

Assembly of EGFR complex in clathrincoated vesicles

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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

This document contains 1 reaction (see Table of Contents)

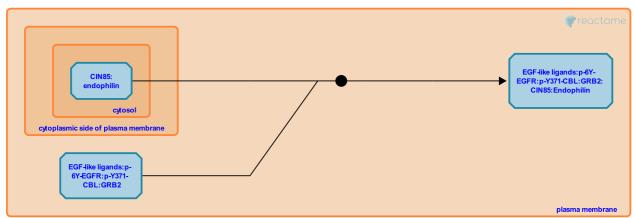
https://reactome.org Page 2

Assembly of EGFR complex in clathrin-coated vesicles

Stable identifier: R-HSA-182994

Type: binding

Compartments: cytosol, plasma membrane



CBL-CIN85-Endophilin complex mediates ligand-induced down-regulation of the EGF receptor. The BAR domain of endophilin induces membrane curvature. The three SH3 domains of CIN85 bind to atypical proline-arginine motifs (PxxxPR) present in the carboxyl termini of CBL and CBL-b. In this way, CIN85 clusters CBL molecules, which is crucial for efficient EGFR endocytosis and degradation (Soubeyran et al. 2002).

Literature references

Szymkiewicz, I., Soubeyran, P., Langdon, WY., Kowanetz, K., Dikic, I. (2002). Cbl-CIN85-endophilin complex mediates ligand-induced downregulation of EGF receptors. *Nature*, 416, 183-7.

Editions

2006-10-10	Authored	Castagnoli, L.
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