TRAF6 binds to hp- IRAK1

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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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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. ↗

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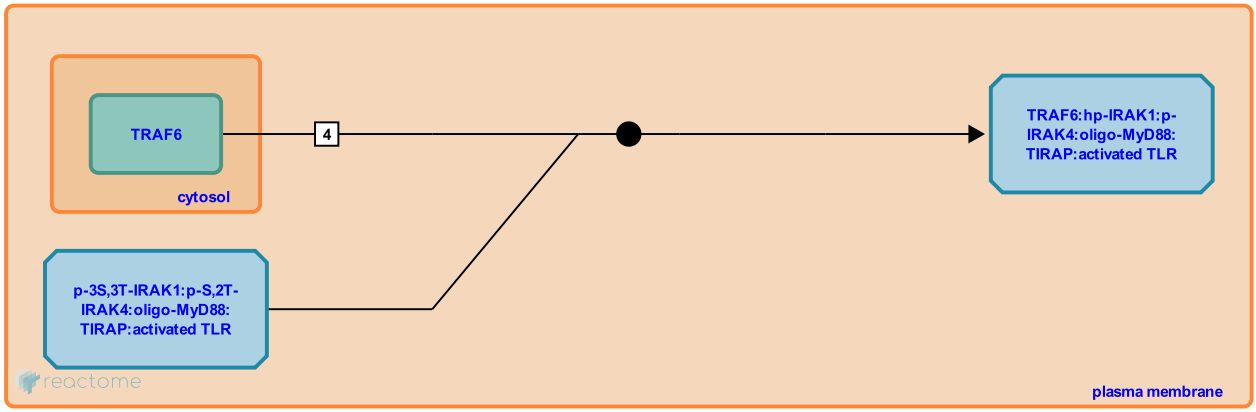
Stable identifier: R-HSA-166363

Type: binding

Compartments: plasma membrane, cytosol



Hyperphosphorylated IRAK1, still within the receptor complex, binds TRAF6 through multiple regions including the death domain, the undefined domain and the C-terminal C1 domain (Li et al. 2001). The C-terminal region of IRAK-1 contains three potential TRAF6-binding sites; mutation of the amino acids (Glu544, Glu587, Glu706) in these sites to alanine greatly reduces activation of NFkappaB (Ye et al. 2002).

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Editions

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