SYVN1 ubiquitinates Hh C-terminal fragments

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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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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. ↗

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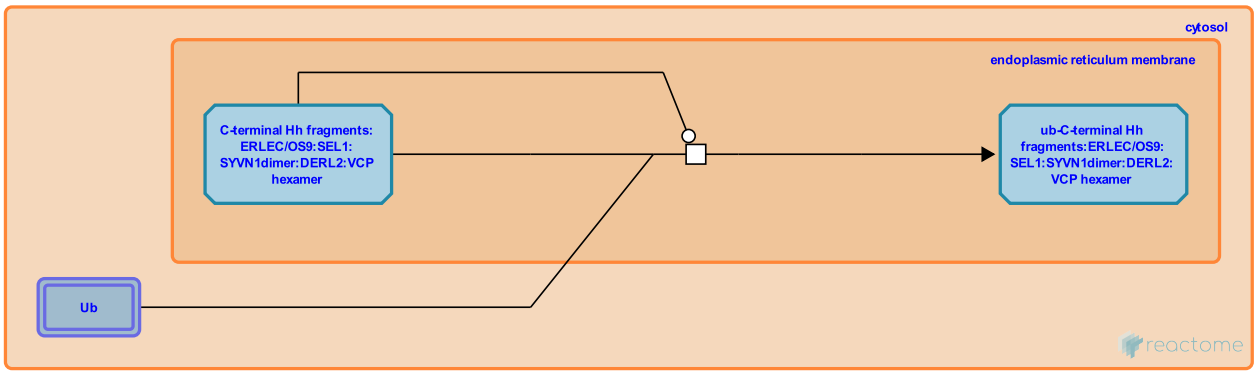
Stable identifier: R-HSA-5362412

Type: transition

Compartments: endoplasmic reticulum membrane



SYVN1 ubiquitinates Hh-C as part of the retrotranslocon that targets these Hh fragments for degradation through the ERAD pathway. Both depletion of SYVN1 by siRNA and expression of a catalytically inactive form of the enzyme strongly inhibits Hh-C degradation. Consistent with this, a dominant negative version of SYVN1 abrogates the polyubiquitination of Hh-C as assessed by IP-Western from HEK293 cells (Chen et al, 2011).

Literature references

Jao, C., Rapoport, TA., Tang, HY., Chu, YR., Schulman, S., Huang, CH. et al. (2011). Processing and turnover of the Hedgehog protein in the endoplasmic reticulum. *J. Cell Biol., 192*, 825-38.

Editions

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