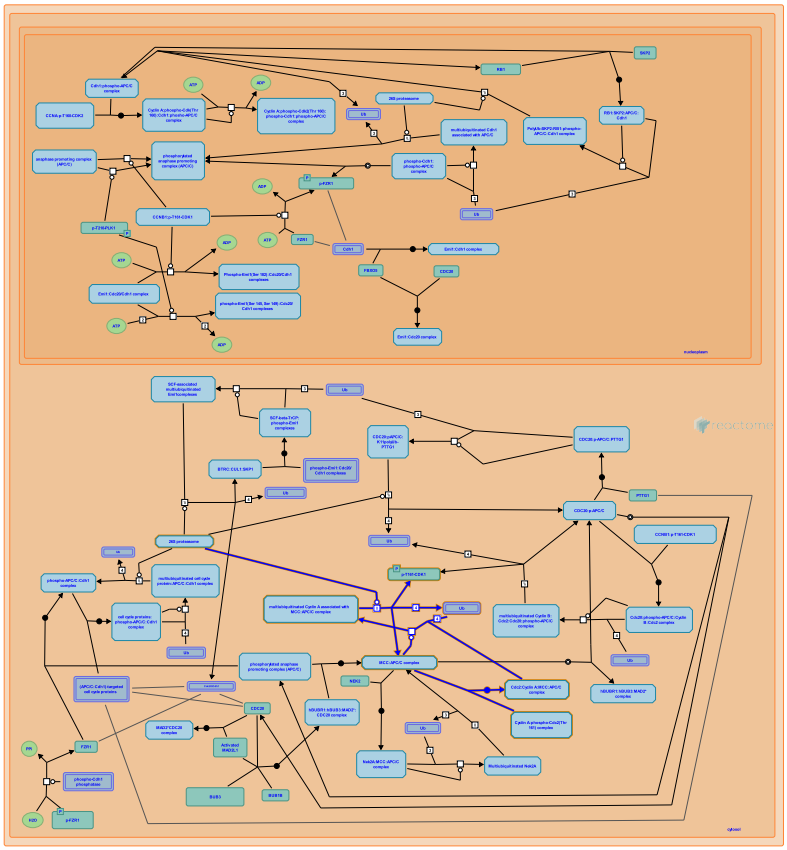
# Cdc20:Phospho-APC/C mediated degradation of Cyclin A



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the Reactome Textbook.

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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.
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. ↗

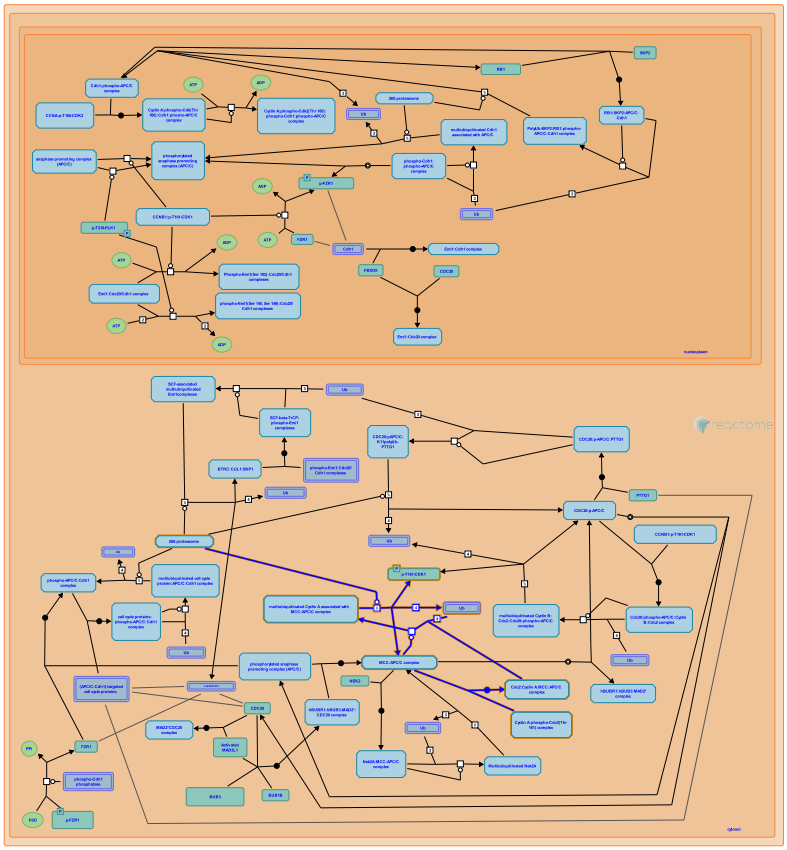
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

## Cdc20:Phospho-APC/C mediated degradation of Cyclin A ↗

**Stable identifier:** R-HSA-174184

**Compartments:** cytosol



Cyclin A, functions in mitosis as well as DNA replication and is degraded in the interim by the APC/C to permit normal chromosome segregation, cell division, and the onset of S phase (see Lukas and Bartek, 2004). Cyclin A is initially degraded early in mitosis by APC/C:Cdc20 when the spindle checkpoint is still active and degradation of securin and cyclin B is inhibited.

