RAS processing

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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


Reactome database release: 79

This document contains 1 pathway and 21 reactions (see Table of Contents)
**RAS processing**

**Stable identifier:** R-HSA-9648002

RAS proteins undergo several processing steps during maturation including farnesylation, carboxy-terminal cleavage and carboxymethylation, among others. These steps are required for their membrane localization and function and ultimately for their ability to activate RAF (reviewed in Gysin et al, 2011; Ahearn et al, 2018).

**Literature references**


**Editions**

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pro-RAS proteins are farnesylated

Location: RAS processing

Stable identifier: R-HSA-9647978