Regulation of APC/C activators between G1/S and early anaphase

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.

18/05/2024

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

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. ↗
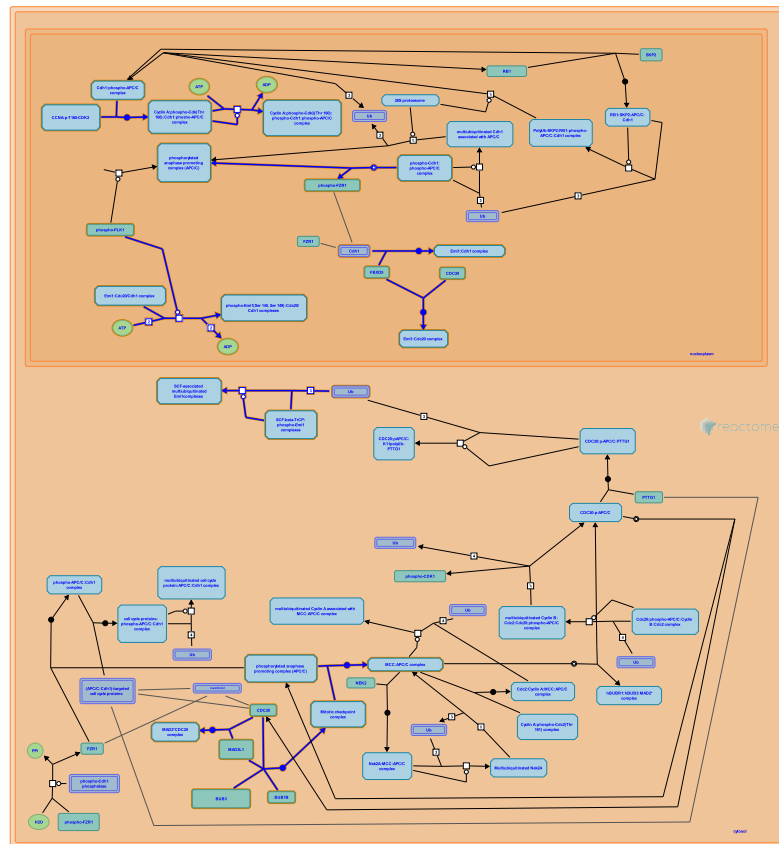
Reactome database release: 88

This document contains 4 pathways and 5 reactions (see Table of Contents)

Regulation of APC/C activators between G1/S and early anaphase ↗

Stable identifier: R-GGA-176408

Inferred from: Regulation of APC/C activators between G1/S and early anaphase (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
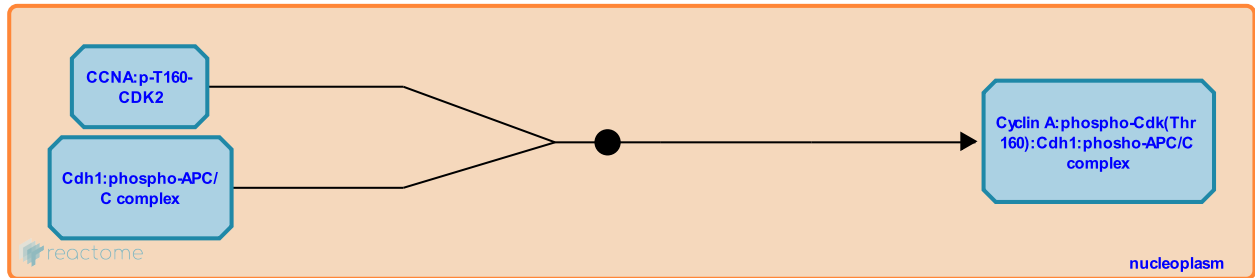
Association of Cyclin A:Cdk2 with Cdh1 ↗

