

Formation of TSC1:TSC2 complex

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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

- 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: 88

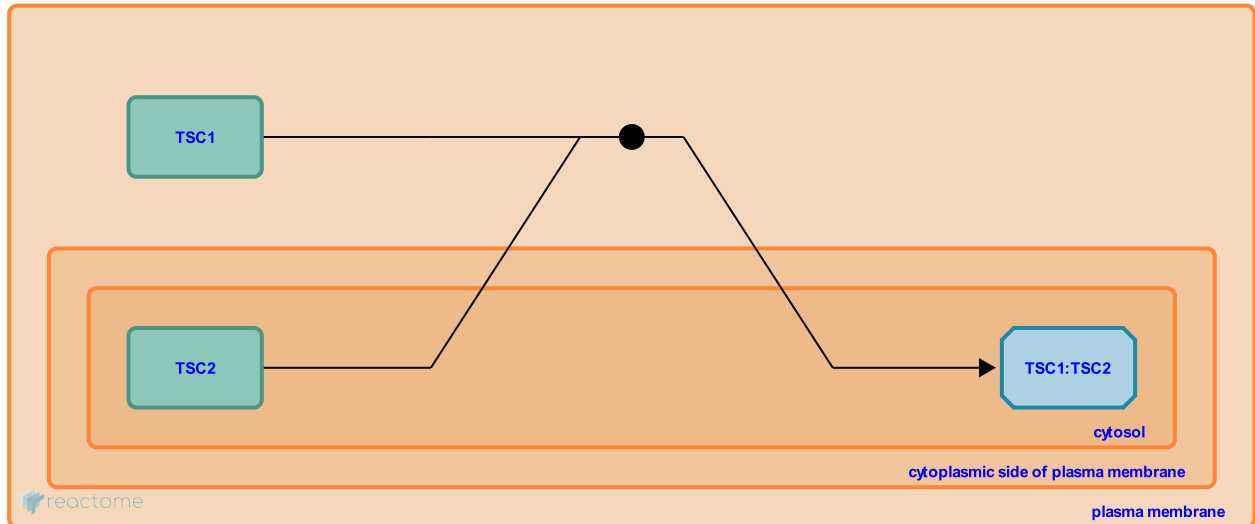
This document contains 1 reaction ([see Table of Contents](#))

Formation of TSC1:TSC2 complex [↗](#)

Stable identifier: R-HSA-165179

Type: binding

Compartments: cytosol, plasma membrane



A membrane-associated TSC1 (hamartin) binds TSC2 (tuberin) and recruits it to the plasma membrane where it can exert its function as a GAP (GTPase activating protein) for the small GTPase RHEB (Cai et al. 2006).

Literature references

Kim, J., Guo, R., Walker, CL., Shen, J., Kiguchi, K., Cai, SL. et al. (2006). Activity of TSC2 is inhibited by AKT-mediated phosphorylation and membrane partitioning. *J. Cell Biol.*, 173, 279-89. [↗](#)

White, MF., Fisher, TL. (2004). Signaling pathways: the benefits of good communication. *Curr Biol*, 14, R1005-7. [↗](#)

Editions

2014-12-23	Authored, Edited	Orlic-Milacic, M.
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