

TRAF6/or TRAF2 ubiquitination within

dsRNA:Mda5:Ips1:Traf6/ or Traf2 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

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This document contains 1 reaction (see Table of Contents)

TRAF6/or TRAF2 ubiquitination within dsRNA:Mda5:Ips1:Traf6/ or Traf2 complex 7

Stable identifier: R-GGA-1227769

Type: omitted

Compartments: mitochondrial outer membrane, cytosol

Inferred from: Recruitment of TRAF6/TRAF2 to IPS-1 (Homo sapiens)



TRAFs are E3 ubiquitin ligases that bind to an E2 - ubiquitin thioester and catalyse Lys63-ubquitination on the associated target proteins and possibly on themselves [Lamothe B et al 2007, Mao AP et al 201]. Although TRAF2 failed to interact with a number of E2 ligases related to Ubc13 and showed considerable difference in its RING domain structure from the known TRAF6 RING structure [Yin Q et al 2009], yet TRAF2 is believed to act as an E3 ubiquitin ligase. Sphingosine-1-phosphate (S1P), which is synthesized during inflammatory responces, was shown to bind to TRAF2 and stimulate TRAF2-mediated K63-linked polyubiquitination [Alvarez SE et al 2010; Napolitano G and Karin M 2010]

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Editions

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