Location: Regulation of APC/C activators between G1/S and early anaphase

Stable identifier: R-GGA-188371

Type: binding

Compartments: nucleoplasm

Inferred from: Association of Cyclin A:Cdk2 with Cdh1 (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Phosphorylation of Cdh1 by Cyclin A:Cdk2
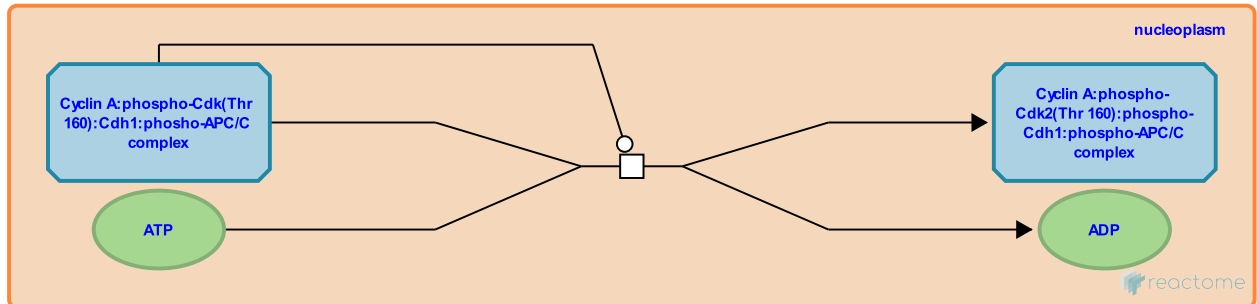
Phosphorylation of Cdh1 by Cyclin A:Cdk2 ↗

Location: Regulation of APC/C activators between G1/S and early anaphase

Stable identifier: R-GGA-174079

Type: transition

Compartments: nucleoplasm

Inferred from: Phosphorylation of Cdh1 by Cyclin A:Cdk2 (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Association of Cyclin A:Cdk2 with Cdh1

Followed by: Dissociation of phospho-Cdh1 from the APC/C complex

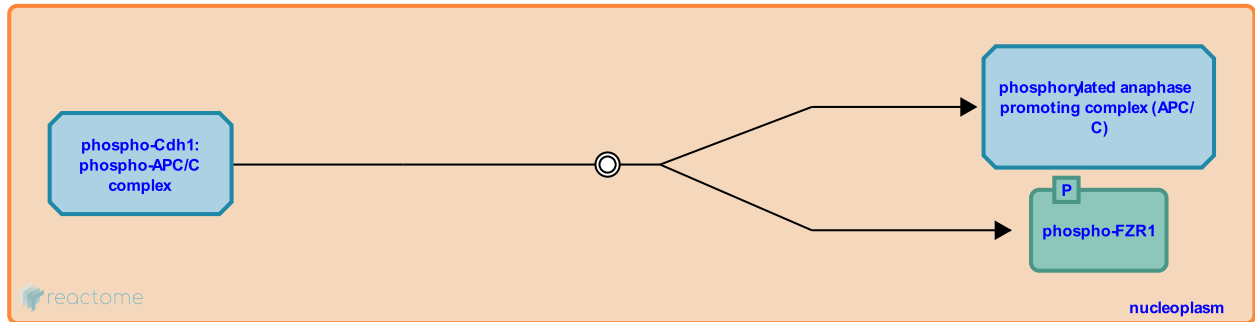# Dissociation of phospho-Cdh1 from the APC/C complex ↗

Location: Regulation of APC/C activators between G1/S and early anaphase

Stable identifier: R-GGA-174139

Type: dissociation

Compartments: nucleoplasm

Inferred from: Dissociation of phospho-Cdh1 from the APC/C 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Phosphorylation of Cdh1 by Cyclin A:Cdk2
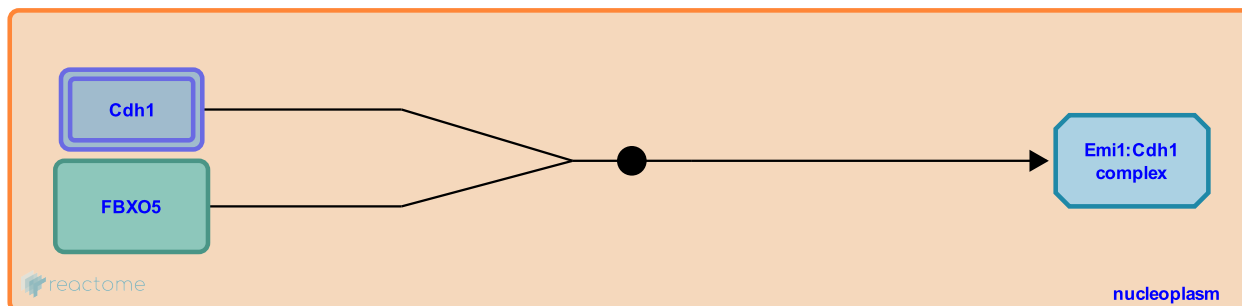
Association of Emi1 with Cdh1 ↗

Location: Regulation of APC/C activators between G1/S and early anaphase

Stable identifier: R-GGA-174097

Type: binding

Compartments: nucleoplasm

Inferred from: Association of Emi1 with Cdh1 (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Followed by: Phosphorylation of Emi1

