SCF(Skp2)-mediated degradation of

p27/p21

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.

19/05/2024

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

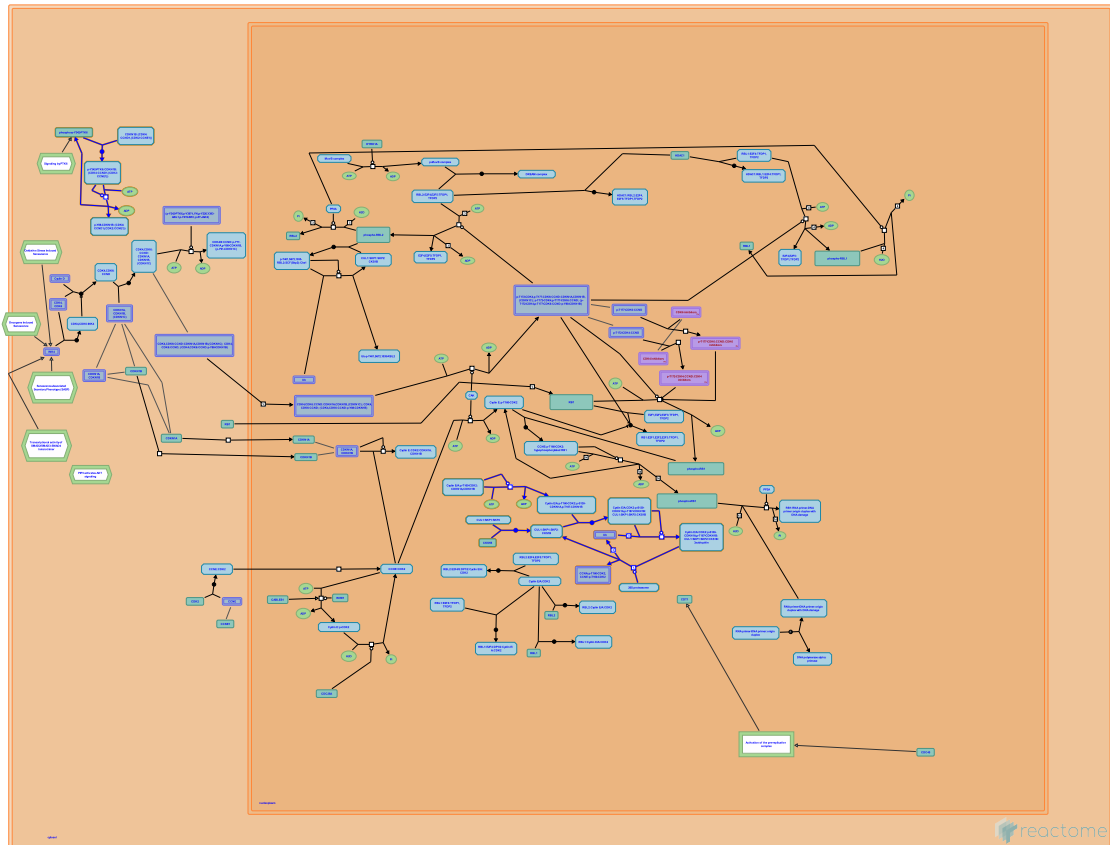This document contains 1 pathway and 7 reactions (see Table of Contents)

SCF(Skp2)-mediated degradation of p27/p21 ↗

Stable identifier: R-BTA-187577

Compartments: nucleoplasm

Inferred from: SCF(Skp2)-mediated degradation of p27/p21 (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

