

3xUb,p-S-NFkB p105:TPL2:ABIN2 dissociates due to degradation of p105

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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. *¬*

Reactome database release: 77

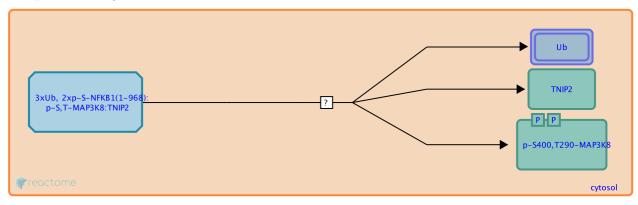
This document contains 1 reaction (see Table of Contents)

3xUb,p-S-NFkB p105:TPL2:ABIN2 dissociates due to degradation of p105 7

Stable identifier: R-HSA-5684273

Type: uncertain

Compartments: cytosol



IKBKB-induced proteolysis of NFkB p105 to p50 releases MAP3K8 (TPL2) from the complex with NFkB p105 and ABIN2. On TLR or IL1beta stimulation, dissociated MAP3K8 with an adequate phosphorylation state activates MAP2K (MKK1/2) and consequently MAPK1/3 (ERK1/2).

Literature references

- Waterfield, MR., Zhang, M., Norman, LP., Sun, SC. (2003). NF-kappaB1/p105 regulates lipopolysaccharide-stimulated MAP kinase signaling by governing the stability and function of the Tpl2 kinase. *Mol Cell, 11*, 685-94.
- Roget, K., Ben-Addi, A., Mambole-Dema, A., Gantke, T., Yang, HT., Janzen, J. et al. (2012). I?B kinase 2 regulates TPL-2 activation of extracellular signal-regulated kinases 1 and 2 by direct phosphorylation of TPL-2 serine 400. *Mol. Cell. Biol.*, 32, 4684-90. *¬*
- Beinke, S., Deka, J., Lang, V., Belich, MP., Walker, PA., Howell, S. et al. (2003). NF-kappaB1 p105 negatively regulates TPL-2 MEK kinase activity. *Mol Cell Biol, 23*, 4739-52.

Editions

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