USP9X deubiquitinates Ub-SNCA

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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

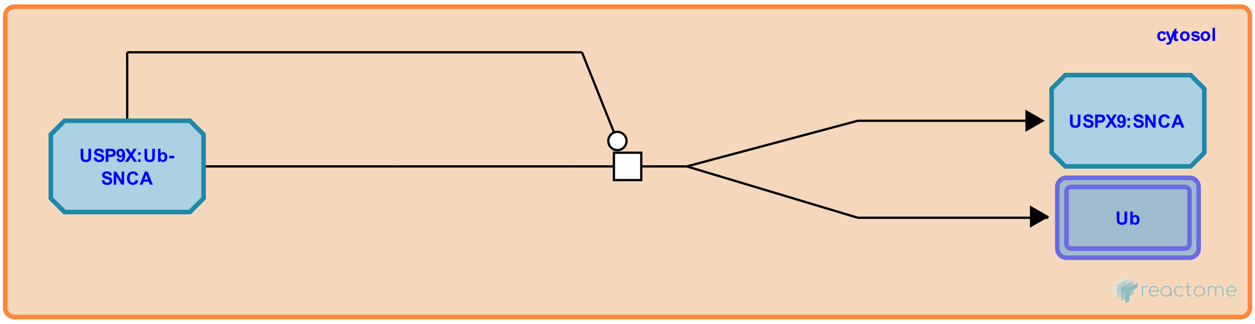
This document contains 1 reaction (see Table of Contents)

USP9X deubiquitinates Ub-SNCA ↗

Stable identifier: R-HSA-5660752

Type: transition

Compartments: cytosol



The deubiquitinase USP9X binds and deubiquitinates alpha-synuclein (SNCA) in vitro and in vivo, showing co-accumulation with SNCA in Lewy Bodies. Knockdown of USP9X expression in conditions of proteolytic inhibition leads to the accumulation of monoubiquitinated SNCA and increases the aggregation of SNCA into toxic inclusions, strengthening the connection between monoubiquitination, inclusion formation, and toxicity of SNCA. USP9X cytosolic levels are lower in Diffuse Lewy Body disease and Parkinson's Disease tissues, which may contribute to the accumulation and aggregation of monoubiquitinated SNCA (Rott et al. 2011).

Literature references

Lees, AJ., Rott, R., Engelender, S., Haskin, J., Szargel, R., Bandopadhyay, R. et al. (2011). ?-Synuclein fate is determined by USP9X-regulated monoubiquitination. *Proc. Natl. Acad. Sci. U.S.A.*, *108*, 18666-71. ↗

Editions

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