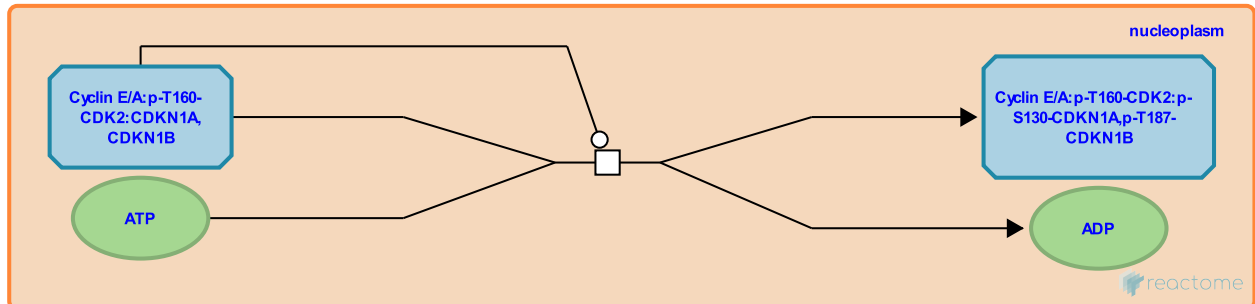# Cyclin E/A:Cdk2-mediated phosphorylation of p27/p21 ↗

Location: SCF(Skp2)-mediated degradation of p27/p21

Stable identifier: R-BTA-187520

Type: transition

Compartments: nucleoplasm

Inferred from: Cyclin E/A:Cdk2-mediated phosphorylation of p27/p21 (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: Binding of phospho-p27/p21:Cdk2:Cyclin E/A to the SCF(Skp2):Cks1 complex
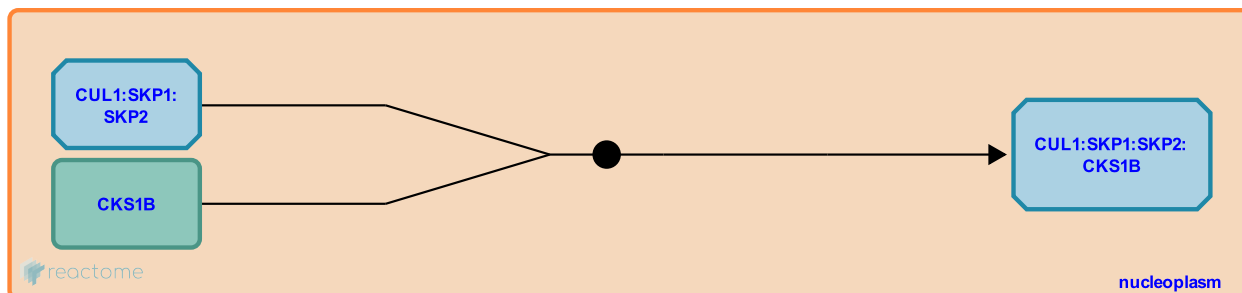
Association of Cks1 with SCF(Skp2) complex ↗

Location: SCF(Skp2)-mediated degradation of p27/p21

Stable identifier: R-BTA-187545

Type: binding

Compartments: nucleoplasm

Inferred from: Association of Cks1 with SCF(Skp2) 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

Followed by: Binding of phospho-p27/p21:Cdk2:Cyclin E/A to the SCF(Skp2):Cks1 complex

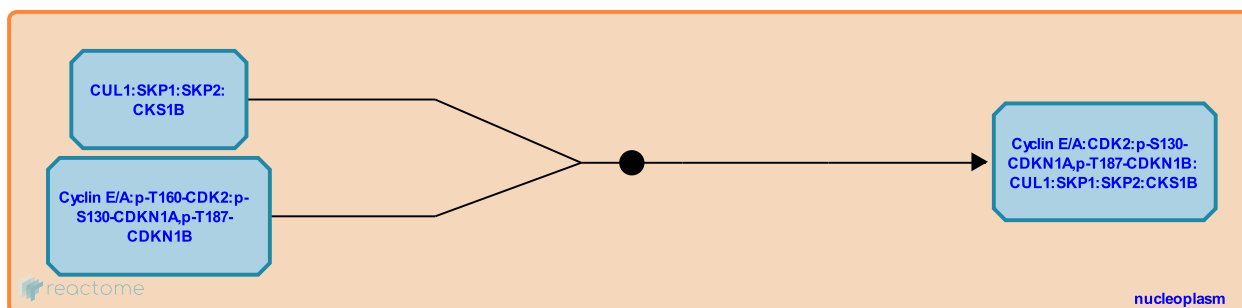**Binding of phospho-p27/p21:Cdk2:Cyclin E/A to the SCF(Skp2):Cks1 complex** ↗

