

# F-actin capping protein binds to the barbed end of elongating F-actin

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https://reactome.org

# 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

- 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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

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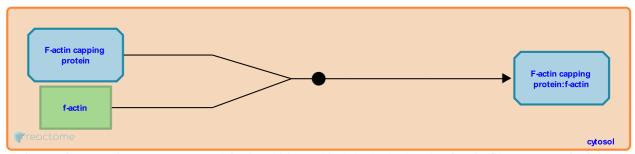
# 

Stable identifier: R-HSA-994169

Type: binding

**Compartments:** cytosol

**Inferred from:** F-actin capping protein binds to elongating F-actin (Gallus gallus)



Actin capping protein (CP) was named for its ability to bind the barbed ends of actin filaments. CP inhibits the addition and loss of actin subunits at the barbed end and is important for the dynamics of actin filament assembly, and therefore important for the control of cell shape and movement. CP was called beta-actinin when first characterized and purified from muscle (Maruyama 1966). Actin polymerization is controlled by a large cellular excess of capping proteins which bind to the barbed end of actin filaments preventing elongation.

# **Editions**

2010-10-29	Authored	Akkerman, JW.
2010-11-12	Edited	Jupe, S.
2010-11-12	Reviewed	Ouwehand, WH.