

HIPK2 phosphorylates RUNX1

Chuang, L.S., Ito, Y., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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

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Reactome database release: 74

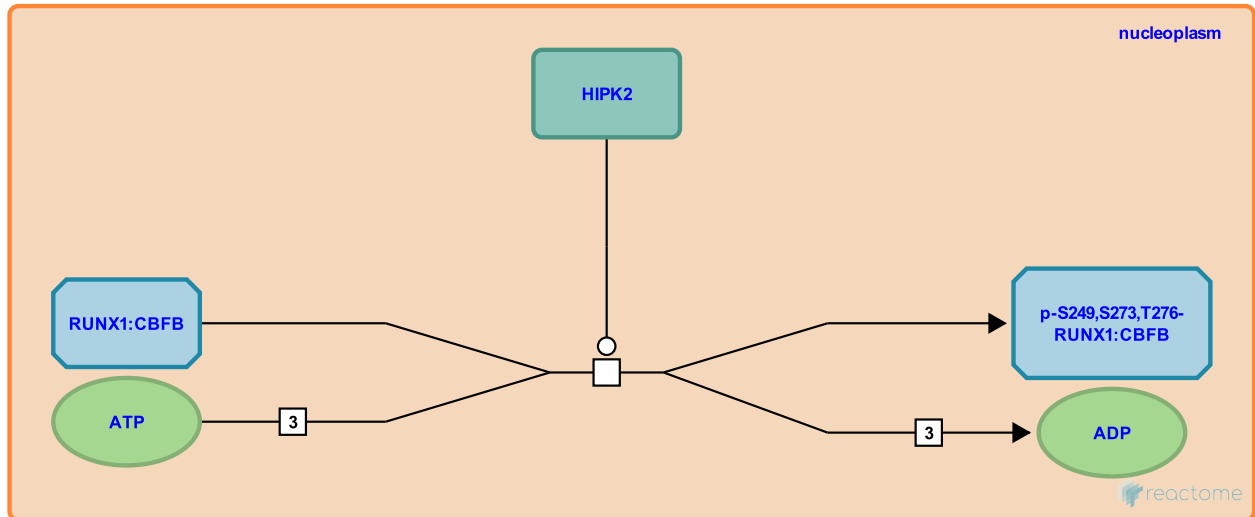
This document contains 1 reaction ([see Table of Contents](#))

HIPK2 phosphorylates RUNX1 [↗](#)

Stable identifier: R-HSA-8878054

Type: transition

Compartments: nucleoplasm



Protein serine/threonine kinase HIPK2 phosphorylates RUNX1 upon formation of the RUNX1:CBFB complex. Serine residues S249 and S273 and threonine residue S276 of RUNX1 are phosphorylated by HIPK2. HIPK2-mediated phosphorylation of RUNX1 is implicated as an important regulatory step in hematopoiesis and is disrupted by leukemogenic mutations in CBFβ (Aikawa et al. 2006, Wee et al. 2008).

Literature references

Wee, HJ., Voon, DC., Bae, SC., Ito, Y. (2008). PEBP2-beta/CBF-beta-dependent phosphorylation of RUNX1 and p300 by HIPK2: implications for leukemogenesis. *Blood*, 112, 3777-87. [↗](#)

Aikawa, Y., Nguyen, LA., Isono, K., Takakura, N., Tagata, Y., Schmitz, ML. et al. (2006). Roles of HIPK1 and HIPK2 in AML1- and p300-dependent transcription, hematopoiesis and blood vessel formation. *EMBO J.*, 25, 3955-65. [↗](#)

Editions

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