

TXNIP binds NLRP3

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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)

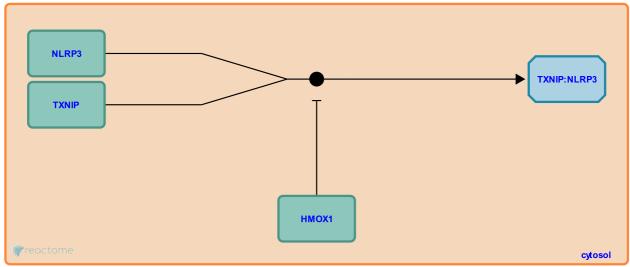
TXNIP binds NLRP3 7

Stable identifier: R-HSA-1250272

Type: binding

Compartments: cytosol

Inferred from: Txnip binds Nlrp3 (Mus musculus)



Thioredoxin-interacting protein (TXNIP) binds NLRP3. Reactive oxygen species (ROS) such as H2O2 increase this interaction, while the ROS inhibitor APDC blocks it (Zhou et al. 2010). This interaction is proposed to activate the NLRP3 inflammasome.

Heme oxygenase (HMOX1), besides its enzymatic activity of the dimeric membrane protein isoform, also occurs as soluble cytosolic protein. It is probably this form that binds to the NACHT domain of NLRP3, suppressing production of epithelial cell-derived cytokines induced by activation of the NLRP3 inflammasome, and protecting airway epithelium in asthma (Lv et al, 2018).

Literature references

Choi, I., Thorens, B., Tardivel, A., Zhou, R., Tschopp, J. (2010). Thioredoxin-interacting protein links oxidative stress to inflammasome activation. *Nat Immunol, 11*, 136-40.

Editions

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