

# CBL ubiquitinates PI3K

Hercus, TR., Jupe, S., Lopez, AF., Ray, KP.

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](#). For more information see our [license](#).

## 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: 73

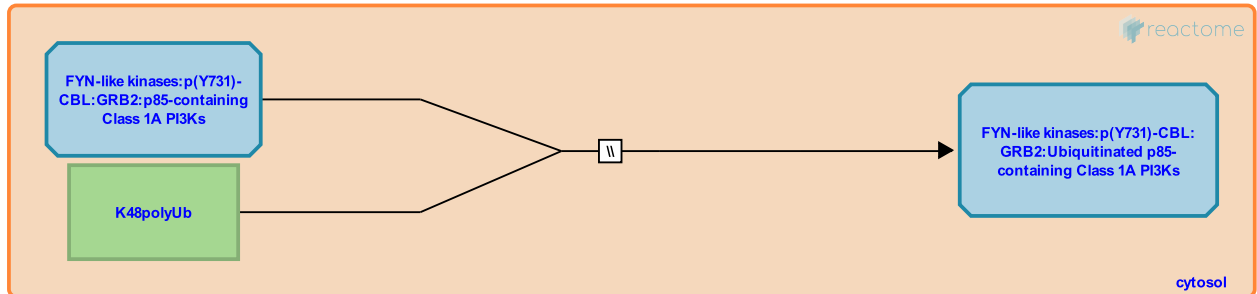
This document contains 1 reaction ([see Table of Contents](#))

## CBL ubiquitinates PI3K [↗](#)

**Stable identifier:** R-HSA-912627

**Type:** omitted

**Compartments:** cytosol



Cbl is an E3 ubiquitin-protein ligase that negatively regulates signaling pathways by targeting proteins for ubiquitination and proteasomal degradation (Rao et al. 2002). Cbl-B targets PI3K for ubiquitination and degradation in T cells (Fang et al. 2000). Similarly, Cbl activation by tyrosine phosphorylation increases PI3K ubiquitination and proteasomal degradation (Dufour et al. 2008).

### Literature references

Dufour, C., Guenou, H., Kaabeche, K., Bouvard, D., Sanjay, A., Marie, PJ. (2008). FGFR2-Cbl interaction in lipid rafts triggers attenuation of PI3K/Akt signaling and osteoblast survival. *Bone*, 42, 1032-9. [↗](#)

### Editions

|            |          |                         |
|------------|----------|-------------------------|
| 2010-05-17 | Authored | Ray, KP.                |
| 2010-08-06 | Edited   | Jupe, S.                |
| 2010-09-06 | Reviewed | Lopez, AF., Hercus, TR. |