

CHEK2 phosphorylates TP53

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19/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)

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Reactome database release: 88

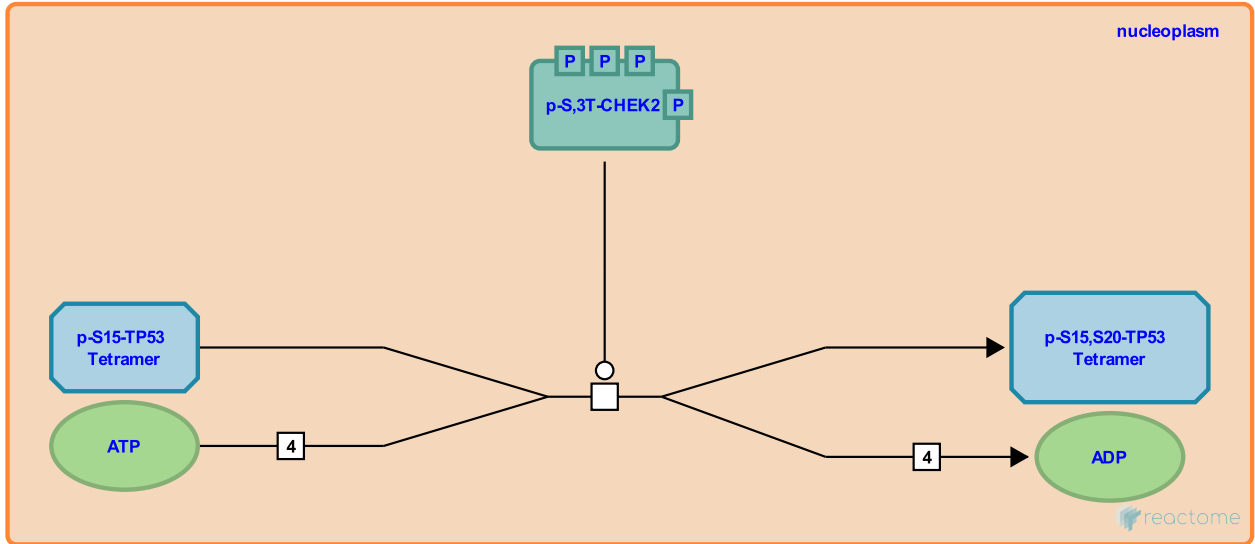
This document contains 1 reaction ([see Table of Contents](#))

CHEK2 phosphorylates TP53 ↗

Stable identifier: R-HSA-69685

Type: transition

Compartments: nucleoplasm



CHEK2 (Chk2) phosphorylates TP53 (p53) at serine residue S20 (Hirao et al. 2000, Shieh et al. 2000, Chehab et al. 2000). Phosphorylation of TP53 at serine residue S20 is necessary for DNA damage-induced TP53 stabilization as it compromises the interaction of TP53 with the ubiquitin ligase MDM2 (Chehab et al. 1999, Chehab et al. 2000). S20 phosphorylation is also required for the induction of TP53-dependent transcripts in response to DNA damage (Hirao et al. 2000).

Literature references

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Editions

2015-10-14	Authored, Edited	Orlic-Milacic, M.
2016-02-04	Reviewed	Inga, A., Zaccara, S.