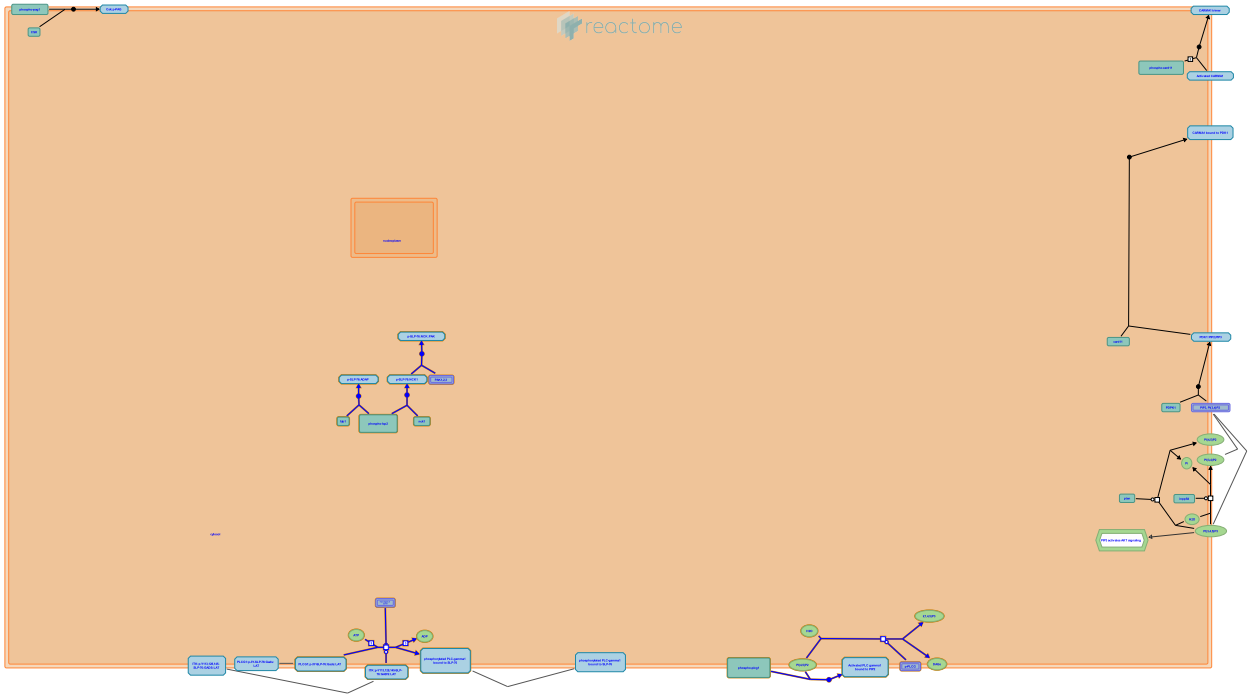
Generation of second messenger molecules



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

This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

12/05/2024

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. ↗

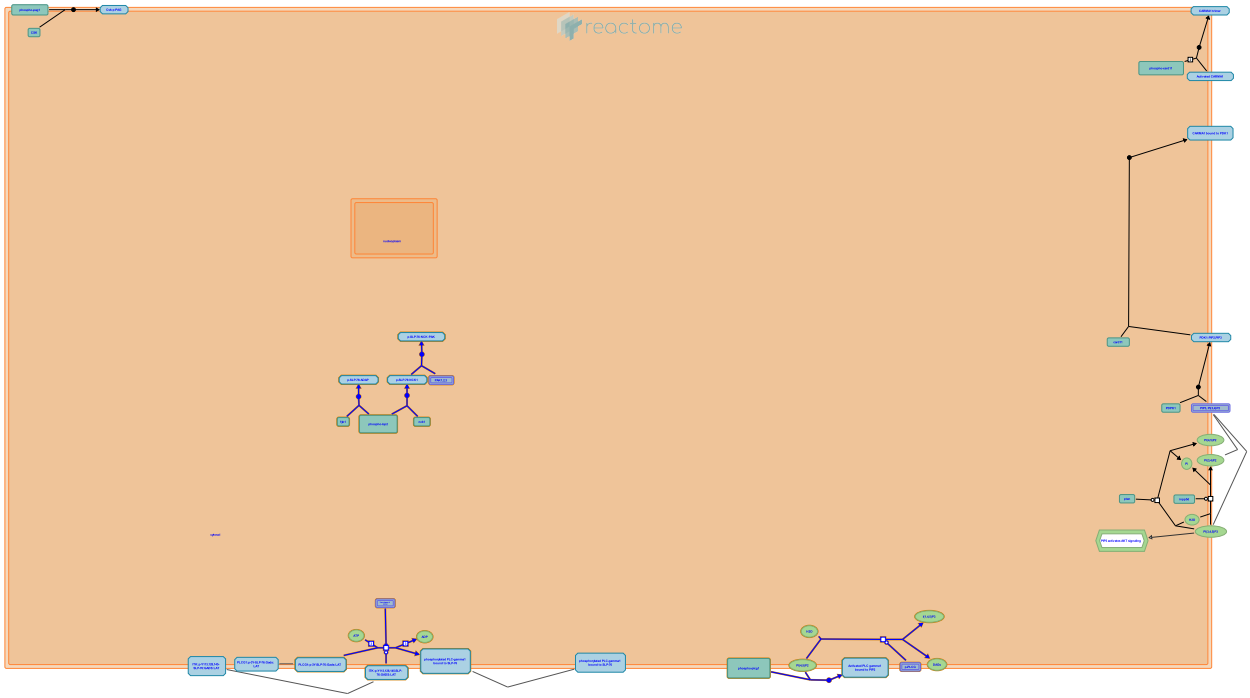
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Generation of second messenger molecules ↗

