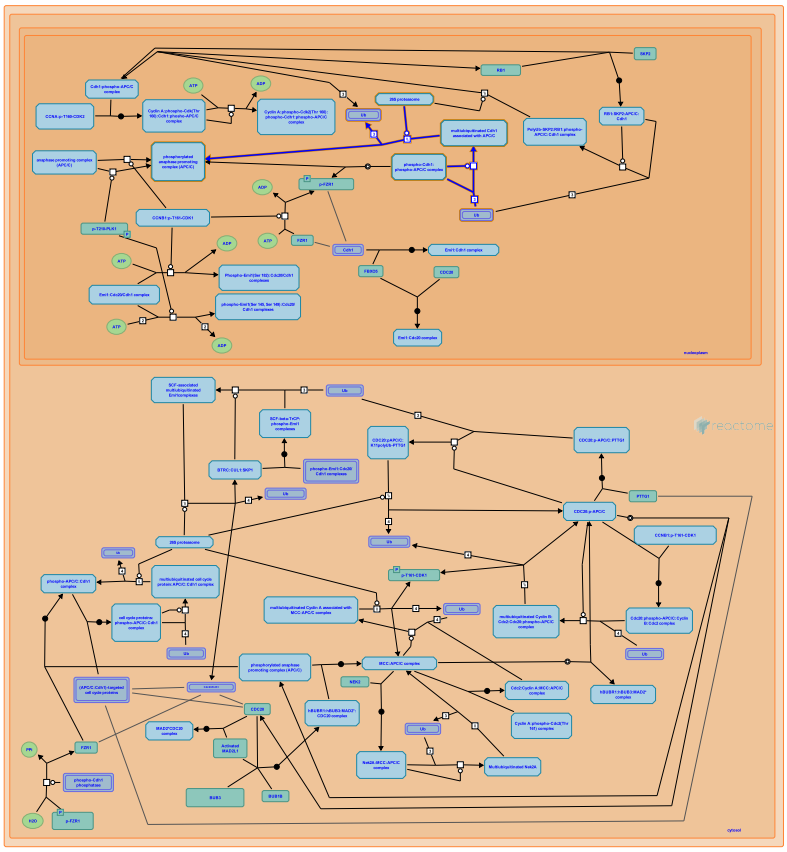
Autodegradation of Cdh1 by Cdh1:APC/C



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16/01/2021

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. ↗

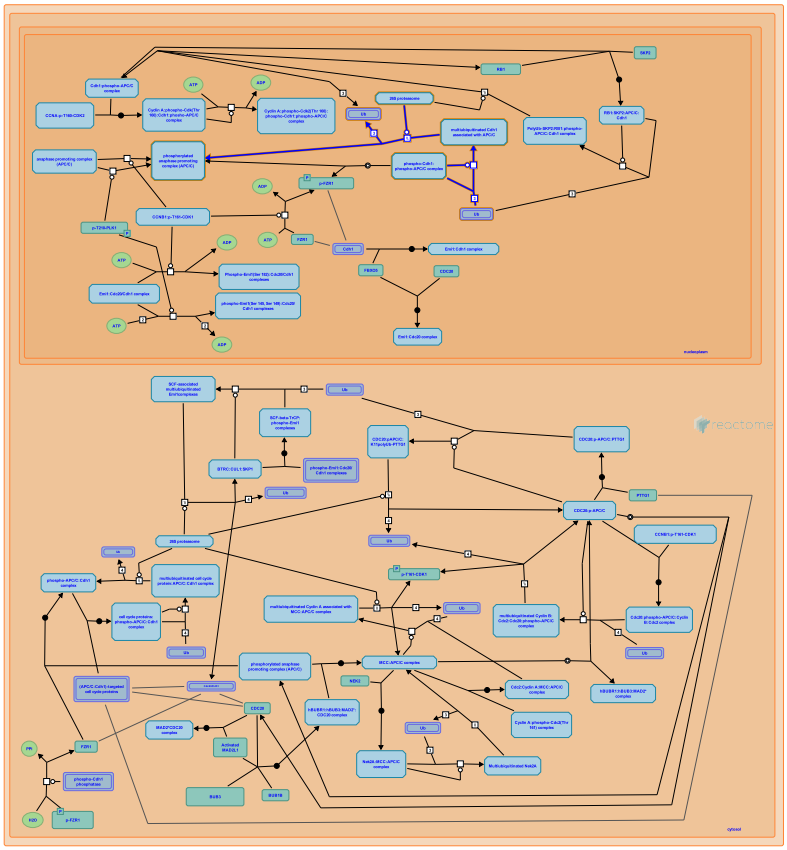
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Autodegradation of Cdh1 by Cdh1:APC/C ↗

Stable identifier: R-HSA-174084

Compartments: nucleoplasm



Cdh1 is degraded by the APC/C during in G1 and G0. This auto-regulation may contribute to reducing the levels of Cdh1 levels during G1 and G0 (Listovsky et al., 2004).

