

# An anchoring protein, Endofin, recruits R- Smad1/5/8

Heldin, CH., Huminiecki, L., Jassal, B., Moustakas, A.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

## 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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- 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. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 76

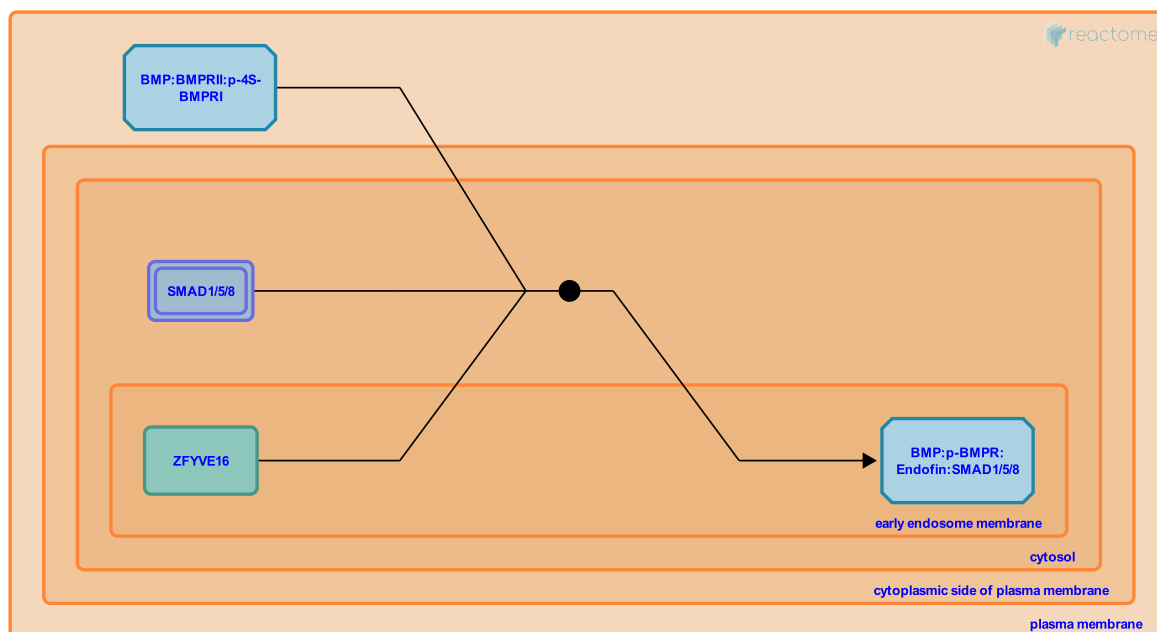
This document contains 1 reaction ([see Table of Contents](#))

## An anchoring protein, Endofin, recruits R-Smad1/5/8 [↗](#)

**Stable identifier:** R-HSA-201648

**Type:** binding

**Compartments:** cytosol, plasma membrane, early endosome membrane



Endofin is a FYVE domain-containing protein that strongly resembles SARA, the Smad anchor for receptor activation that facilitates TGF-beta signalling. Endofin acts in a similar manner as SARA, it binds to BMP-specific R-Smads, it localizes in early endosomes and it facilitates their phosphorylation, thus promoting signal transduction by the BMP receptors. However, it should be noted that endofin has also been reported to bind to the Co-Smad, Smad4, and to the TGF-beta type receptor, thus enhancing TGF-beta signalling. Since Smad4 is a common Smad that operates in the BMP-specific pathways, the latter observation might imply that endofin could regulate both TGF-beta and BMP signalling, a hypothesis still open for investigation.

### Literature references

Shi, W., Chang, C., Nie, S., Xie, S., Wan, M., Cao, X. (2007). Endofin acts as a Smad anchor for receptor activation in BMP signaling. *J Cell Sci*, 120, 1216-24. [↗](#)

### Editions

2007-09-03	Edited	Jassal, B.
2007-11-07	Authored	Moustakas, A., Huminiecki, L.
2007-11-12	Reviewed	Heldin, CH.