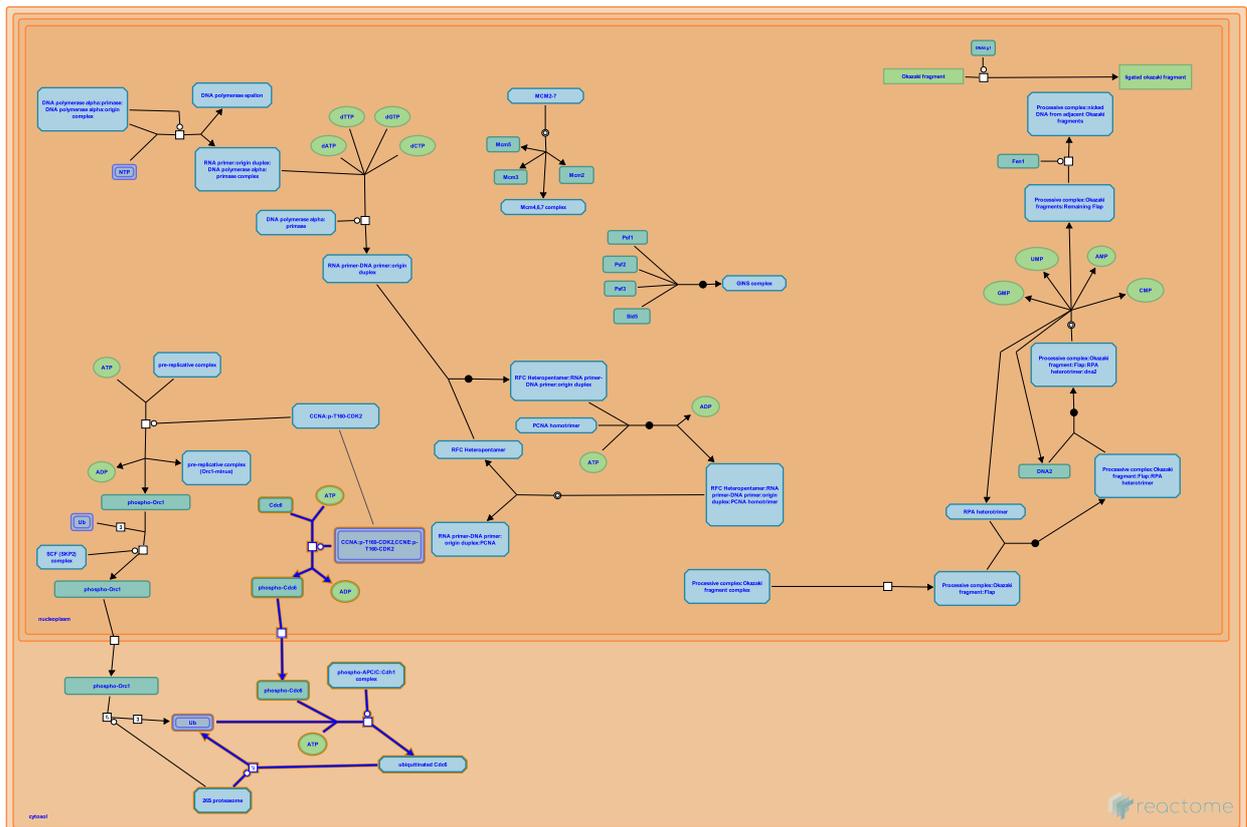


# CDK-mediated phosphorylation and removal of Cdc6



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://creativecommons.org/licenses/by/4.0/).

## 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

- 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: 76

This document contains 1 pathway and 4 reactions ([see Table of Contents](#))



## Cdc6 protein is phosphorylated by CDK ↗

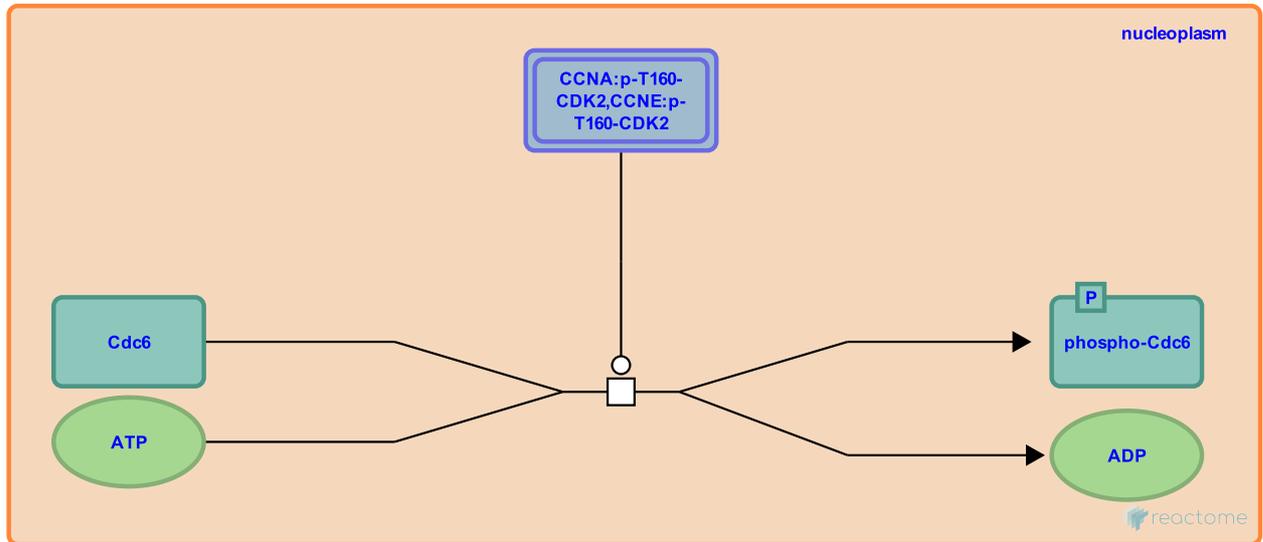
**Location:** [CDK-mediated phosphorylation and removal of Cdc6](#)

