

PEX7 binds cargo proteins containing PTS2

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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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Reactome database release: 88

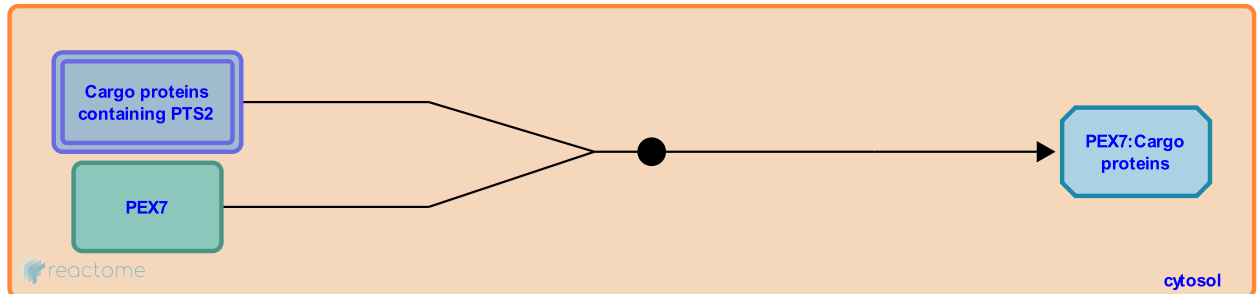
This document contains 1 reaction ([see Table of Contents](#))

PEX7 binds cargo proteins containing PTS2 [↗](#)

Stable identifier: R-HSA-9033232

Type: binding

Compartments: cytosol



Cytosolic PEX7 binds peroxisome targeting signal 2 (PTS2), a sequence of nine amino acid residues functionally identified in 3 human peroxisomal matrix proteins (Braverman et al. 1997, Motley et al. 1997, Purdue et al. 1997, Braverman et al. 2000, Ghys et al. 2002, Motley et al. 2002, Kunze et al. 2011, Kunze et al. 2015). According to molecular modeling, the PTS2 consensus sequence binds a groove in PEX7 (Kunze et al. 2011). Mutations in PEX7 cause rhizomelic chondrodysplasia punctata type 1 (Braverman et al. 1997, Motley et al. 1997, Purdue et al. 1997).

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Editions

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