

PEX19 binds class I peroxisomal membrane proteins

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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

- 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

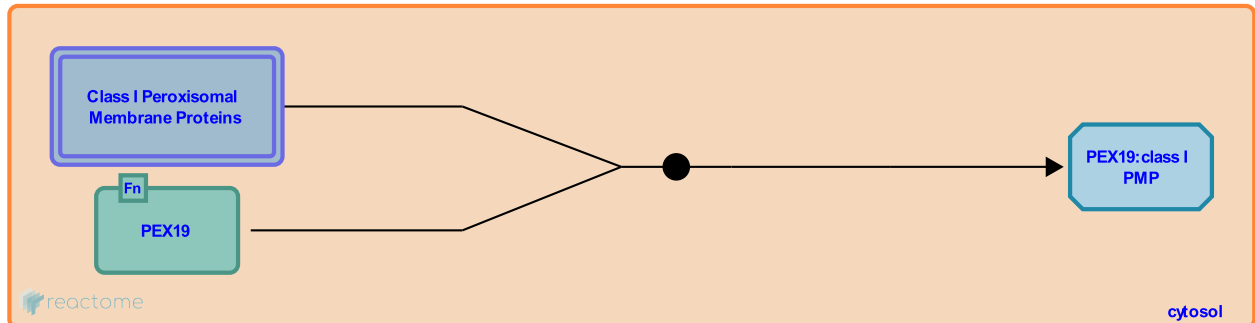
This document contains 1 reaction ([see Table of Contents](#))

PEX19 binds class I peroxisomal membrane proteins [↗](#)

Stable identifier: R-HSA-9603804

Type: binding

Compartments: cytosol



In the cytosol, PEX19 binds newly synthesized class I peroxisomal membrane proteins (Sacksteder et al. 2000, Fransen et al. 2001, Jones et al. 2004, reviewed in Fujiki et al. 2006). The C-terminal region and a conserved N-terminal helical segment of PEX19 bind to peroxisomal membrane proteins (Fransen et al. 2005, Schueller et al. 2010) and PEX19 acts both as a chaperone and as an import receptor (Jones et al. 2004). PEX19 is farnesylated (Götte et al. 1998, Sacksteder et al. 2000, Vastiau et al. 2006) and the farnesyl group is buried in a hydrophobic cavity which alters the conformation of PEX19 to yield two hydrophobic pockets involved in binding peroxisomal membrane proteins (Emmanouilidis et al. 2017). The number of positively charged amino acid residues in the transmembrane domain of the PMP appears to determine binding by PEX19 and, hence, targeting to the peroxisomal membrane protein (Costello et al. 2017).

Class I membrane proteins are inserted into the peroxisomal membrane after peroxisomal progenitors have budded from the endoplasmic reticulum (Jones et al. 2004). Human class I peroxisomal membrane proteins that are bound by PEX19 include PEX10 (Sacksteder et al. 2000), PEX11B (Fransen et al. 2005), PEX12 (Sacksteder et al. 2000, Fransen et al. 2001, Fransen et al. 2005), PEX13 (Sacksteder et al. 2000, Fransen et al. 2001, Fransen et al. 2005, Vastiau et al. 2006, Liu et al. 2016), PEX14 (Sacksteder et al. 2000, Fransen et al. 2005, Vastiau et al. 2006), PEX16 (Fransen et al. 2001, Fransen et al. 2005, Matsuzono and Fujiki 2006, Schueller et al. 2010, Yagita et al. 2013, Liu et al. 2016), PEX26 (Fransen et al. 2005, Matsuzono and Fujiki 2006), ABCD1 (ALDP, Mayerhofer et al. 2002, Halbach et al. 2005), ABCD2 (ALDRP, Mayerhofer et al. 2002), ABCD3 (PMP70, Sacksteder et al. 2000, Mayerhofer et al. 2002), PXMP2 (PMP22, Jones et al. 2001, Brosius et al. 2002), PXMP4 (PMP24, Pinto et al. 2006), SLC25A17 (PMP34, Sacksteder et al. 2000, Liu et al. 2016), ATAD1 (Liu et al. 2016), FIS1 (Delille and Schrader 2008), and GDAP1 (Huber et al. 2013).

Literature references

- Milewski, M., Schliebs, W., Wilmanns, M., Wolf, J., Konarev, P., Song, YH. et al. (2010). The peroxisomal receptor Pex19p forms a helical mPTS recognition domain. *EMBO J.*, 29, 2491-500. [↗](#)
- Schrader, M., Suter, U., Guimaraes, S., Niemann, A., Huber, N. (2013). Charcot-Marie-Tooth disease-associated mutants of GDAP1 dissociate its roles in peroxisomal and mitochondrial fission. *EMBO Rep.*, 14, 545-52. [↗](#)
- Lorenzen, S., Rottensteiner, H., Volkmer-Engert, R., Landgraf, C., Erdmann, R., Halbach, A. (2005). Function of the PEX19-binding site of human adrenoleukodystrophy protein as targeting motif in man and yeast. PMP targeting is evolutionarily conserved. *J. Biol. Chem.*, 280, 21176-82. [↗](#)
- Mannaerts, GP., Brams, M., Van de Velde, S., Vastiau, IM., Van Veldhoven, PP., Anthonio, EA. et al. (2006). Farnesylation of Pex19p is not essential for peroxisome biogenesis in yeast and mammalian cells. *Cell. Mol. Life Sci.*, 63, 1686-99. [↗](#)
- Hiromasa, T., Yagita, Y., Fujiki, Y. (2013). Tail-anchored PEX26 targets peroxisomes via a PEX19-dependent and TRC40-independent class I pathway. *J. Cell Biol.*, 200, 651-66. [↗](#)

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