

Multiple IRAK1 autophosphorylation steps

Gay, NJ., Gillespie, ME., Napetschnig, J., Shamovsky, V., de Bono, B.

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

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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. [↗](#)

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: 88

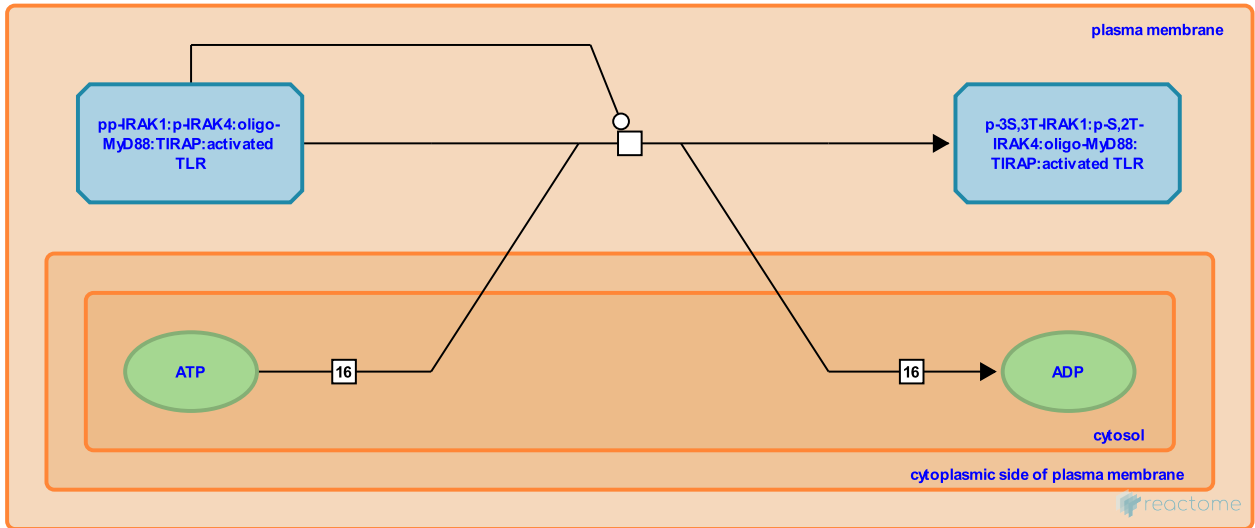
This document contains 1 reaction ([see Table of Contents](#))

Multiple IRAK1 autophosphorylation steps ↗

Stable identifier: R-HSA-166286

Type: transition

Compartments: plasma membrane, cytosol



Phosphorylation of IRAK-1 is due to three sequential phosphorylation steps, which leads to full or hyperphosphorylation of IRAK1. Under in vitro conditions these are all autophosphorylation events. First, Thr-209 is phosphorylated resulting in a conformational change of the kinase domain. Next, Thr-387 in the activation loop is phosphorylated, leading to full enzymatic activity. Several additional residues are phosphorylated in the proline-, serine-, and threonine-rich (ProST) region between the N-terminal death domain and kinase domain. Hyperphosphorylation of this region leads to dissociation of IRAK1 from the activated receptor complex. The kinase activity of IRAK1 is dispensable for IL1-induced NFκB and MAP kinase activation (Knop & Martin, 1999), unlike that of IRAK4 (Suzuki et al. 2002; Kozicak-Holbro et al. 2007), It has been suggested that IRAK1 primarily acts as an adaptor for TRAF6 (Conze et al. 2008).

Literature references

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Editions

2005-08-16	Authored	de Bono, B.
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