## Literature references


Peters, JM., Gannon, J., Geley, S., Kramer, E., Gieffers, C., Hunt, T. (2001). Anaphase-promoting complex/cyclosome-dependent proteolysis of human cyclin A starts at the beginning of mitosis and is not subject to the spindle assembly checkpoint. *J Cell Biol, 153*, 137-48. ↗


## Editions

| | | |
|---|---|---|
| 2006-01-26 | Authored | Lorca, T., Castro, A. |
| 2006-01-30 | Edited | Matthews, L. |
| 2006-03-28 | Reviewed | Peters, JM. |

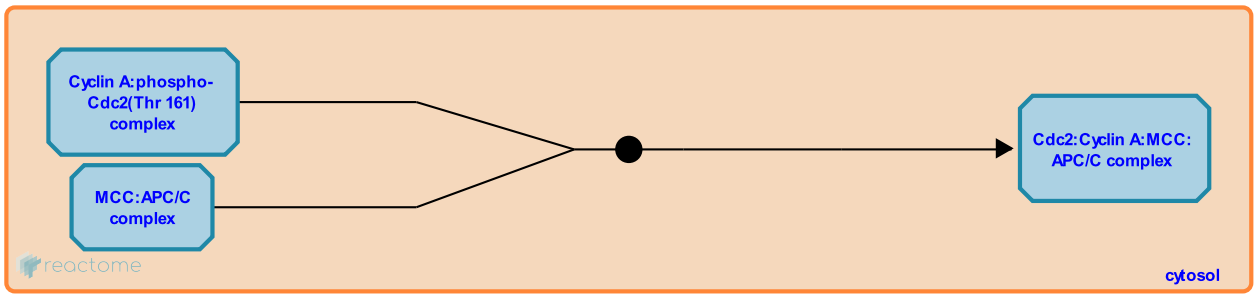
## Association of Cyclin A with the APC/C ↗

**Location:** Cdc20:Phospho-APC/C mediated degradation of Cyclin A

**Stable identifier:** R-HSA-174171

**Type:** binding

**Compartments:** cytosol




Cyclin A is believed to be recognized by the APC/C:Cdc20 complex through its D-box sequence, which is 10-20 residues longer than the D-box of cyclin B (Geley et al., 2001).

**Followed by:** Ubiquitination of Cyclin A by APC/C:Cdc20 complex

## Literature references


Peters, JM., Gannon, J., Geley, S., Kramer, E., Gieffers, C., Hunt, T. (2001). Anaphase-promoting complex/cyclosome-dependent proteolysis of human cyclin A starts at the beginning of mitosis and is not subject to the spindle assembly checkpoint. *J Cell Biol, 153*, 137-48. ↗

Hatakeyama, M., Maeda, T., Ashizawa, S., Higashi, H., Ohtoshi, A. (2000). Human p55(CDC)/Cdc20 associates with cyclin A and is phosphorylated by the cyclin A-Cdk2 complex. *Biochem Biophys Res Commun, 268*, 530-4. ↗


## Editions

| | | |
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| 2006-03-28 | Reviewed | Peters, JM. |

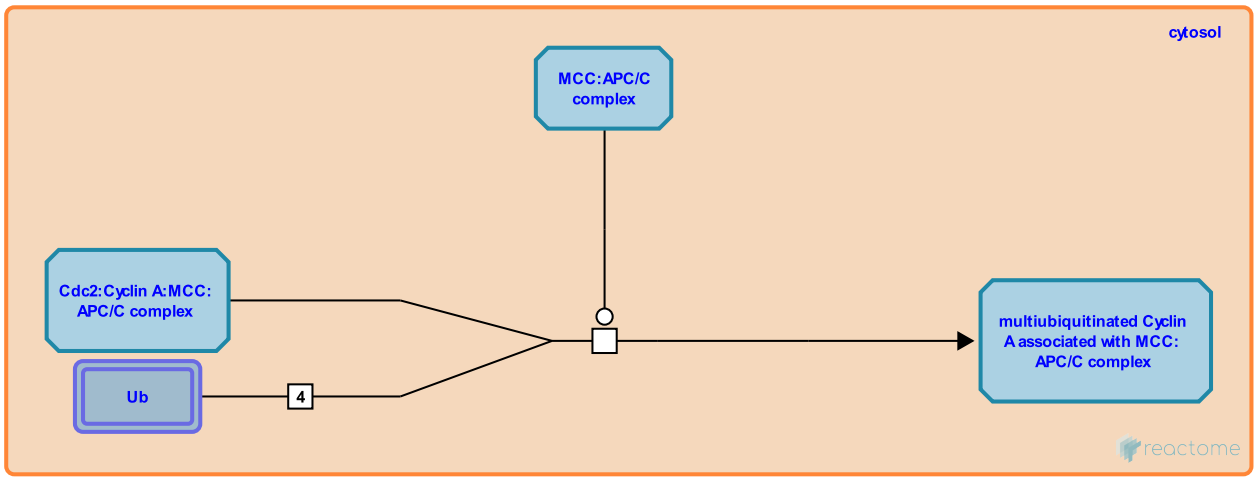
## Ubiquitination of Cyclin A by APC/C:Cdc20 complex ↗

