RCE1 cleaves S-Farn proRAS proteins

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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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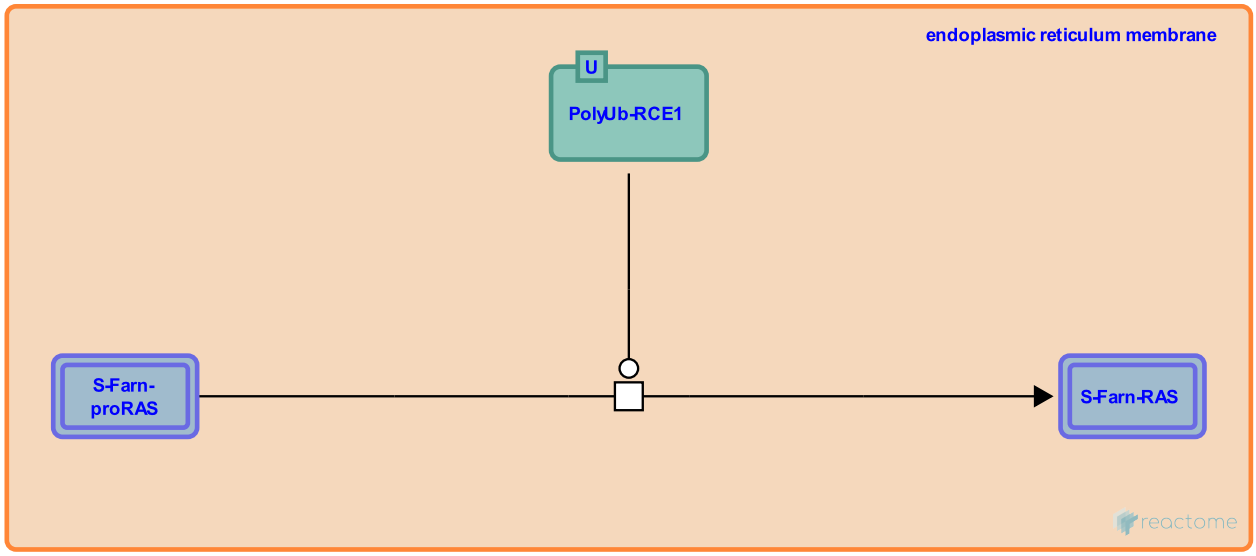
Stable identifier: R-HSA-9647999

Type: transition

Compartments: endoplasmic reticulum membrane



After prenylation, RAS proteins undergo C-terminal endoproteolysis by RAS-converting enzyme I (RCE1), which removes the aaX residues of the CaaX motif (Otto et al, 1999; Hollander et al, 2000; reviewed in Hampton et al, 2018; Ahearn et al, 2018). RCE1-mediated cleavage is required for RAS plasma membrane localization and function (Michaelson et al, 2005). RCE1 is ubiquitinated in its active form, and deubiquitination by USP17L2 abrogates its catalytic activity and inhibits signaling through the RAS-RAF MAP kinase pathway (Burrows et al, 2009). RCE1 has thus been investigated as a potential therapeutic target in RAS driven disease. Despite some promising studies, the effects of RCE1 inactivation appear unpredictable and can lead to unexpected activation of RAS signaling through mechanisms that are not fully understood (Bergo et al, 2002; Aiyagari et al, 2003; Kim et al, 1999; Chen et al, 1998; Chen et al, 1999; Wahlstrom et al, 2007).

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Editions

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