USP9X hydrolyzes Ub:PEX5L yielding PEX5L and Ubiquitin

Azevedo, JE., Fransen, M., May, B., Van Veldhoven, PP.
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: 78

This document contains 1 reaction (see Table of Contents)
USP9X hydrolyzes Ub:PEX5L yielding PEX5L and Ubiquitin

Stable identifier: R-HSA-9033491

Type: transition

Compartments: cytosol

The deubiquitinating enzyme USP9X hydrolyzes the thioester bond between the carboxyl terminus of ubiquitin and cysteine-11 of PEX5L (Grou et al. 2012). The thioester bond is unstable and appears to be also spontaneously (non-enzymatically) disrupted by nucleophilic attack of small metabolites such as reduced glutathione (Grou et al. 2009).

Literature references


Editions

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