ITCH homolog downregulates MDA5/IPS1 signaling

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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. ↗

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. ↗

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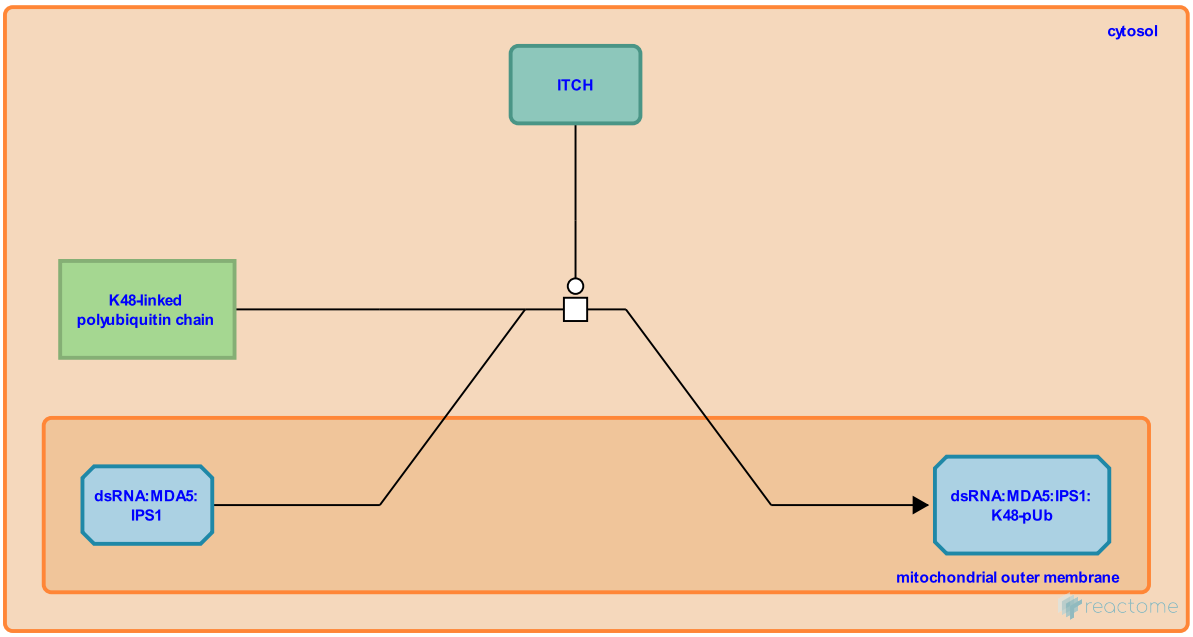
Stable identifier: R-GGA-1227860

Type: transition

Compartments: mitochondrial outer membrane, cytosol

Inferred from: Recruitment of ITCH and K48 ubiquitination of MAVS (Homo sapiens)



Predicted chicken ITCH shows 86% amino acid sequence identiti to its human ortholog. In mammals, ITCH, also known as AIP4 (atrophin 1-interacting protein-4), negatively regulates RLR signaling through Lys-48 linked polyubiquitination of IPS-1 resulting in IPS-1 proteasomal degradation.

Literature references

Sun, W., Jiang, Z., You, F., Liang, S., Sun, H., Zhai, Z. et al. (2009). PCBP2 mediates degradation of the adaptor MAVS via the HECT ubiquitin ligase AIP4. *Nat Immunol, 10*, 1300-8. ↗

Editions

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