# Assembly of the PGN:PGRP-LC oligomer receptor 'signalling complex'

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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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

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Stable identifier: R-DME-209221

Type: binding

#### Compartments: cytosol, plasma membrane

**Inferred from:** TNF:TNFR1 binds TRADD, TRAF2 and RIPK1 (Homo sapiens), FasL:Fas binds FADD (Homo sapiens)



Upon ligand binding and receptor multimerisation at the plasma membrane, a 'signalling complex' is assembled. The adaptor protein, IMD, binds to the cytoplasmic part of the receptors, while another adaptor protein, DFADD (BG4), binds to IMD through their respective death domains. The caspase-8 orthologue, DREDD, binds to BG4 through interaction between their respective death-inducing (DID) domains.

#### Literature references

- Yano, T., Kaneko, T., Silverman, N., Lim, JH., Kurata, S., Peach, C. et al. (2006). PGRP-LC and PGRP-LE have essential yet distinct functions in the drosophila immune response to monomeric DAP-type peptidoglycan. *Nat Immunol*, 7, 715-23.
- Hu, S., Yang, X. (2000). dFADD, a novel death domain-containing adapter protein for the Drosophila caspase DREDD. *J Biol Chem*, 275, 30761-4.
- Belvin, M., Georgel, P., Kappler, C., Rosse, C., Naitza, S., Reichhart, JM. et al. (2002). The Drosophila immune defense against gram-negative infection requires the death protein dFADD. *Immunity*, 17, 575-81.
- Lee, H., Anderson, KV., Choe, KM. (2005). Drosophila peptidoglycan recognition protein LC (PGRP-LC) acts as a signal-transducing innate immune receptor. *Proc Natl Acad Sci U S A*, 102, 1122-6. 7

### Editions

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