Tyrosine phosphorylation of PRLR

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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. ↗

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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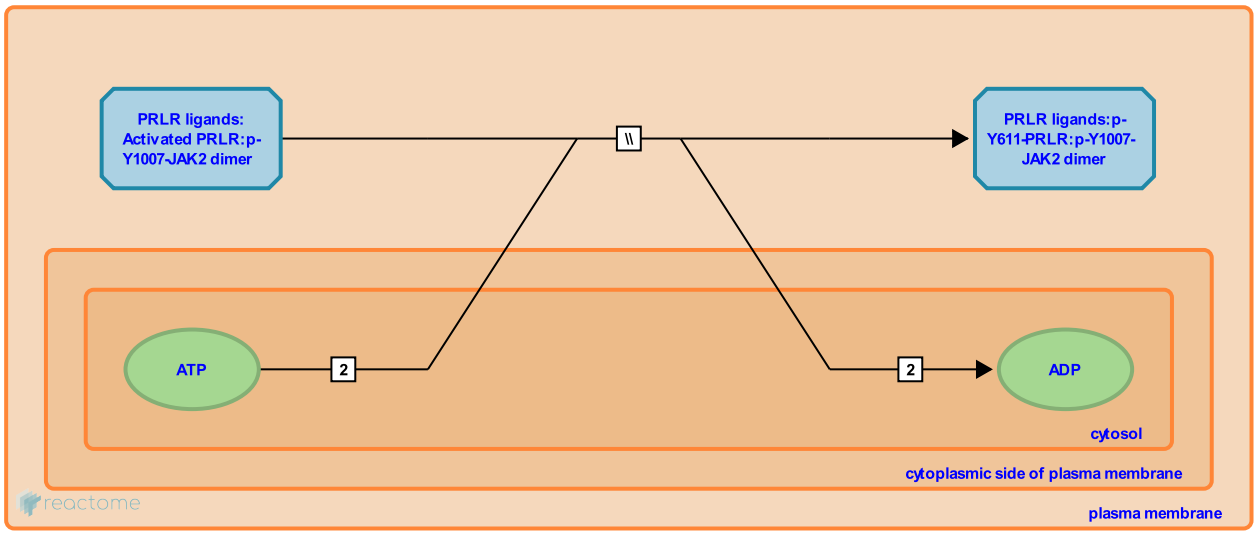
Stable identifier: R-HSA-1364043

Type: omitted

Compartments: plasma membrane, cytosol

Inferred from: Tyrosine phosphorylation of Prlr (Rattus norvegicus)



The model for PRL-induced PRLR activation suggests that JAK2 phosphorylates PRLR on specific tyrosine residues. Consistent with this, JAK2 and PRLR are phosphorylated in response to activating ligand (Lebrun et al. 1994) and PRLR tyrosine phosphorylation is required for subsequent Stat signaling (Pezet et al. 1997). Though this evidence is consistent with a role for JAK2, it has not been formally demonstrated that JAK2 is the kinase responsible for PRLR tyrosine phosphorylation.

Editions

2011-06-13	Authored	Jupe, S.
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