</th>
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<tr>
<td>2019-10-29</td>
<td>Authored, Edited</td>
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<td>2019-10-30</td>
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ATM binds PEX5

Location: Pexophagy

Stable identifier: R-HSA-9664850