

Dissociation of hp-IRAK1:TRAF6 from the activated TLR:oligo-Myd88:TIRAP:p-IRAK4 complex

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.

The contents of this document may be freely copied and distributed in any media, provided the authors,
plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 Inter-
national \(CC BY 4.0\) License](#). For more information see our [license](#).

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: 75

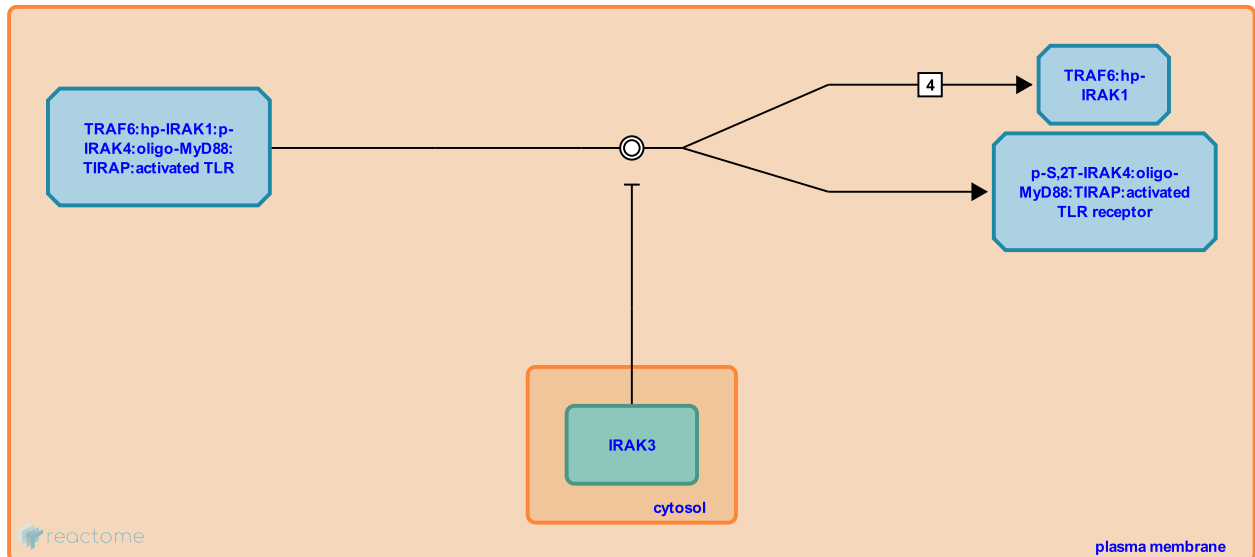
This document contains 1 reaction ([see Table of Contents](#))

Dissociation of hp-IRAK1:TRAF6 from the activated TLR:oligo-Myd88:TIRAP:p-IRAK4 complex ↗

Stable identifier: R-HSA-166362

Type: dissociation

Compartments: plasma membrane, cytosol



Hyperphosphorylated IRAK1 and TRAF6 are thought to dissociate from the activated receptor. (Gottipati et al. 2007) but the IRAK1:TRAF6 complex may remain associated with the membrane (Dong et al. 2006).

Phosphorylated IRAK2, like its paralog IRAK1, possibly dissociates from the activated receptor as shown here, although mechanism of IRAK2 activation by IRAK4 followed by TRAF6 binding remains to be deciphered.

Literature references

Kollewe, C., Mackensen, AC., Neumann, D., Knop, J., Cao, P., Li, S. et al. (2004). Sequential autophosphorylation steps in the interleukin-1 Receptor-associated Kinase-1 Regulate its Availability as an Adapter in Interleukin-1 Signaling. *J Biol Chem*, 279, 5227-36. ↗

Gottipati, S., Rao, NL., Fung-Leung, WP. (2008). IRAK1: a critical signaling mediator of innate immunity. *Cell Signal*, 20, 269-76. ↗

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.