

# Second phosphorylation of IRAK1 by

# **IRAK4** bound to activated

TLR:MyD88:TIRAP

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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

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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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 77

This document contains 1 reaction (see Table of Contents)

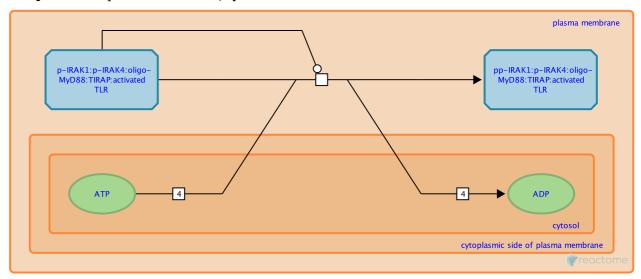
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# Second phosphorylation of IRAK1 by IRAK4 bound to activated TLR:MyD88:TIRAP **₹**

Stable identifier: R-HSA-166284

Type: transition

Compartments: plasma membrane, cytosol



Second, Thr387 in the activation loop is phosphorylated, leading to full enzymatic activity.

#### Literature references

## **Editions**

2005-08-16	Authored	de Bono, B.
2006-04-24	Reviewed	Gay, NJ.
2010-11-30	Reviewed	Gillespie, ME.
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2012-11-16	Reviewed	Napetschnig, J.

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