Stable identifier: R-XTR-202433

Compartments: plasma membrane

Inferred from: Generation of second messenger molecules (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Phosphorylation of PLC-gamma1 ↗

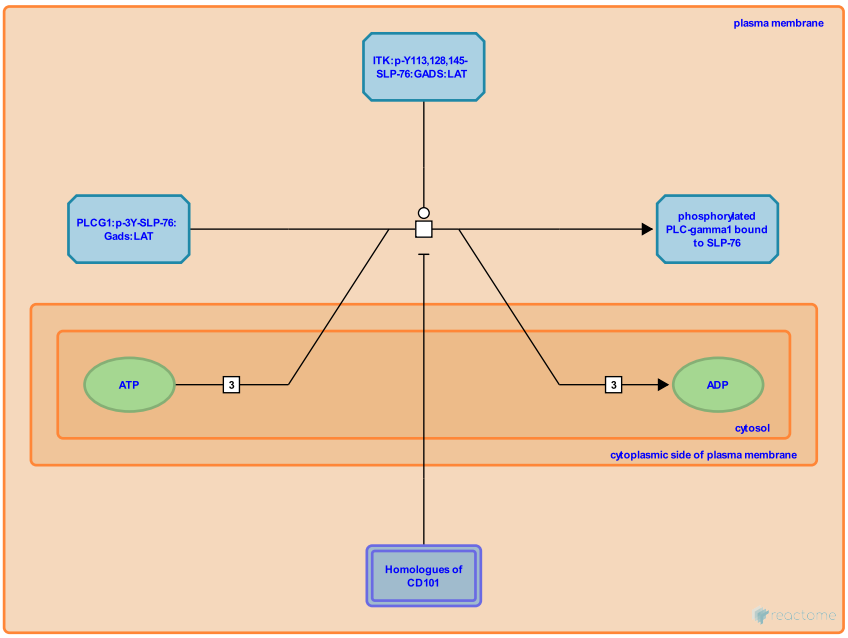
Location: Generation of second messenger molecules

Stable identifier: R-XTR-202248

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: Phosphorylation of PLC-gamma1 (Homo sapiens)



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Followed by: Translocation of PLC-gamma1 to PIP2

