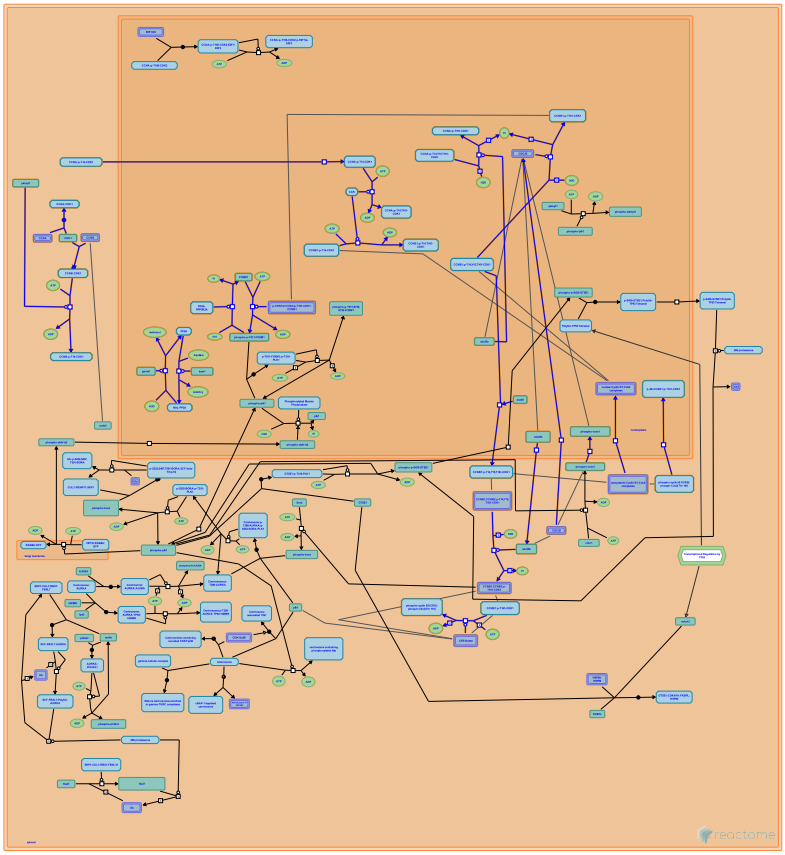
Cyclin A/B1/B2 associated events during G2/M transition



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

26/02/2021

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.

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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. ↗

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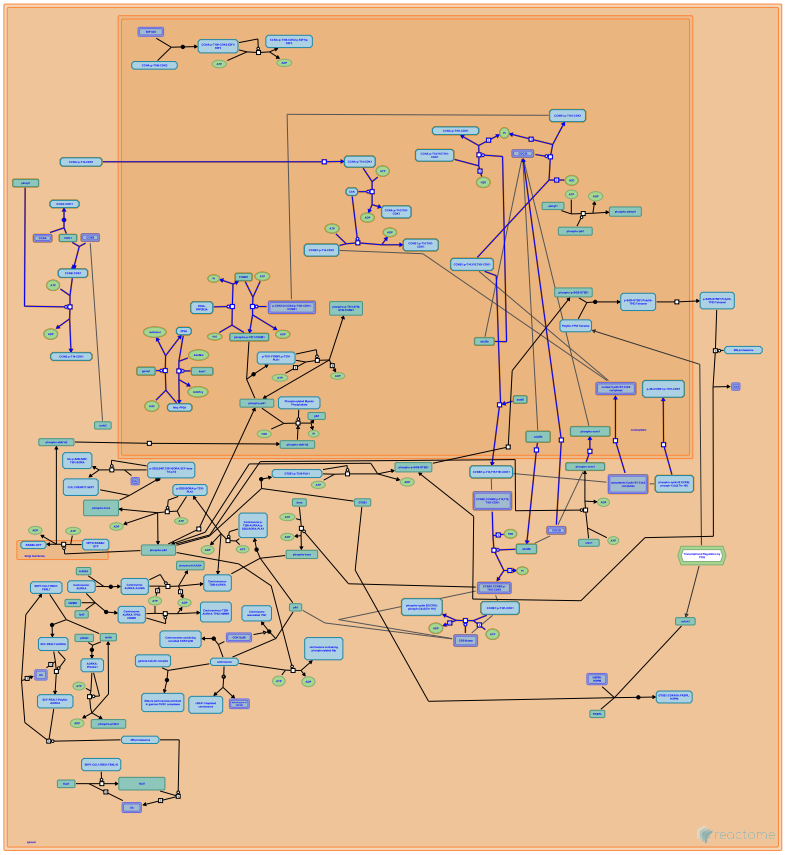
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Cyclin A/B1/B2 associated events during G2/M transition ↗

