

Ubiquitin-dependent degradation controls basal levels of R-Smad1/5/8

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03/05/2024

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

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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 88

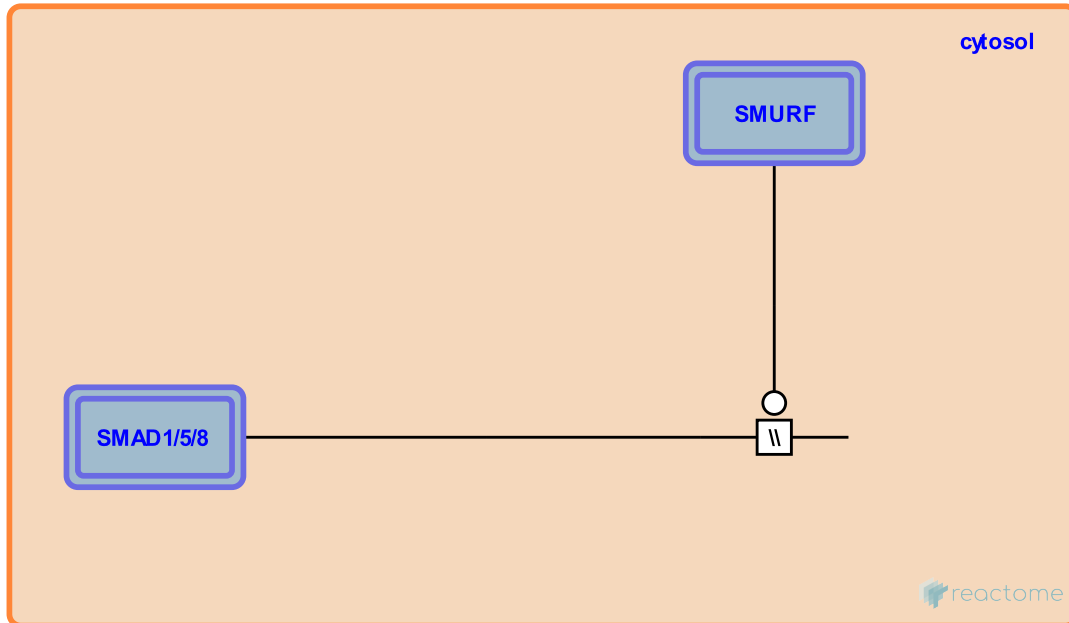
This document contains 1 reaction ([see Table of Contents](#))

Ubiquitin-dependent degradation controls basal levels of R-Smad1/5/8 [↗](#)

Stable identifier: R-HSA-201445

Type: omitted

Compartments: cytosol



SMAD2 is polyubiquitinated by SMURF2 and targeted for proteasome-mediated degradation.

Literature references

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Editions

2007-11-07	Authored	Moustakas, A., Huminiecki, L.
2007-11-12	Reviewed	Heldin, CH.
2019-02-08	Revised	Mi, H.