Translocation of PLC-gamma1 to PIP2 ↗

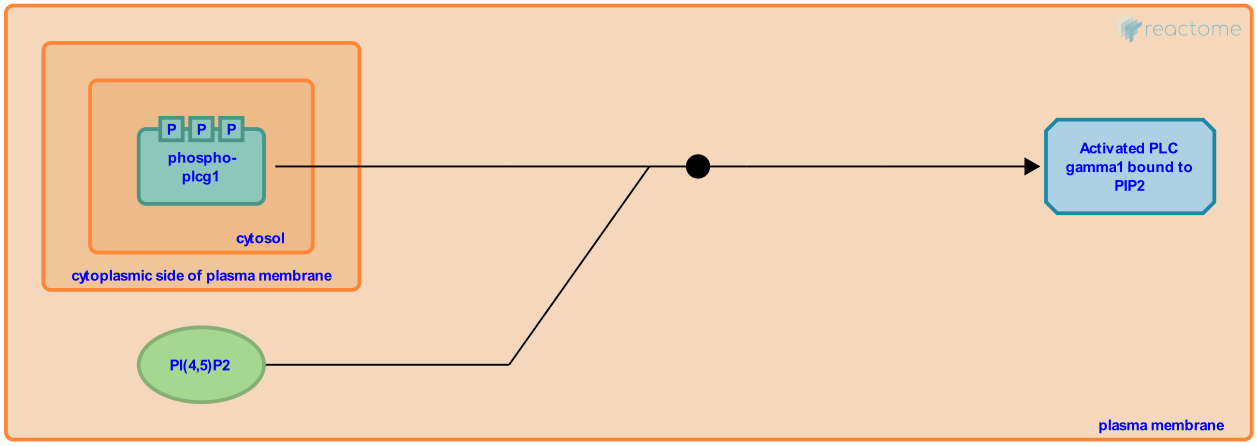
Location: Generation of second messenger molecules

Stable identifier: R-XTR-202354

Type: binding

Compartments: plasma membrane, cytosol

Inferred from: Translocation of PLC-gamma1 to PIP2 (Homo sapiens)



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Preceded by: Phosphorylation of PLC-gamma1

Followed by: PLC-gamma1 hydrolyses PIP2

PLC-gamma1 hydrolyses PIP2 ↗

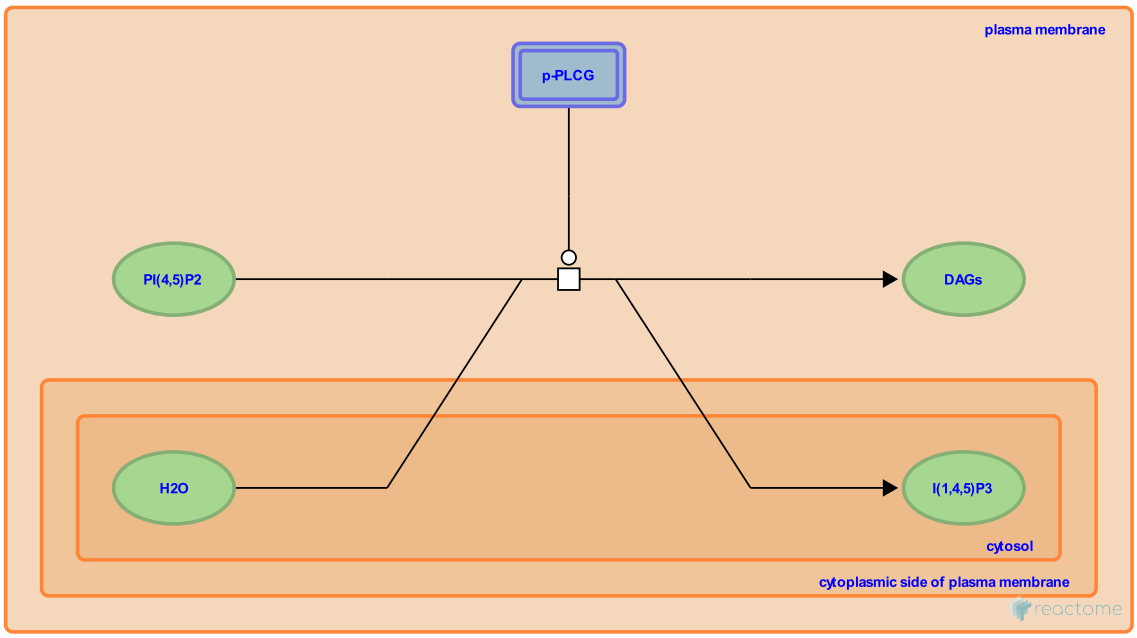
Location: Generation of second messenger molecules

Stable identifier: R-XTR-202407

Type: transition

Compartments: plasma membrane, cytosol

Inferred from: PLC-gamma1 hydrolyses PIP2 (Homo sapiens)



