Binding of CBL to EGFR

Castagnoli, L., Heldin, CH., Orlic-Milacic, M.

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

04/05/2024

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. ↗

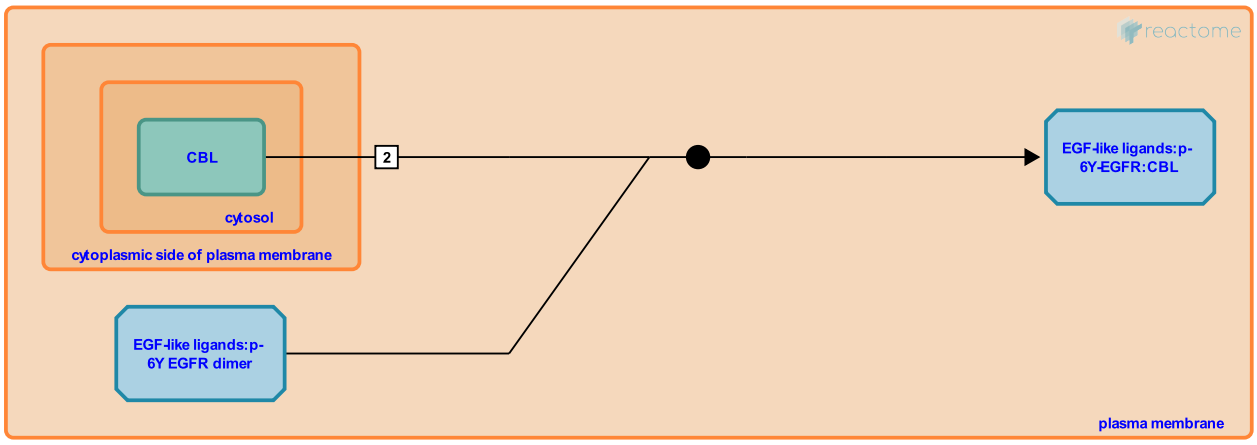
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Binding of CBL to EGFR ↗

Stable identifier: R-HSA-183055

Type: binding

Compartments: plasma membrane, extracellular region



Phosphorylation at tyrosine Y1069 (i.e. Y1045 in the mature protein) of EGFR creates a major docking site for E3 ubiquitin-protein ligase, CBL (Casitas B-lineage lymphoma proto- oncogene) and is required to sort the EGFR to lysosomes for degradation. The E3 ligase CBL plays a crucial role in these events as it dually participates in early events of internalization via a CIN85-endophilin dependent mechanism and endocytic sorting by mediating multiple monoubiquitylation of the receptor.

Literature references

Grovdal, LM., Madshus, IH., Stang, E., Sorkin, A. (2004). Direct interaction of Cbl with pTyr 1045 of the EGF receptor (EGFR) is required to sort the EGFR to lysosomes for degradation. *Exp Cell Res, 300*, 388-95. ↗

Editions

2006-10-10	Authored	Castagnoli, L.
2008-02-12	Reviewed	Heldin, CH.
2011-08-25	Edited	Orlic-Milacic, M.