**Stable identifier:** R-DME-69005

**Type:** transition

**Compartments:** nucleoplasm

**Inferred from:** [Cdc6 protein is phosphorylated by CDK \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Followed by:** [Phosphorylated Cdc6 is exported from the nucleus](#)

## Phosphorylated Cdc6 is exported from the nucleus ↗

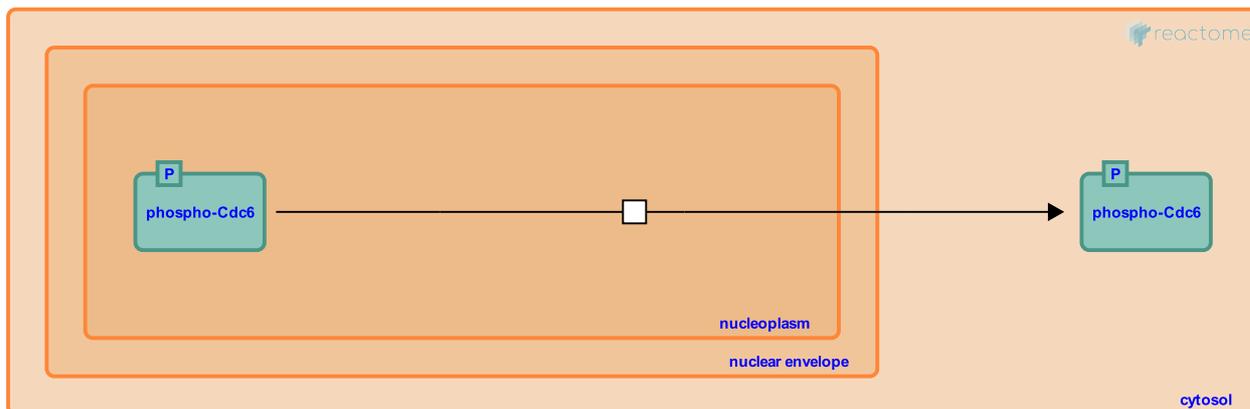
**Location:** [CDK-mediated phosphorylation and removal of Cdc6](#)

**Stable identifier:** R-DME-69006

**Type:** transition

**Compartments:** nucleoplasm, cytosol

**Inferred from:** [Phosphorylated Cdc6 is exported from the nucleus \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Cdc6 protein is phosphorylated by CDK](#)