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Preceded by: Translocation of PLC-gamma1 to PIP2

p-SLP-76 binds ADAP ↗

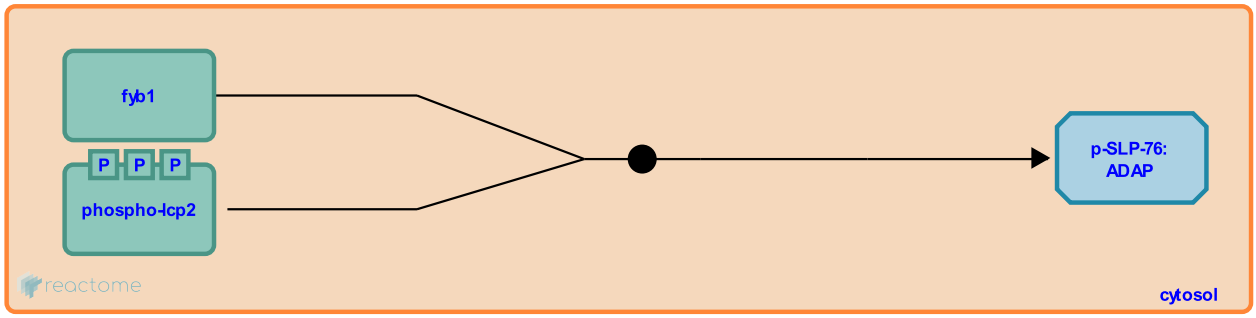
Location: Generation of second messenger molecules

Stable identifier: R-XTR-430135

Type: binding

Compartments: cytosol

Inferred from: p-SLP-76 binds ADAP (Homo sapiens)



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The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

p-SLP-76 binds NCK ↗

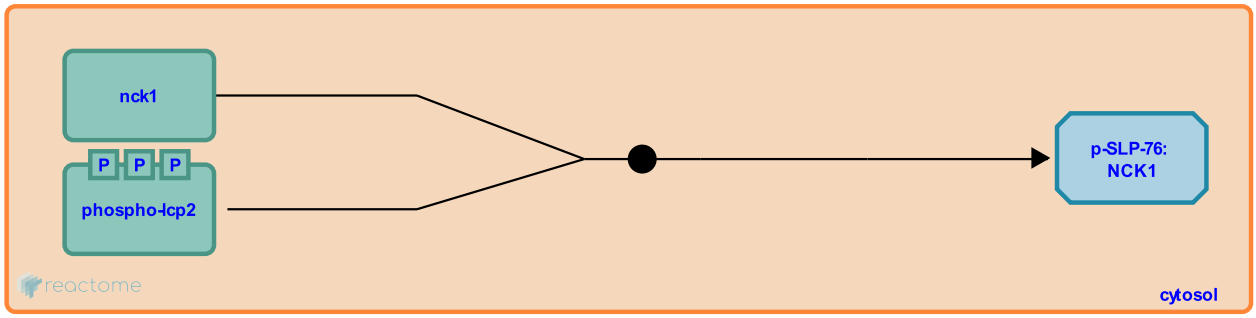
Location: Generation of second messenger molecules

Stable identifier: R-XTR-430190

Type: binding

Compartments: cytosol

Inferred from: p-SLP-76 binds NCK (Homo sapiens)



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NCK binds PAK ↗

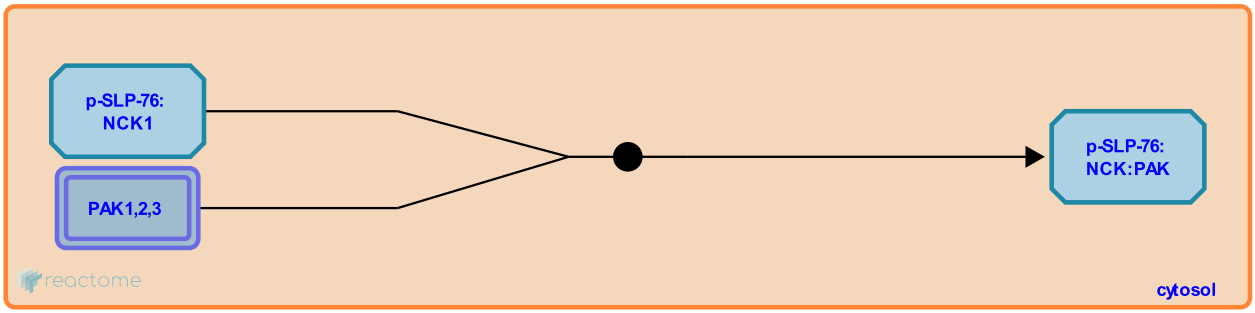
Location: Generation of second messenger molecules

Stable identifier: R-XTR-430183

Type: binding

Compartments: cytosol

Inferred from: NCK binds PAK (Homo sapiens)



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More details and caveats of the event inference in Reactome. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Table of Contents