Location: SCF(Skp2)-mediated degradation of p27/p21

Stable identifier: R-BTA-187552

Type: binding

Compartments: nucleoplasm

Inferred from: Binding of phospho-p27/p21:Cdk2:Cyclin E/A to the SCF(Skp2):Cks1 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: Association of Cks1 with SCF(Skp2) complex, Cyclin E/A:Cdk2-mediated phosphorylation of p27/p21

Followed by: Ubiquitination of phospho-p27/p21
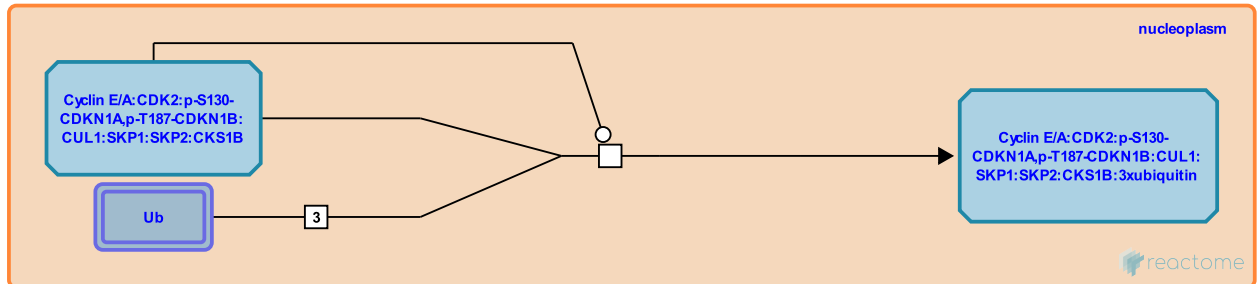
Ubiquitination of phospho-p27/p21 ↗

Location: SCF(Skp2)-mediated degradation of p27/p21

Stable identifier: R-BTA-187575

Type: transition

Compartments: nucleoplasm

Inferred from: Ubiquitination of phospho-p27/p21 (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: Binding of phospho-p27/p21:Cdk2:Cyclin E/A to the SCF(Skp2):Cks1 complex

Followed by: Degradation of ubiquitinated p27/p21 by the 26S proteasome

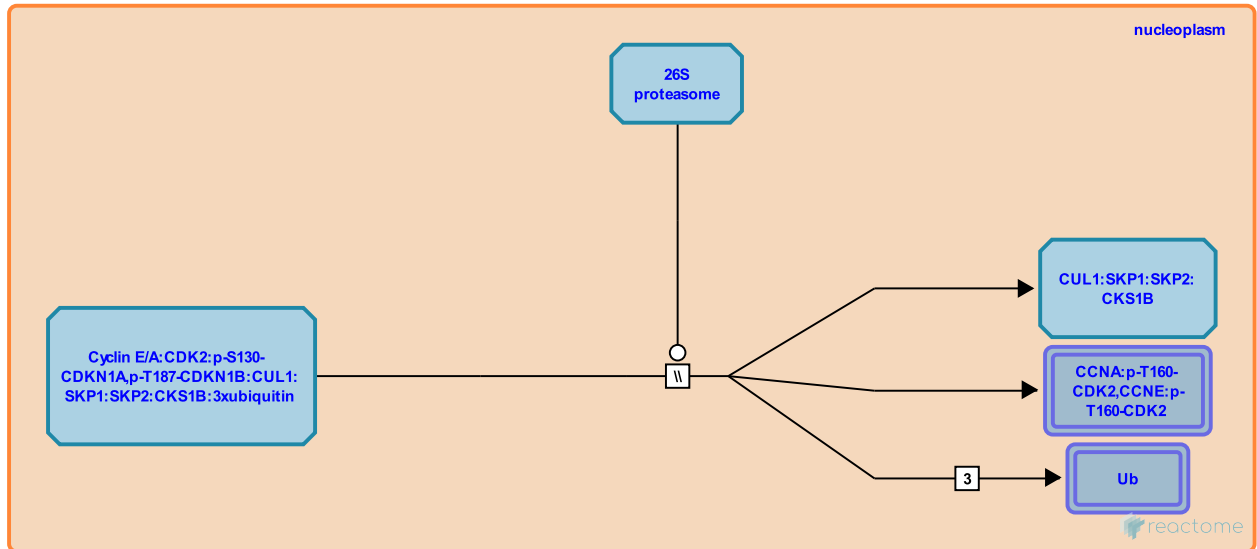## Degradation of ubiquitinated p27/p21 by the 26S proteasome ↗

