

# MyD88 forms a complex with TIRAP- :activated TLR2/4

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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.

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. [↗](#)

Reactome database release: 76

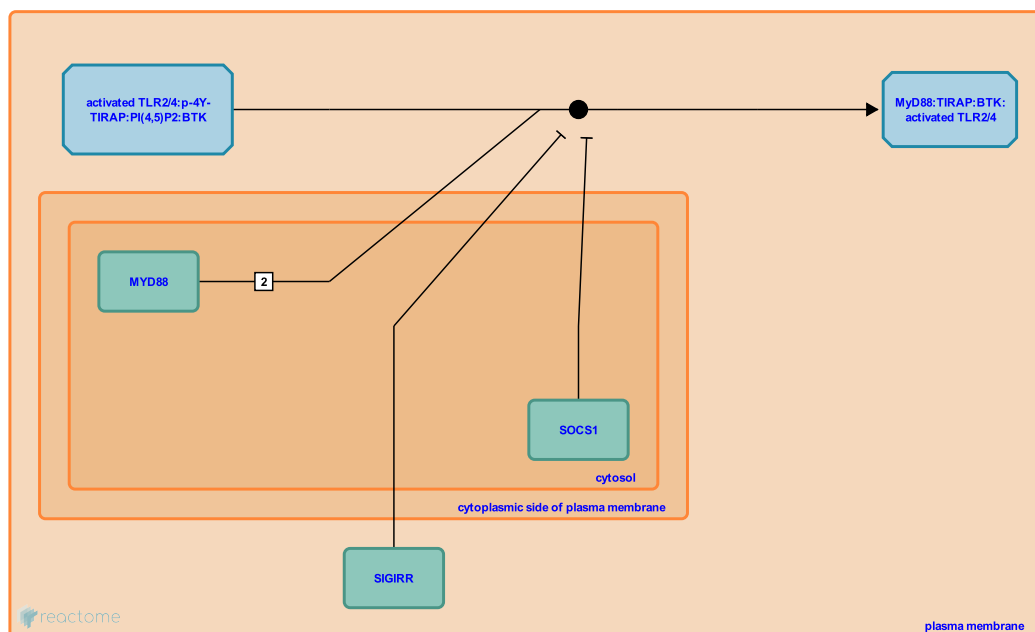
This document contains 1 reaction ([see Table of Contents](#))

## MyD88 forms a complex with TIRAP:activated TLR2/4 [↗](#)

**Stable identifier:** R-HSA-166072

**Type:** binding

**Compartments:** plasma membrane, cytosol



MyD88 binds to IRAK (IL-1 receptor-associated kinase) and the receptor heterocomplex (the signaling complex) and thereby mediates the association of IRAK with the receptor. MyD88 therefore couples a serine/threonine protein kinase to the receptor complex.

### Literature references

Yamamoto, M., Sato, S., Hemmi, H., Sanjo, H., Uematsu, S., Kaisho, T. et al. (2002). Essential role for TIRAP in activation of the signalling cascade shared by TLR2 and TLR4. *Nature*, 420, 324-9. [↗](#)

Hornig, T., Barton, GM., Flavell, RA., Medzhitov, R. (2002). The adaptor molecule TIRAP provides signalling specificity for Toll-like receptors. *Nature*, 420, 329-33. [↗](#)

Wesche, H., Henzel, WJ., Shillinglaw, W., Li, S., Cao, Z. (1997). MyD88: an adapter that recruits IRAK to the IL-1 receptor complex. *Immunity*, 7, 837-47. [↗](#)

### Editions

2005-08-16	Authored	de Bono, B.
2006-04-24	Reviewed	Gay, NJ.
2010-08-25	Revised	Shamovsky, V.
2010-11-30	Reviewed	Gillespie, ME.
2012-11-06	Edited	Shamovsky, V.
2012-11-16	Reviewed	Napetschnig, J.