TRAF3/or TRAF6 ubiquitination within dsRNA:MDA5:IPS1:TRAF3/TRAF6 complex

Garapati, P V., Shamovsky, V.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

14/05/2024

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. ↗

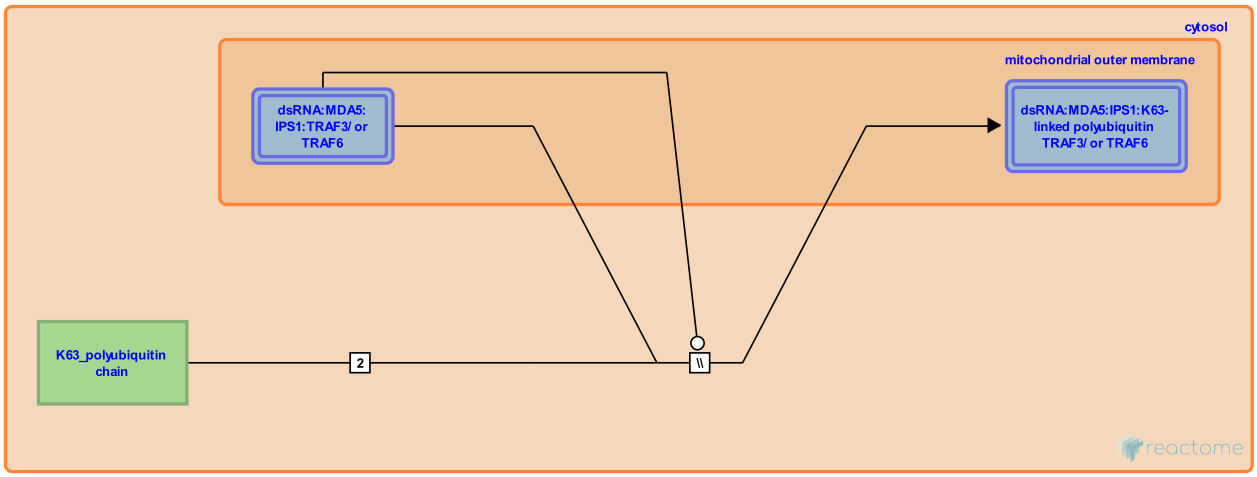
TRAF3/or TRAF6 ubiquitination within dsRNA:MDA5:IPS1:TRAF3/TRAF6 complex ↗

Stable identifier: R-GGA-1227893

Type: omitted

Compartments: mitochondrial outer membrane, cytosol

Inferred from: Recruitment of TRAF3 to MAVS (Homo sapiens)



TRAFs are E3 ubiquitin ligases that catalyse Lys63-polyubquitination of associated target proteins and possibly on themselves.
Virus- triggered Lys63-polyubiquitination of TRAF3/ or TRAF6 was shown to be essential for induction of IFN production [Mao AP et al 2010]. Furthermore, Kayagaki et al. demonstrated that deubiquitinating enzyme A (DUBA) specifically removed Lys63-linked polyubiquitin chains from TRAF3, resulting in its dissociation from the IFN signaling complex [Kayagaki N et al 2007].

Literature references

Lamothe, B., Wu, H., Darnay, BG., Besse, A., Campos, AD., Webster, WK. (2007). Site-specific Lys-63-linked tumor necrosis factor receptor-associated factor 6 auto-ubiquitination is a critical determinant of I kappa B kinase activation. *J Biol Chem, 282*, 4102-12. ↗

Hura, G., Lo, YC., Lin, SC., Rich, RL., Yin, Q., Lamothe, B. et al. (2009). E2 interaction and dimerization in the crystal structure of TRAF6. *Nat Struct Mol Biol, 16*, 658-66. ↗

Adhikari, A., Zeng, W., Chen, ZJ., Pineda, G., Sun, L., Chen, X. et al. (2009). Direct activation of protein kinases by unanchored polyubiquitin chains. *Nature*. ↗

Editions

2011-01-05	Authored	Shamovsky, V.
2011-05-11	Edited	Shamovsky, V.
2011-05-16	Reviewed	Garapati, P V.