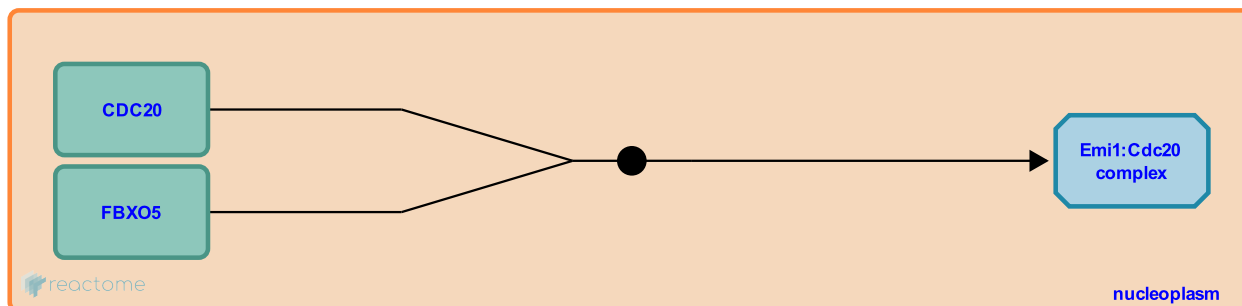# Association of Emi1 with Cdc20 ↗

Location: Regulation of APC/C activators between G1/S and early anaphase

Stable identifier: R-GGA-174235

Type: binding

Compartments: nucleoplasm

Inferred from: Association of Emi1 with Cdc20 (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
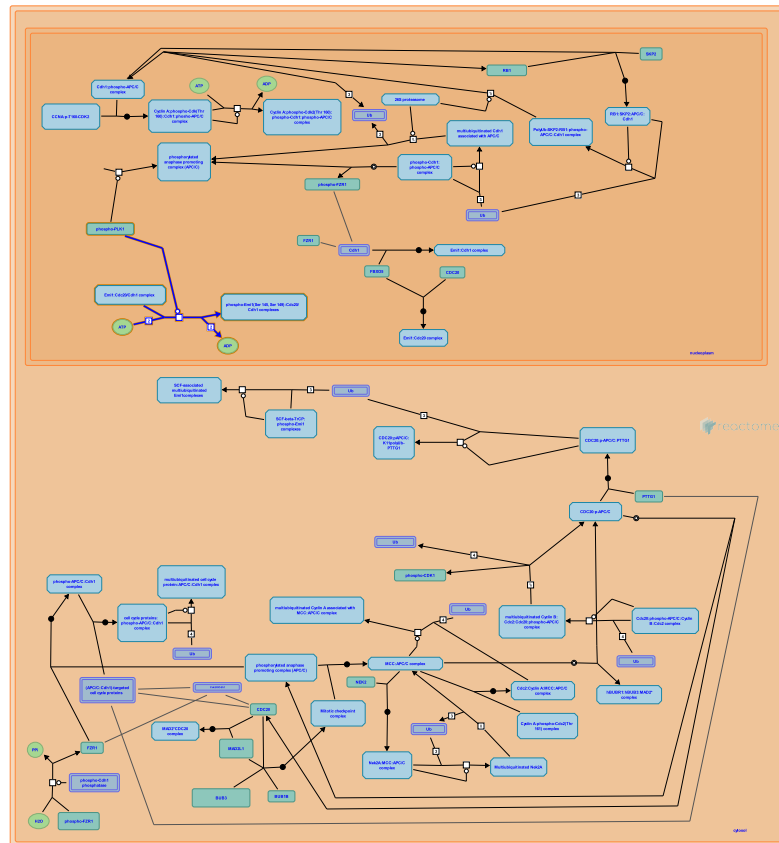
Followed by: Phosphorylation of Emi1

