cIAP1,2 ubiquitinates NIK in cIAP1,2:TRAF2::TRAF3:NIK

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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. ↗

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. ↗

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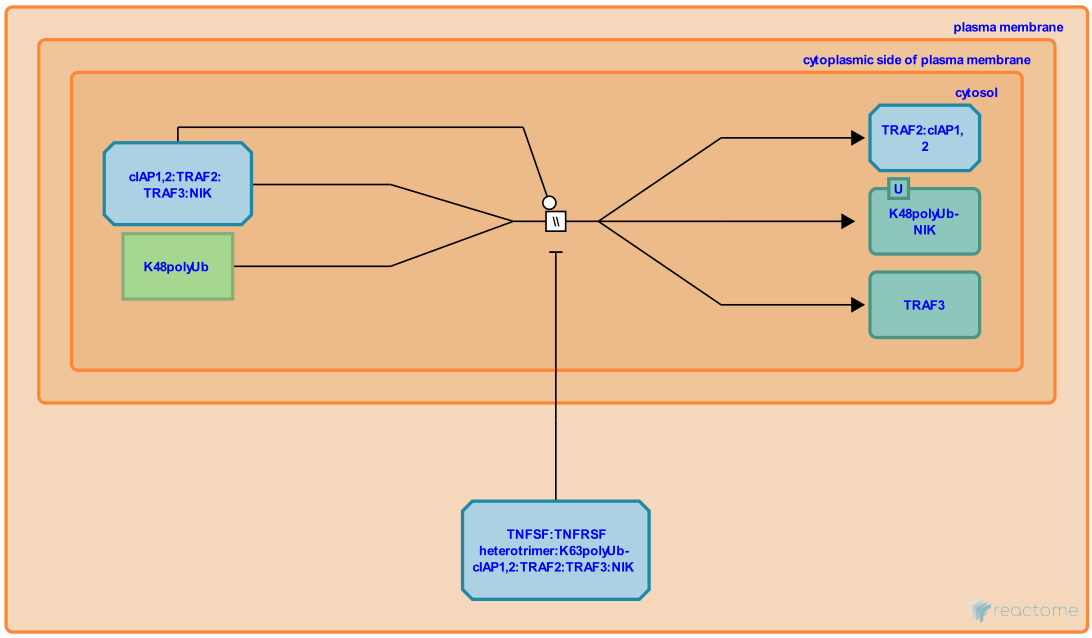
Stable identifier: R-HSA-5668534

Type: omitted

Compartments: cytosol



TNF receptor-associated factor 2 (TRAF2) and cellular inhibitors of apoptosis 1 and 2 (cIAP1,2) are both RING-containing ubiquitin protein ligase (E3), and the interplay between these two protein families and other molecules in the receptor complex is critical in the propagation of downstream signals (Rothe et al. 1995, Yang et al., 2000). cIAP1,2 initiates proteasomal degradation of NIK by mediating its K48-linked ubiquitination (K48-(Ub)n).

Literature references

Mahoney, DJ., Wang, Y., Shiba, T., Mak, TW., Yeh, WC., Cheng, G. et al. (2008). Noncanonical NF-kappaB activation requires coordinated assembly of a regulatory complex of the adaptors cIAP1, cIAP2, TRAF2 and TRAF3 and the kinase NIK. *Nat. Immunol., 9*, 1371-8. ↗

Yang, Y., Weissman, AM., Ashwell, JD., Jensen, JP., Fang, S. (2000). Ubiquitin protein ligase activity of IAPs and their degradation in proteasomes in response to apoptotic stimuli. *Science, 288*, 874-7. ↗

Editions

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