Literature references

Listovsky, T., Oren, YS., Yudkovsky, Y., Mahbubani, HM., Weiss, AM., Lebendiker, M. et al. (2004). Mammalian Cdh1/Fzr mediates its own degradation. *EMBO J, 23*, 1619-26. ↗

Editions

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

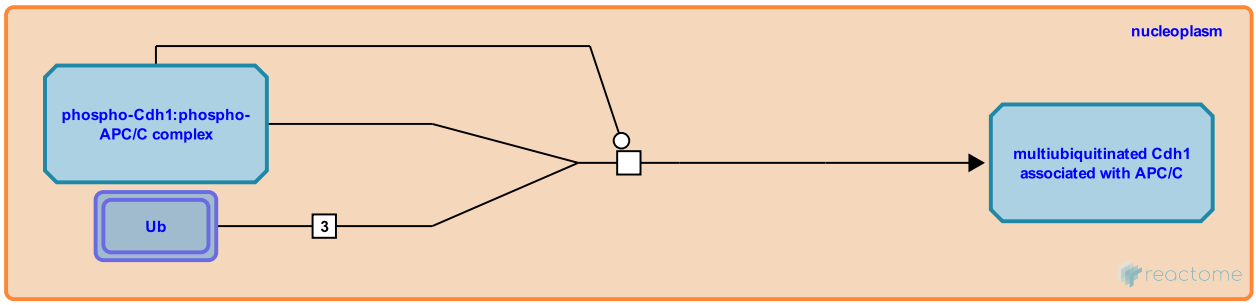
Multiubiquitination of APC/C-associated Cdh1 ↗

Location: Autodegradation of Cdh1 by Cdh1:APC/C

Stable identifier: R-HSA-174057

Type: transition

Compartments: nucleoplasm



Cdh1 is multiubiquitinated by the APC/C:Cdh1 complex prior to degradation by the 26S proteasome.

Followed by: Degradation of multiubiquitinated Cdh1

Literature references

Listovsky, T., Oren, YS., Yudkovsky, Y., Mahbubani, HM., Weiss, AM., Lebendiker, M. et al. (2004). Mammalian Cdh1/Fzr mediates its own degradation. *EMBO J, 23*, 1619-26. ↗

Editions

2006-01-26	Authored	Lorca, T., Castro, A.
2006-02-17	Edited	Matthews, L.
2006-03-28	Reviewed	Peters, JM.

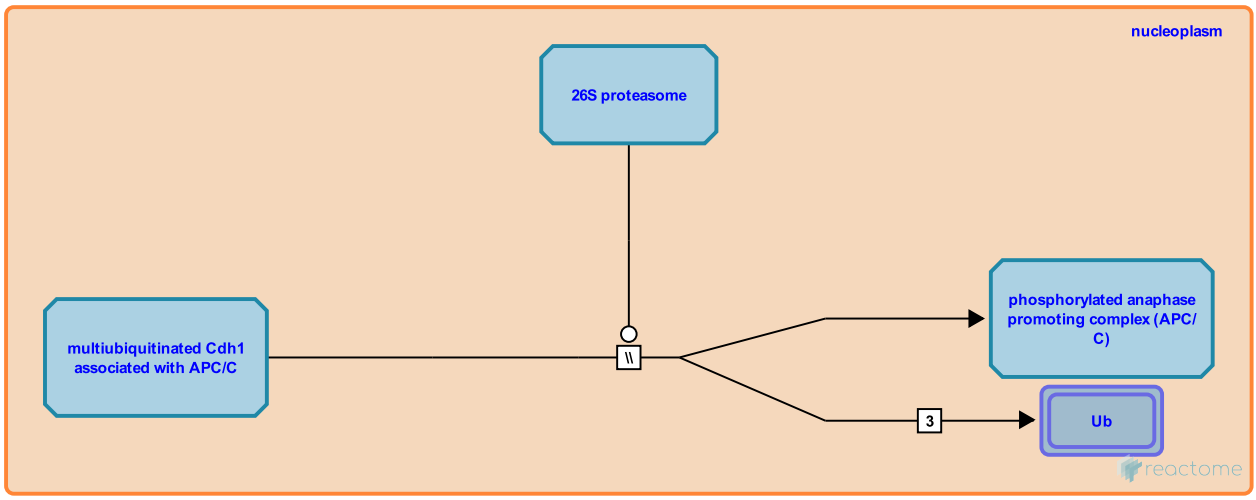
Degradation of multiubiquitinated Cdh1 ↗

Location: Autodegradation of Cdh1 by Cdh1:APC/C

Stable identifier: R-HSA-174058

Type: omitted

Compartments: nucleoplasm



At the beginning of this reaction, 1 molecule of 'multiubiquitinated Cdh1 associated with APC/C' is present. At the end of this reaction, 1 molecule of 'phosphorylated anaphase promoting complex (APC/C)', and 3 molecules of 'ubiquitin' are present.

This reaction takes place in the 'nucleoplasm' and is mediated by the 'endopeptidase activity' of '26S proteasome'.

Preceded by: Multiubiquitination of APC/C-associated Cdh1

Literature references

Listovsky, T., Oren, YS., Yudkovsky, Y., Mahbubani, HM., Weiss, AM., Lebendiker, M. et al. (2004). Mammalian Cdh1/Fzr mediates its own degradation. *EMBO J, 23*, 1619-26. ↗

Editions

2006-01-30	Authored, Edited	Matthews, L.
2006-03-28	Reviewed	Peters, JM.

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