**Followed by:** [Cytoplasmic phosphorylated Cdc6 is ubiquitinated by the anaphase-promoting complex](#)

## Cytoplasmic phosphorylated Cdc6 is ubiquitinated by the anaphase-promoting complex [↗](#)

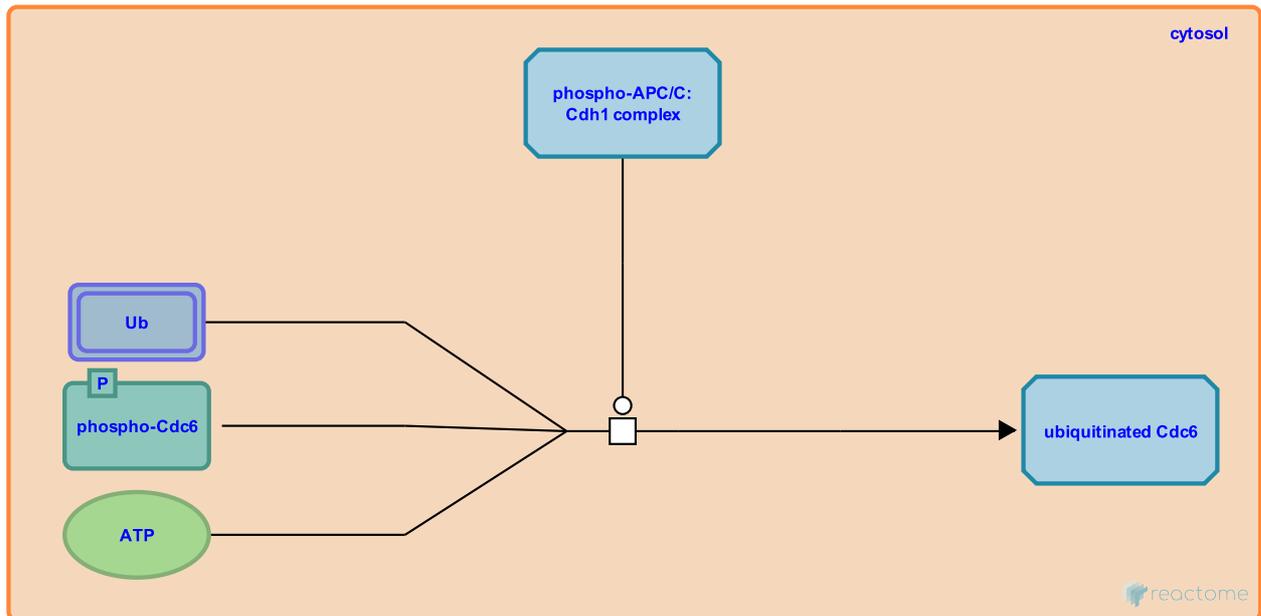
**Location:** [CDK-mediated phosphorylation and removal of Cdc6](#)

**Stable identifier:** R-DME-69015

**Type:** transition

**Compartments:** cytosol

**Inferred from:** [Cytoplasmic phosphorylated Cdc6 is ubiquitinated by the anaphase-promoting complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Phosphorylated Cdc6 is exported from the nucleus](#)

**Followed by:** [Ubiquitinated Cdc6 is degraded by the proteasome](#)

## Ubiquitinated Cdc6 is degraded by the proteasome ↗

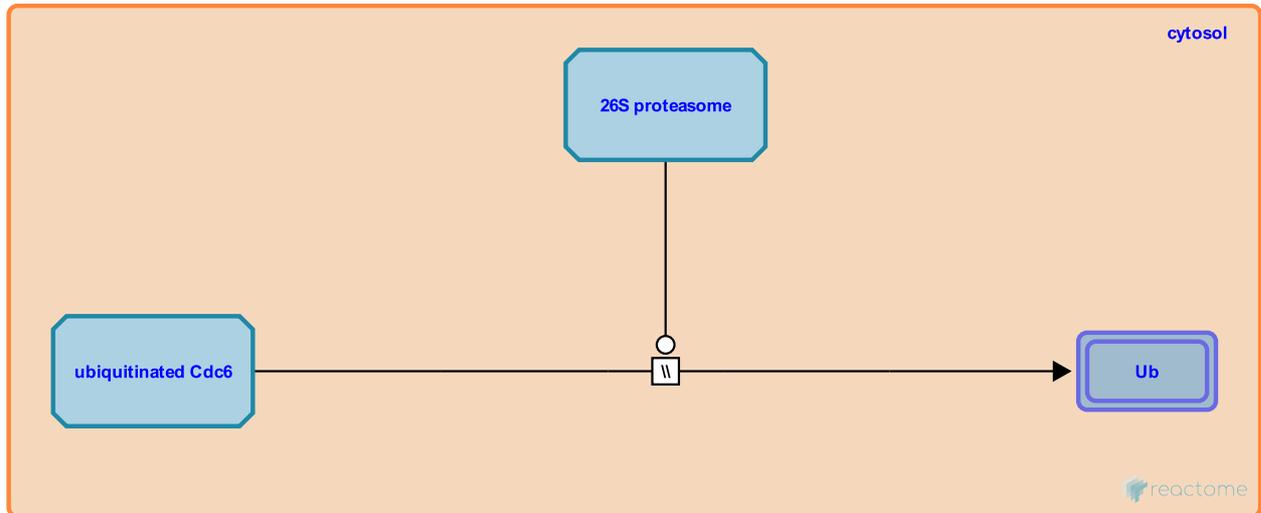
**Location:** [CDK-mediated phosphorylation and removal of Cdc6](#)

**Stable identifier:** R-DME-69016

**Type:** omitted

**Compartments:** cytosol

**Inferred from:** [Ubiquitinated Cdc6 is degraded by the proteasome \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [Cytoplasmic phosphorylated Cdc6 is ubiquitinated by the anaphase-promoting complex](#)

# Table of Contents

Introduction	1
☒ CDK-mediated phosphorylation and removal of Cdc6	2
↳ Cdc6 protein is phosphorylated by CDK	3
↳ Phosphorylated Cdc6 is exported from the nucleus	4
↳ Cytoplasmic phosphorylated Cdc6 is ubiquitinated by the anaphase-promoting complex	5
☒ Ubiquitinated Cdc6 is degraded by the proteasome	6
Table of Contents	7