

USP9X binds Ub:PEX5S

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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](#))

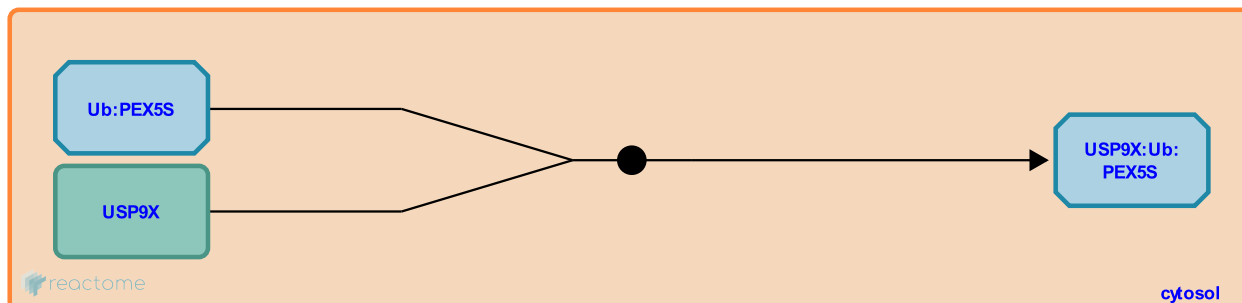
USP9X binds Ub:PEX5S [↗](#)

Stable identifier: R-HSA-9033526

Type: binding

Compartments: cytosol

Inferred from: [USP9X binds Ub:PEX5L \(Homo sapiens\)](#)



The deubiquitinating enzyme USP9X binds cytosolic ubiquitinated PEX5S (Ub:PEX5S) and then hydrolyzes the thioester bond between the carboxyl terminus of ubiquitin and cysteine-11 of PEX5S (inferred from the large isoform of PEX5 in Grou et al. 2012).

Literature references

Domingues, P., Sá-Miranda, C., Rodrigues, TA., Freitas, MO., Grou, CP., Carvalho, AF. et al. (2012). Identification of ubiquitin-specific protease 9X (USP9X) as a deubiquitinase acting on ubiquitin-peroxin 5 (PEX5) thioester conjugate. *J. Biol. Chem.*, 287, 12815-27. [↗](#)

Editions

2017-12-20	Authored, Edited	May, B.
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