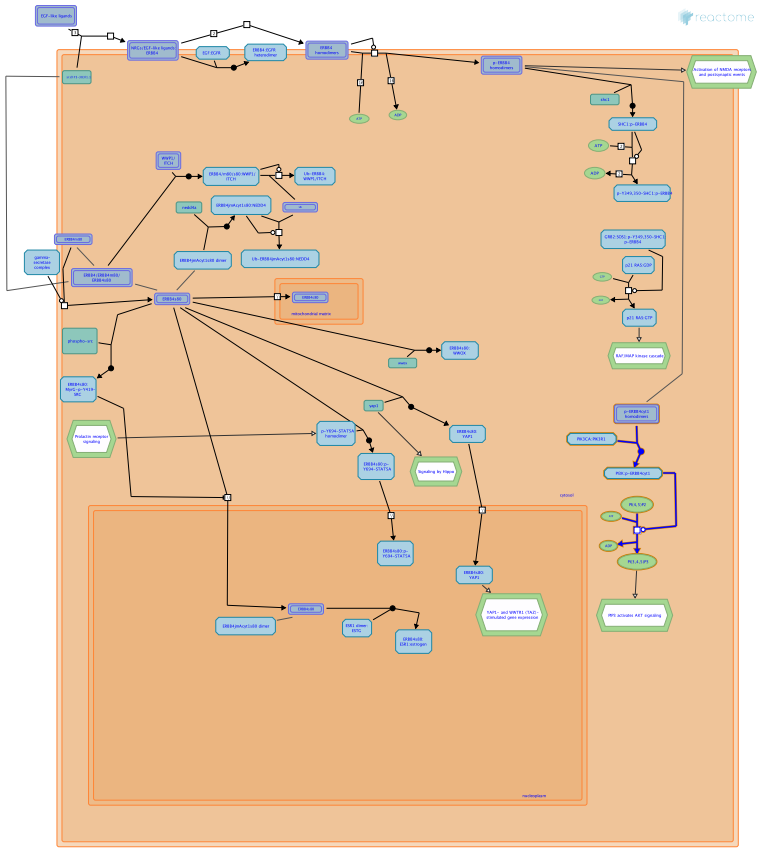
PI3K events in ERBB4 signaling



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

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11/09/2021

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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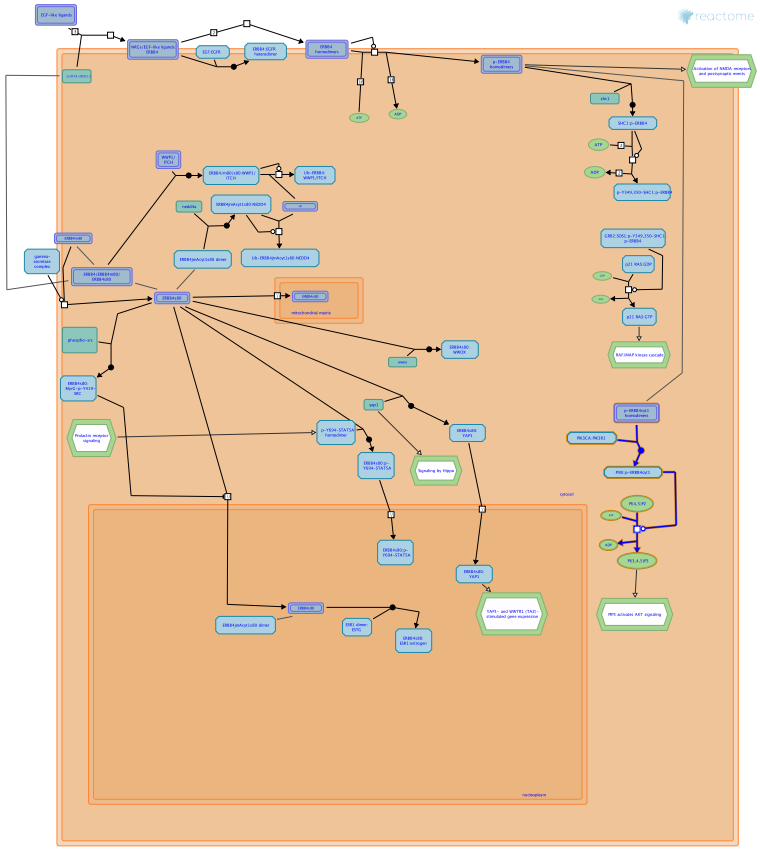
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

PI3K events in ERBB4 signaling ↗

Stable identifier: R-DRE-1250342

Inferred from: PI3K events in ERBB4 signaling (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Binding of p85 subunit of PI3K (PIK3R1) to p-ERBB4cyt1 homodimers ↗

