Phosphorylation of Cdc25C at Ser216 by CHEK2

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06/05/2024

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. ↗

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. ↗

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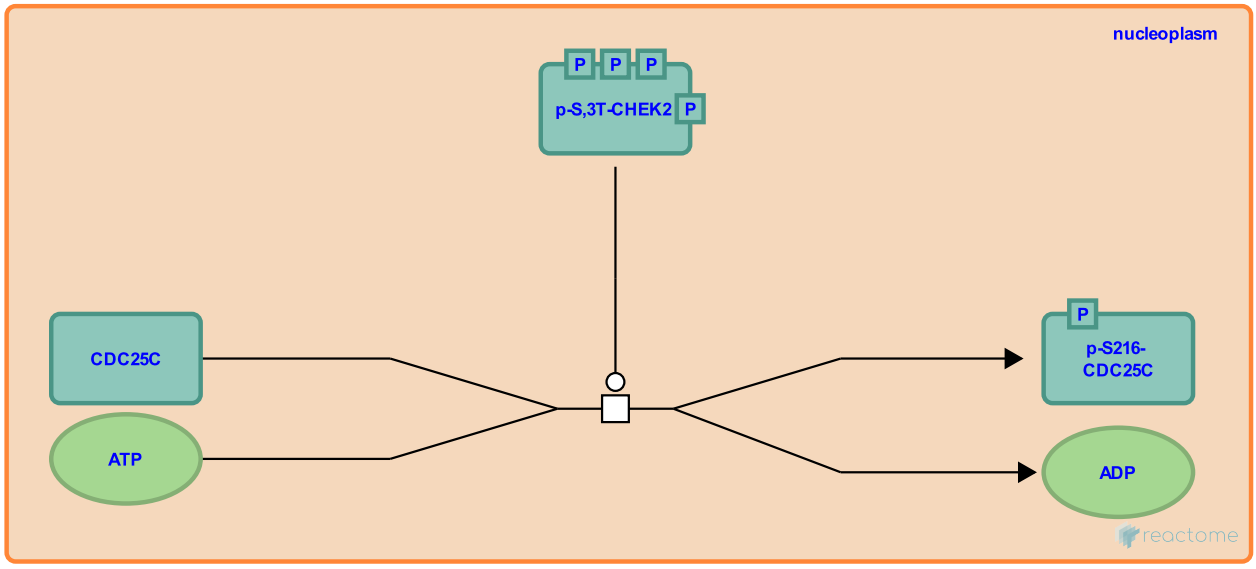
Stable identifier: R-HSA-75809

Type: transition

Compartments: nucleoplasm



Cdc25C is negatively regulated by phosphorylation on Ser 216, the 14-3-3-binding site. This is an important regulatory mechanism used by cells to block mitotic entry under normal conditions and after DNA damage (Chaturvedi et al, 1999; Bulavin et al., 2003).

Literature references

Carr, SA., Winkler, JD., Mattern, MR., Zhou, BB., Johnson, RK., Chaturvedi, P. et al. (1999). Mammalian Chk2 is a downstream effector of the ATM-dependent DNA damage checkpoint pathway. *Oncogene, 18*, 4047-54. ↗

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Editions

2004-02-11	Authored	Sanchez, Y.
2004-03-23	Edited	Matthews, L.
2008-01-15	Revised	Matthews, L.
2018-07-10	Reviewed	Manfredi, JJ.