USP9X hydrolyzes Ub:PEX5S yielding PEX5S and Ubiquitin

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

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

22/04/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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. ↗

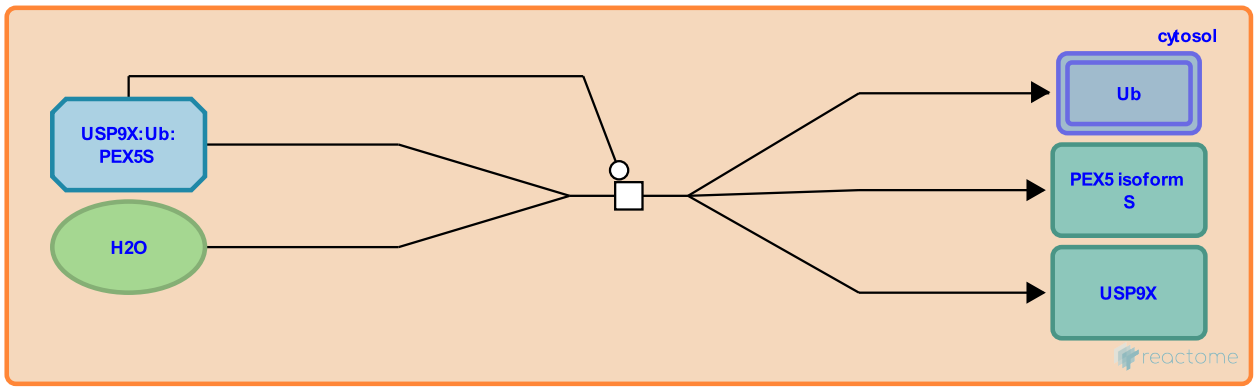
USP9X hydrolyzes Ub:PEX5S yielding PEX5S and Ubiquitin ↗

Stable identifier: R-HSA-9033478

Type: transition

Compartments: cytosol

Inferred from: USP9X hydrolyzes Ub:PEX5L yielding PEX5L and Ubiquitin (Homo sapiens)



The deubiquitinating enzyme USP9X hydrolyzes the thioester bond between the carboxyl terminus of ubiquitin and cysteine-11 of PEX5S (inferred from the large isoform of PEX5L in Grou et al. 2012). The thioester bond is unstable and appears also to be spontaneously disrupted by nucleophilic attack of small metabolites such as reduced glutathione (Grou et al. 2009).

Literature references

Huybrechts, SJ., Sá-Miranda, C., Grou, CP., Carvalho, AF., Azevedo, JE., Pinto, MP. et al. (2009). Properties of the ubiquitin-pex5p thiol ester conjugate. *J. Biol. Chem., 284*, 10504-13. ↗

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.
2018-02-13	Reviewed	Van Veldhoven, PP., Fransen, M.
2018-03-12	Reviewed	Azevedo, JE.