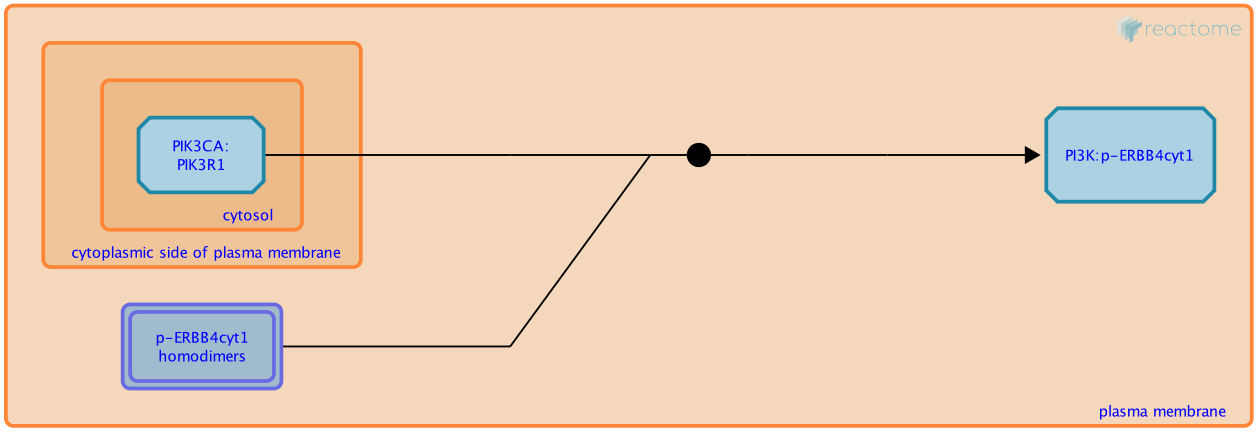
Location: PI3K events in ERBB4 signaling

Stable identifier: R-DRE-1250353

Type: binding

Compartments: plasma membrane, extracellular region

Inferred from: Binding of p85 subunit of PI3K (PIK3R1) to p-ERBB4cyt1 homodimers (Homo sapiens)



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

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Followed by: Conversion of PIP2 into PIP3 by PI3K bound to p-ERBB4cyt1 homodimers

Conversion of PIP2 into PIP3 by PI3K bound to p-ERBB4cyt1 homodimers ↗

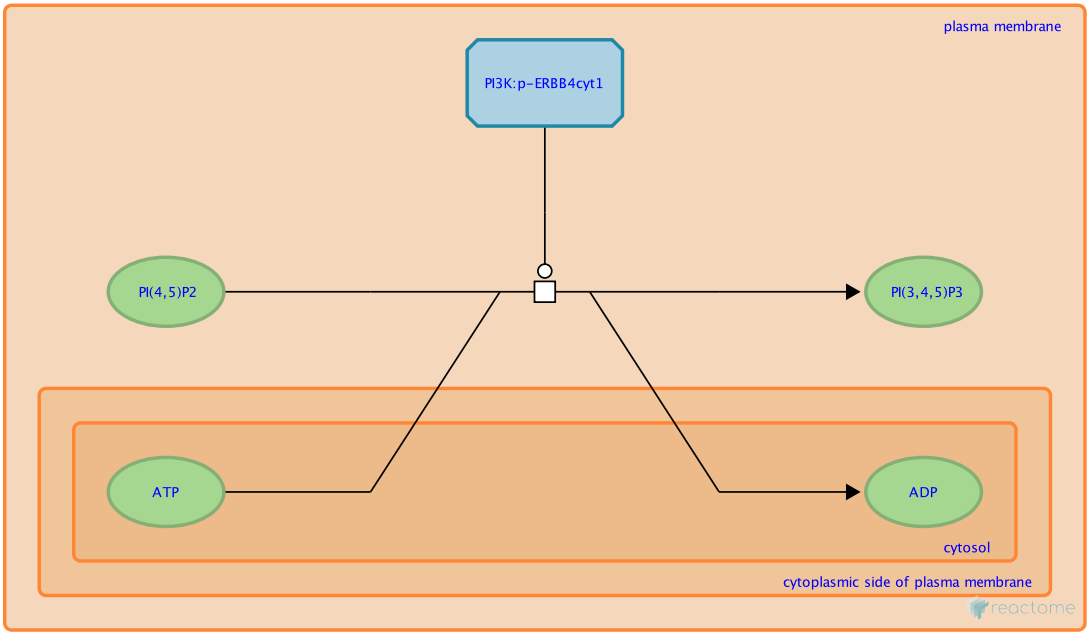
Location: PI3K events in ERBB4 signaling

Stable identifier: R-DRE-1250370

Type: transition

Compartments: plasma membrane, cytosol, extracellular region

Inferred from: Conversion of PIP2 into PIP3 by PI3K bound to p-ERBB4cyt1 homodimers (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.

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Preceded by: Binding of p85 subunit of PI3K (PIK3R1) to p-ERBB4cyt1 homodimers

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