

# IKBA is phosphorylated by Phospho IKKB kinase

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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. [↗](#)

Reactome database release: 88

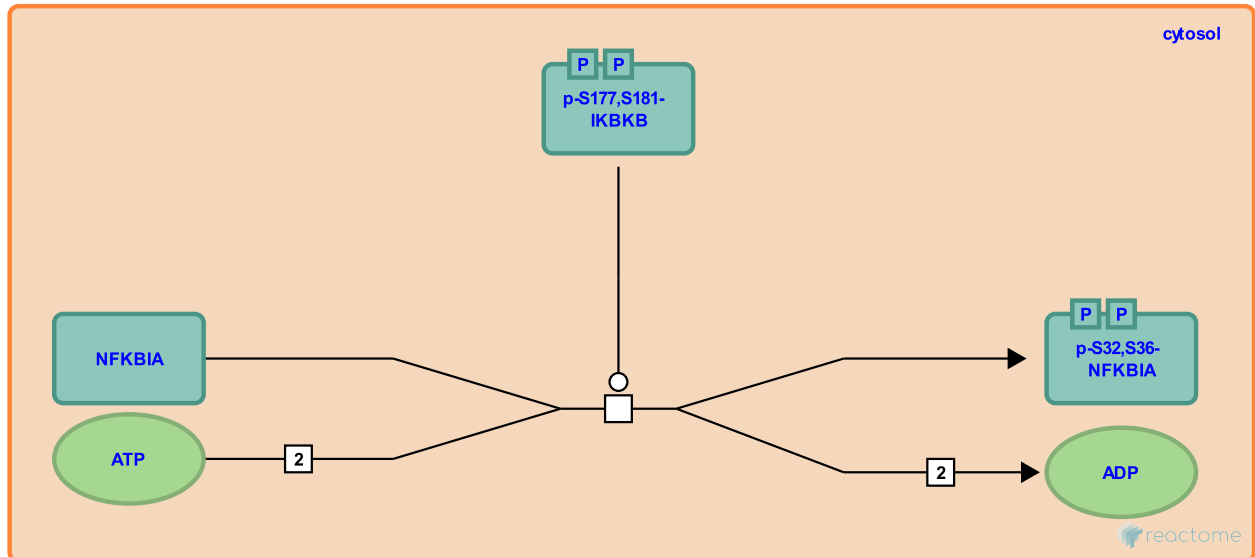
This document contains 1 reaction ([see Table of Contents](#))

## IKBA is phosphorylated by Phospho IKKB kinase [↗](#)

**Stable identifier:** R-HSA-209087

**Type:** transition

**Compartments:** cytosol



Human IKBA, orthologue of *Drosophila* Cactus (CACT), is phosphorylated by activated IKKB kinase at residues Ser32 and Ser36.

### Literature references

Bennett, BL., Rao, A., Barbosa, M., Shevchenko, A., Young, DB., Mann, M. et al. (1997). IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation. *Science*, 278, 860-6. [↗](#)

Wu, C., Ghosh, S. (2003). Differential phosphorylation of the signal-responsive domain of I kappa B alpha and I kappa B beta by I kappa B kinases. *J Biol Chem*, 278, 31980-7. [↗](#)

### Editions

2010-05-17	Edited	Jupe, S.
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