

EGFR non-clathrin mediated endocytosis

Castagnoli, L., Heldin, CH.

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](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

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

- 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

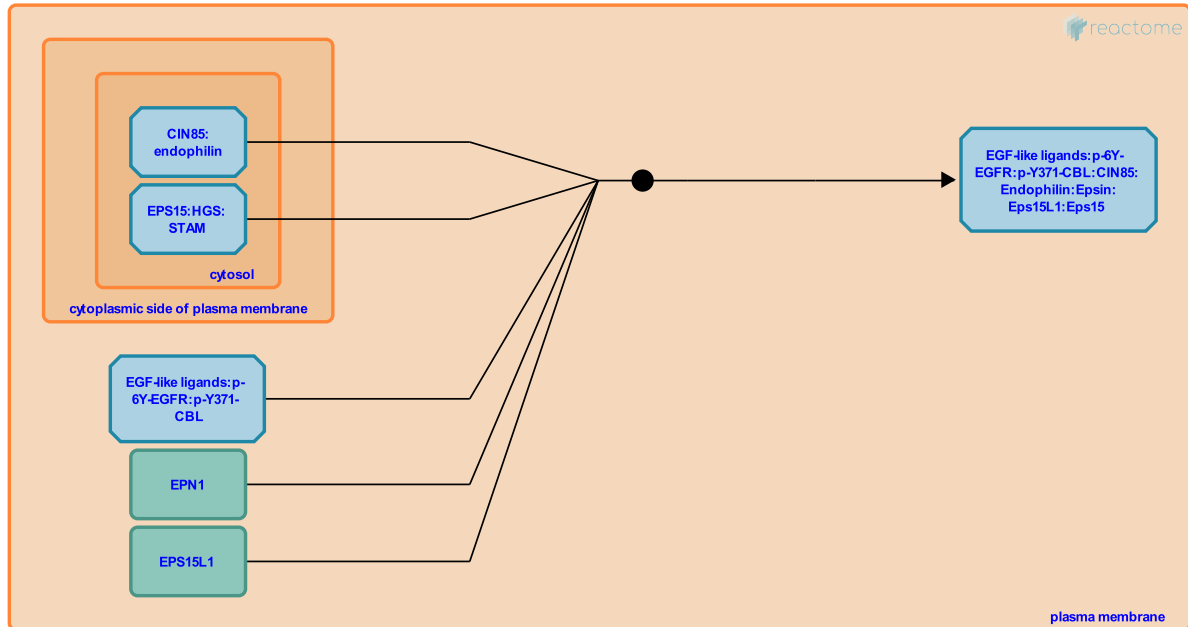
This document contains 1 reaction ([see Table of Contents](#))

EGFR non-clathrin mediated endocytosis [↗](#)

Stable identifier: R-HSA-183072

Type: binding

Compartments: cytosol, plasma membrane



At higher concentrations of ligand, a substantial fraction of the receptor (>50%) is endocytosed through a clathrin independent, lipid-raft-dependent route as the receptor becomes Y1069 (i.e. Y1045 in the mature protein) phosphorylated and ubiquitinated. Eps15 and Epsin are found in caveolae. Eps15 and Epsin are immunoprecipitated with the EGF receptor. Non-clathrin internalization of ubiquitinated EGFR depends on its interaction with proteins harbouring the UIM Ub-interacting motif, as shown through the ablation of three Ub-interacting motif-containing proteins, Eps15, Eps15R and Epsin.

Literature references

- Pijnenburg, M., Lemeer, S., van Bergen en Henegouwen, PM., Sorokina, I., Klapisz, E., Verkleij, AJ. (2002). A ubiquitin-interacting motif (UIM) is essential for Eps15 and Eps15R ubiquitination. *J Biol Chem*, 277, 30746-53. [↗](#)
- Di Fiore, PP., Tacchetti, C., Transidico, P., Puri, C., Maspero, E., Polo, S. et al. (2005). Clathrin-independent endocytosis of ubiquitinated cargos. *Proc Natl Acad Sci U S A*, 102, 2760-5. [↗](#)

Editions

2006-10-10

Authored

Castagnoli, L.

2008-02-12

Reviewed

Heldin, CH.