

viral dsRNA:IFIH1, viral dsRNA:K63poly-Ub-DDX58 bind MAVS

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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

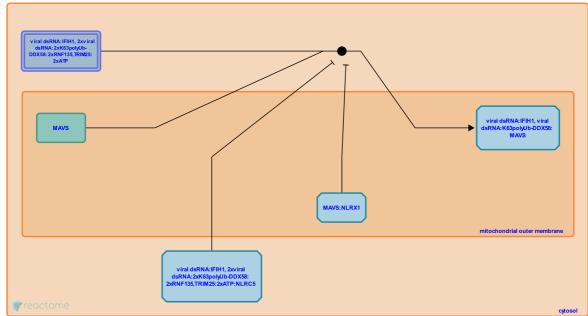
- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18,* 142. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

This document contains 1 reaction (see Table of Contents)

viral dsRNA:IFIH1, viral dsRNA:K63polyUb-DDX58 bind MAVS 7

Stable identifier: R-HSA-168909

Type: binding



Compartments: cytosol, mitochondrial outer membrane

NLRC5 competes with IPS-1 for binding to the CARD domain of RIG-I/MDA5. NLRC5 specifically recognize the CARD domains of RIG-I/MDA5 when the CARD domains become accessible after viral infection, leading to dampened activation of IRF3.

NLRX1 is a member of nucleotide-binding domain and leucine-rich repeat containing (NLR) protein family. NLRX1 competes with RIG-I for IPS-1 interaction and has been identified as a negative regulator of RLR signaling. NLRX1 resides at the outer mitochondrial membrane where IPS-1 is located and this interaction is mediated by the CARD region of IPS-1 and a putative nucleotide-binding domain (NBD) of NLRX1. This interaction between NLRX1 and IPS-1 prevents the association between RIG-1/MDA5 and IPS-1.

Upon binding viral dsRNA, Probable ATP-dependent RNA helicase DDX58 (DDX58, RIG-I, RIG-1) and Interferon-induced helicase C domain-containing protein 1 (IFIH1, MDA5) recruit the downstream signal transducer Mitochondrial antiviral-signaling protein (MAVS, IPS-1). This mitochondria-bound adaptor has an N-terminal CARD-like domain (CLD) which associates with the CARD regions of DDX58 and IFIH1 to mediate induction of interferons.

Literature references

- Xu, LG., Shu, HB., Han, KJ., Wang, YY., Zhai, Z., Li, LY. (2005). VISA is an adapter protein required for virustriggered IFN-beta signaling. *Mol Cell*, 19, 727-40. *¬*
- Seth, RB., Chen, ZJ., Sun, L., Ea, CK. (2005). Identification and characterization of MAVS, a mitochondrial antiviral signaling protein that activates NF-kappaB and IRF 3. *Cell, 122*, 669-82. 7
- Taylor, GL., Potter, JA., Randall, RE. (2008). Crystal structure of human IPS-1/MAVS/VISA/Cardif caspase activation recruitment domain. *BMC Struct Biol*, *8*, 11. 7
- Takeuchi, O., Ishii, KJ., Kumar, H., Sato, S., Kawai, T., Takahashi, K. et al. (2005). IPS-1, an adaptor triggering RIG-Iand Mda5-mediated type I interferon induction. *Nat Immunol*, *6*, 981-8. *¬*

Editions

2010-08-02	Authored, Edited	Garapati, P V.
2010-10-30	Reviewed	Akira, S., Kawai, T.