

p62:MEKK3 binds to TRAF6

Jupe, S., Pinteaux, E., Ray, KP.

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 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

20/11/2024

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: 90

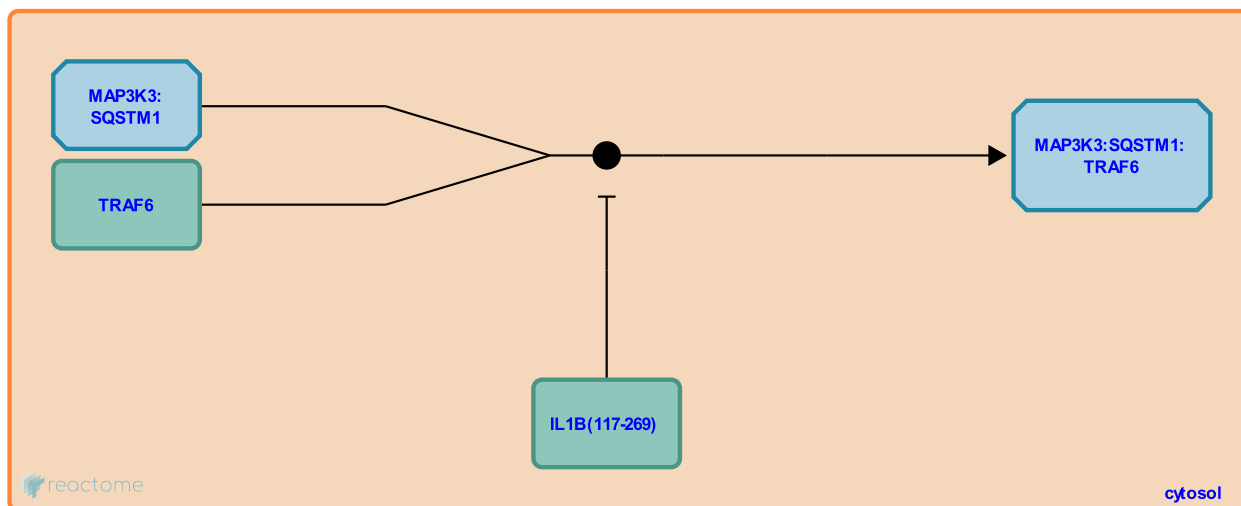
This document contains 1 reaction ([see Table of Contents](#))

p62:MEKK3 binds to TRAF6 [↗](#)

Stable identifier: R-HSA-507719

Type: binding

Compartments: cytosol



p62, MEKK3 and TRAF6 co-localize in cytoplasmic aggregates that are thought to be centres for organizing TRAF6-regulated NF-kappaB signaling and the assembly of polyubiquinated proteins sorting to sequestosomes and proteasomes. p62/Sequestosome-1 is a scaffold protein involved in the regulation of autophagy, trafficking of proteins to the proteasome and activation of NF-kB. p62 binds the basic region of MEKK3. MEKK3 is known to bind TRAF6 in response to IL1B (Huang et al. 2004). Recently p62 was shown to be required for the association of MEKK3 with TRAF6. RNA knockdown of p62 inhibited IL1B and MEKK3 activation of NF-kB. IL1B stimulation resulted in dissociation of MEKK3 from p62:TRAF6 (Nakamura et al. 2010).

Literature references

Siderovski, DP., Nakamura, K., Johnson, GL., Kimple, AJ. (2010). PB1 domain interaction of p62/sequestosome 1 and MEKK3 regulates NF-kappaB activation. *J Biol Chem*, 285, 2077-89. [↗](#)

Editions

2010-05-17	Edited	Jupe, S.
2010-05-17	Reviewed	Pinteaux, E.
2010-05-17	Authored	Ray, KP.