Stable identifier: R-XTR-69273

Inferred from: Cyclin A/B1/B2 associated events during G2/M transition (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Formation of Cyclin A:Cdc2 complexes ↗

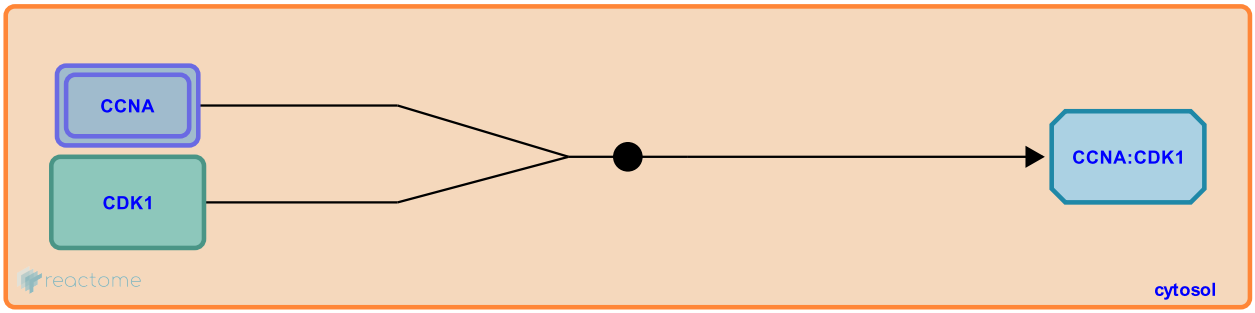
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170084

Type: binding

Compartments: cytosol

Inferred from: Formation of Cyclin A:Cdc2 complexes (Homo sapiens)



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Translocation of Cyclin A:phospho-Cdc2 (Thr 14) to the nucleus ↗

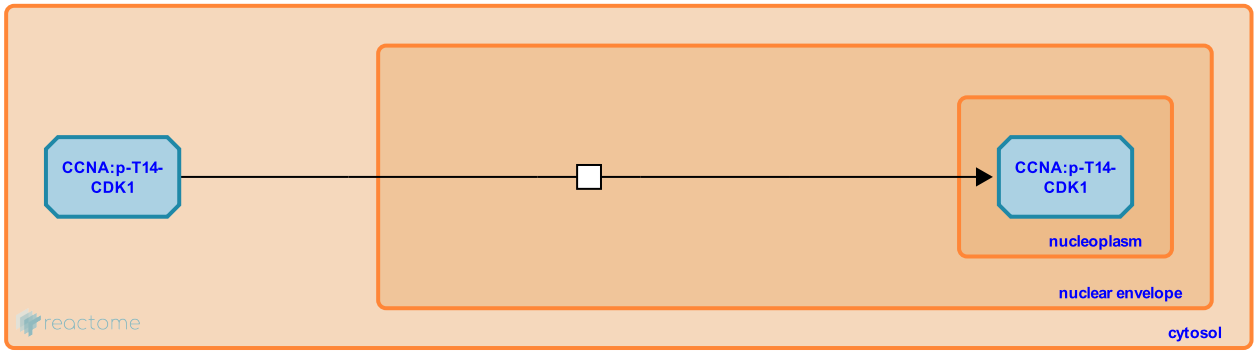
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170088

Type: transition

Compartments: nuclear envelope

Inferred from: Translocation of Cyclin A:phospho-Cdc2 (Thr 14) to the nucleus (Homo sapiens)



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Followed by: CAK-mediated phosphorylation of Cyclin A:Cdc2 complexes

