

Phosphorylation of CBL (EGFR:CBL)

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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

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- 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. [↗](#)
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Reactome database release: 88

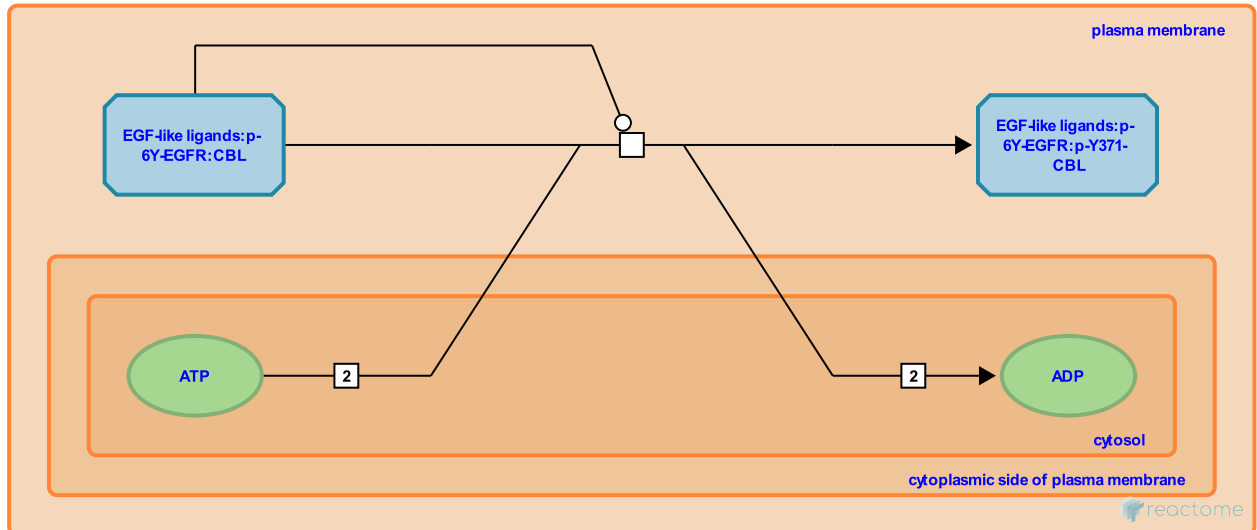
This document contains 1 reaction ([see Table of Contents](#))

Phosphorylation of CBL (EGFR:CBL) ↗

Stable identifier: R-HSA-182969

Type: transition

Compartments: cytosol, plasma membrane



EGF (and indeed FGF, PDGF and NGF) stimulation results in CBL phosphorylation on Tyr-371. Phosphorylation is necessary for CBL to exhibit ubiquitin ligase activity.

Literature references

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Kassenbrock, CK., Anderson, SM. (2004). Regulation of ubiquitin protein ligase activity in c-Cbl by phosphorylation-induced conformational change and constitutive activation by tyrosine to glutamate point mutations. *J Biol Chem*, 279, 28017-27. ↗

Editions

2006-10-10	Authored	Castagnoli, L.
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