**Location:** Cdc20:Phospho-APC/C mediated degradation of Cyclin A

**Stable identifier:** R-HSA-174104

**Type:** transition

**Compartments:** cytosol




Rape et al. have recently demonstrated that the order in which APC/C targeted proteins are degraded is determined by the processivity of multiubiquitination of these substrates. Processive substrates acquire a polyubiquitin chain upon binding to the APC/C once and are degraded. Distributive substrates bind, dissociate and reassociate with the APC/C multiple times before acquiring an ubiquitin chain of sufficient length to insure degradation. In addition, distributive substrates that dissociate from the APC/C with short ubiquitin chains are targeted for deubiquitination (Rape et al., 2006). Paradoxically, although the multiubiquitination of cyclin A is distributive and later substrates of APC-Cdc20 such as Securin are processive (Rape et al., 2006), Cyclin A is degraded prior to Securin and Cyclin B. The mechanisms insuring this order have not yet be determined.

**Preceded by:** Association of Cyclin A with the APC/C

**Followed by:** Degradation multiubiquitinated Cyclin A

## Literature references

Peters, JM., Gannon, J., Geley, S., Kramer, E., Gieffers, C., Hunt, T. (2001). Anaphase-promoting complex/cyclosome-dependent proteolysis of human cyclin A starts at the beginning of mitosis and is not subject to the spindle assembly checkpoint. *J Cell Biol, 153*, 137-48. ↗

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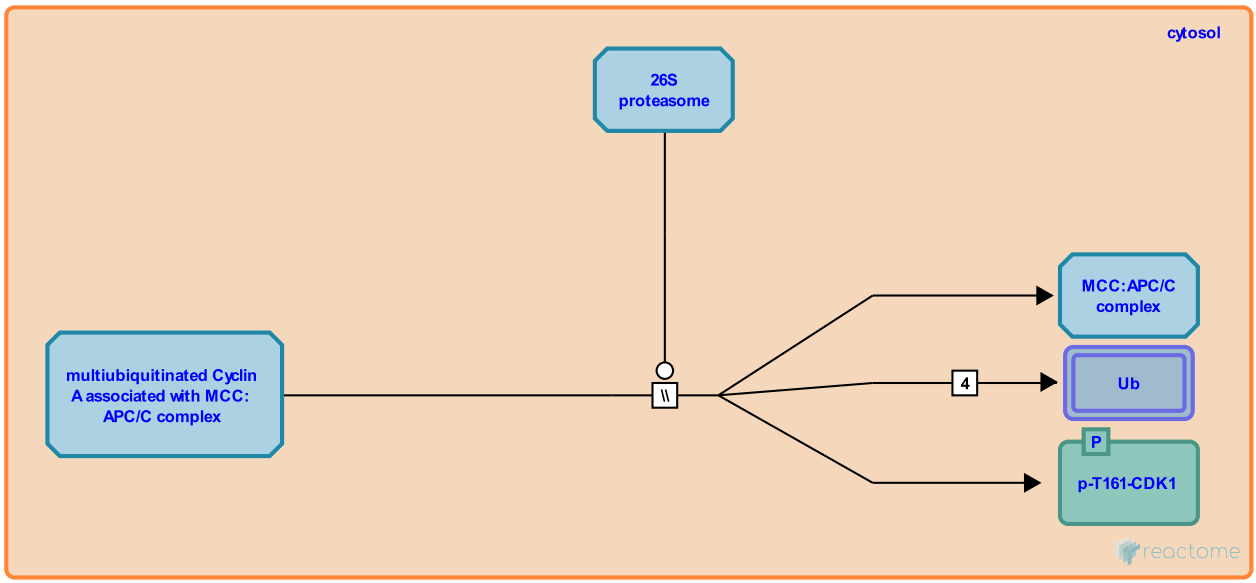
## Degradation multiubiquitinated Cyclin A ↗

**Location:** Cdc20:Phospho-APC/C mediated degradation of Cyclin A

**Stable identifier:** R-HSA-174255

**Type:** omitted

**Compartments:** cytosol




Following multiubiquitination, Cyclin A is targeted for destruction by the 26S proteasome.

**Preceded by:** Ubiquitination of Cyclin A by APC/C:Cdc20 complex

## Literature references

Peters, JM., Gannon, J., Geley, S., Kramer, E., Gieffers, C., Hunt, T. (2001). Anaphase-promoting complex/cyclosome-dependent proteolysis of human cyclin A starts at the beginning of mitosis and is not subject to the spindle assembly checkpoint. *J Cell Biol, 153*, 137-48. ↗

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# Table of Contents