Recruitment of TRAF6 to CBM complex by binding to MALT1

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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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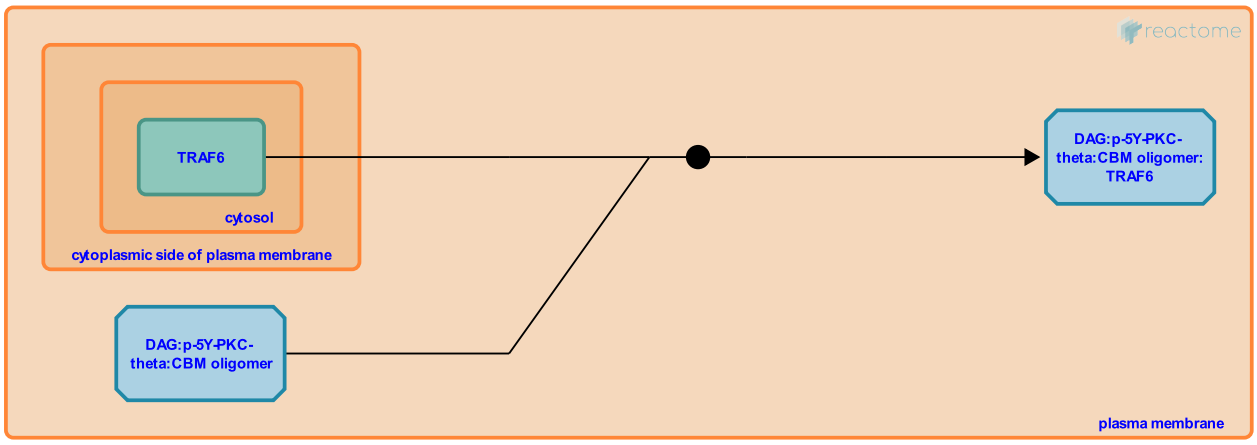
Stable identifier: R-HSA-2730864

Type: binding

Compartments: plasma membrane, cytosol



TRAF6 is a ubiquitin ligase that plays a central role in the IKK-dependent canonical NF-kB pathway. It is recruited to the CBM complex by binding to MALT1. The MALT1 C-terminal Ig domain and extension contain two binding motifs for TRAF6 (Noels et al 2007). After oligomerzation TRAF6, together with Ubc13/Uev1A, activates TAK1 and IKK. It also acts as an E3 ligase for MALT1 and mediates lysine 63-linked ubiquitination (Oeckinghaus et al. 2007).

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Editions

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