Location: SCF(Skp2)-mediated degradation of p27/p21

Stable identifier: R-BTA-187574

Type: omitted

Compartments: nucleoplasm

Inferred from: Degradation of ubiquitinated p27/p21 by the 26S 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. For details on PANTHER see also: http://www.pantherdb.org/about.jsp

Preceded by: Ubiquitination of phospho-p27/p21
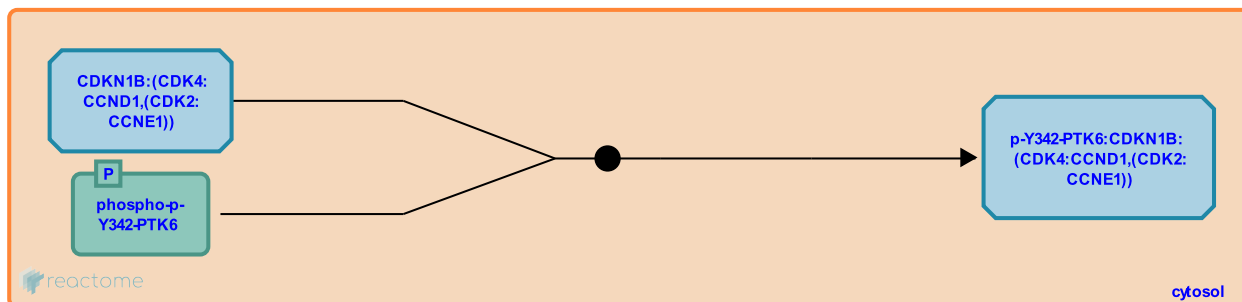
Activated PTK6 binds CDKN1B ↗

Location: SCF(Skp2)-mediated degradation of p27/p21

Stable identifier: R-BTA-8848414

Type: binding

Compartments: cytosol

Inferred from: Activated PTK6 binds CDKN1B (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: PTK6 phosphorylates CDKN1B
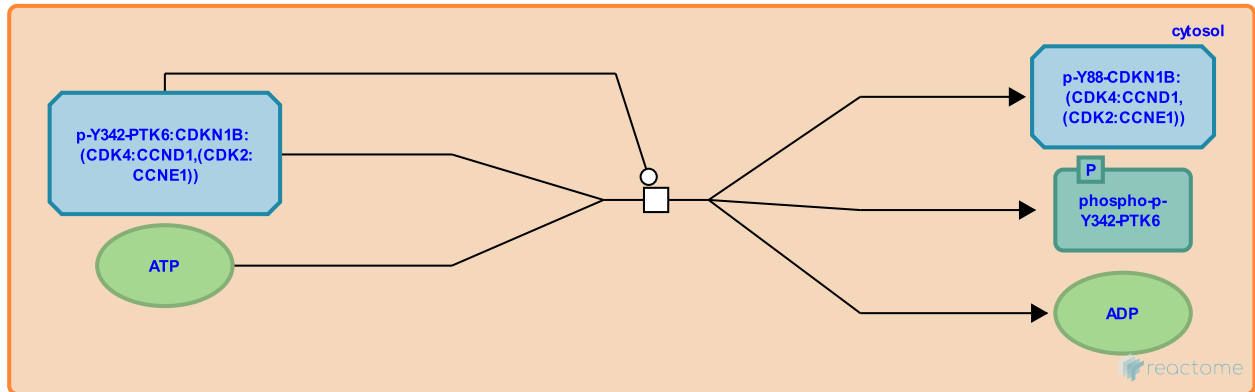
PTK6 phosphorylates CDKN1B ↗

Location: SCF(Skp2)-mediated degradation of p27/p21

Stable identifier: R-BTA-8848436

Type: transition

Compartments: cytosol

Inferred from: PTK6 phosphorylates CDKN1B (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: Activated PTK6 binds CDKN1B

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