

PI3-kinase binds to the active receptor

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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

- 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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

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Stable identifier: R-HSA-186780

Type: binding

Compartments: cytosol, plasma membrane



Phosphatidylinositol 3'-kinases (PI3Ks) are a family of enzymes which can phosphorylate phosphoinositides. PI3Ks bind to and are activated by PDGF receptors. Tyr 740 and Tyr 751 in PDGF beta-receptor, and Tyr 731 and Tyr 742 in PDGF alpha-receptor have been shown to be autophosphorylation sites and to bind PI3-kinase.

Literature references

- Escobedo, JA., Coughlin, SR., Williams, LT. (1989). Role of phosphatidylinositol kinase in PDGF receptor signal transduction. *Science*, 243, 1191-4. ↗
- Ostman, A., Heldin, CH., Rönnstrand, L. (1998). Signal transduction via platelet-derived growth factor receptors. *Biochim Biophys Acta*, 1378, F79-113. 7
- McCormick, F., del Rosario, M., Turck, CW., Escobedo, JA., Martin, GA., Williams, LT. et al. (1992). Distinct phosphotyrosines on a growth factor receptor bind to specific molecules that mediate different signaling pathways. *Cell*, 69, 413-23.

Editions

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