Phosphorylation of Emi1 ↗

Location: Regulation of APC/C activators between G1/S and early anaphase

Stable identifier: R-GGA-176417

Compartments: nucleoplasm

Inferred from: Phosphorylation of Emi1 (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
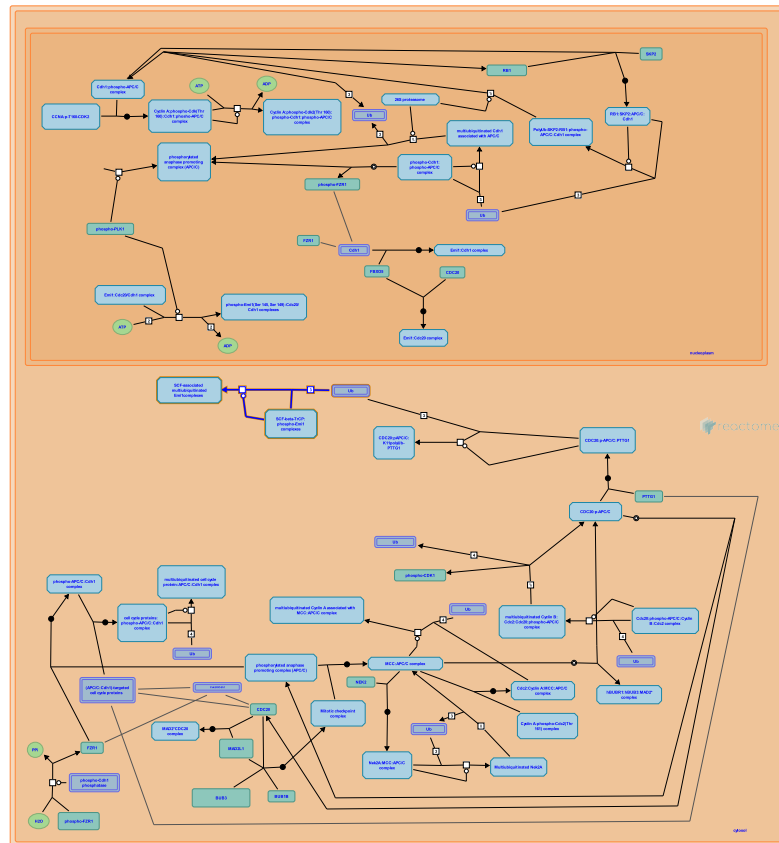
SCF-beta-TrCP mediated degradation of Emi1 ↗

Location: Regulation of APC/C activators between G1/S and early anaphase

Stable identifier: R-GGA-174113

Compartments: cytosol

Inferred from: SCF-beta-TrCP mediated degradation of Emi1 (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp
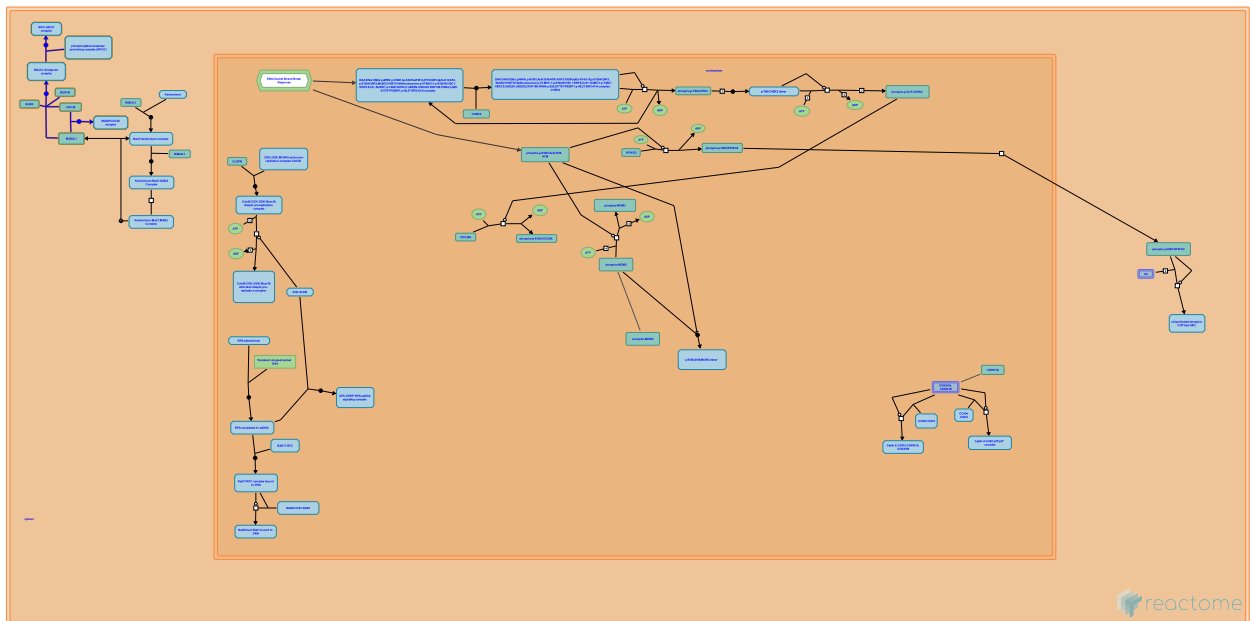
Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components ↗

Location: Regulation of APC/C activators between G1/S and early anaphase

Stable identifier: R-GGA-141405

Compartments: cytosol

Inferred from: Inhibition of the proteolytic activity of APC/C required for the onset of anaphase by mitotic spindle checkpoint components (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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Table of Contents