CAK-mediated phosphorylation of Cyclin A:Cdc2 complexes ↗

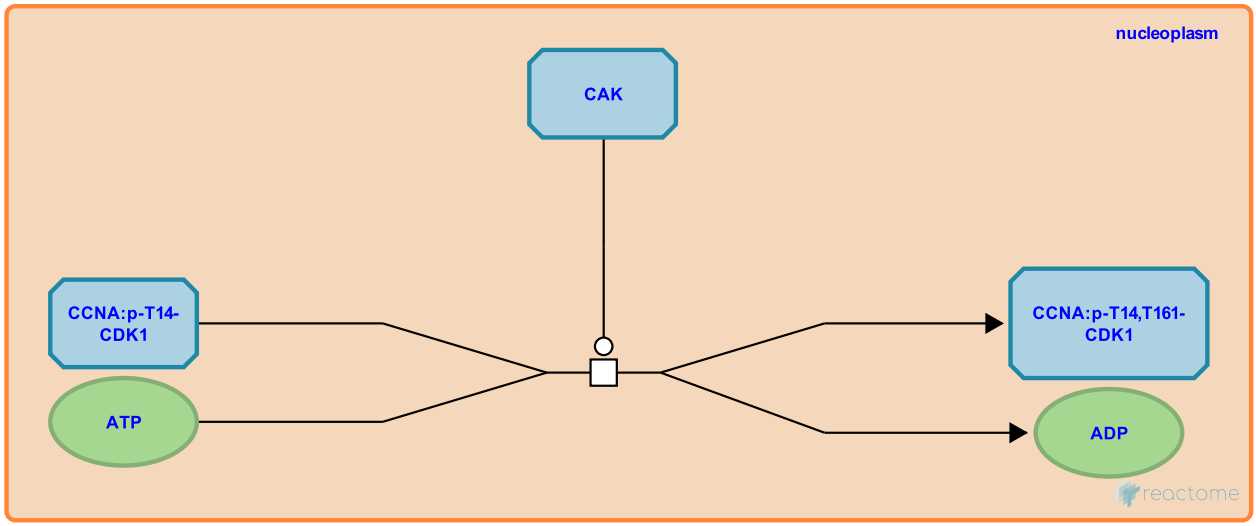
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170087

Type: transition

Compartments: nucleoplasm

Inferred from: CAK-mediated phosphorylation of Cyclin A:Cdc2 complexes (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.

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Preceded by: Translocation of Cyclin A:phospho-Cdc2 (Thr 14) to the nucleus

Translocation of active Cdc25C to the nucleus ↗

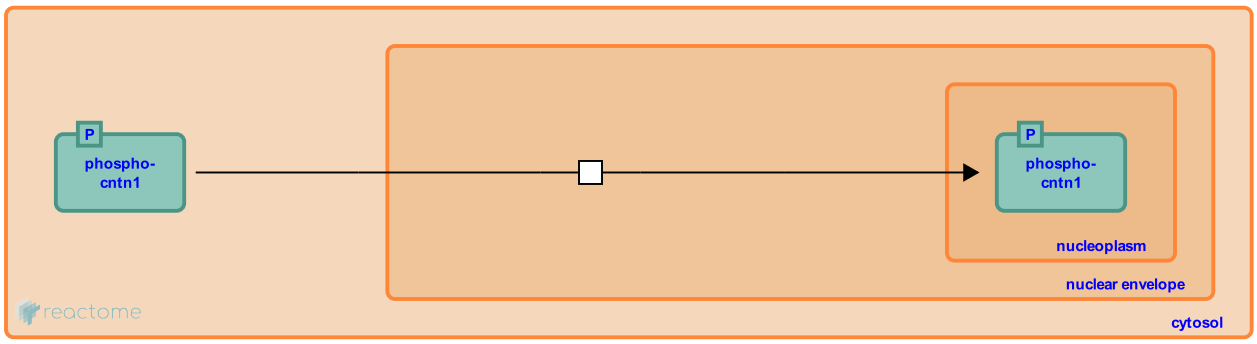
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170149

Type: transition

Compartments: nuclear envelope

Inferred from: Translocation of active Cdc25C to 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.

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Followed by: Dephosphorylation of nuclear Cyclin A:phospho-Cdc2 complexes

Dephosphorylation of nuclear Cyclin A:phospho-Cdc2 complexes ↗

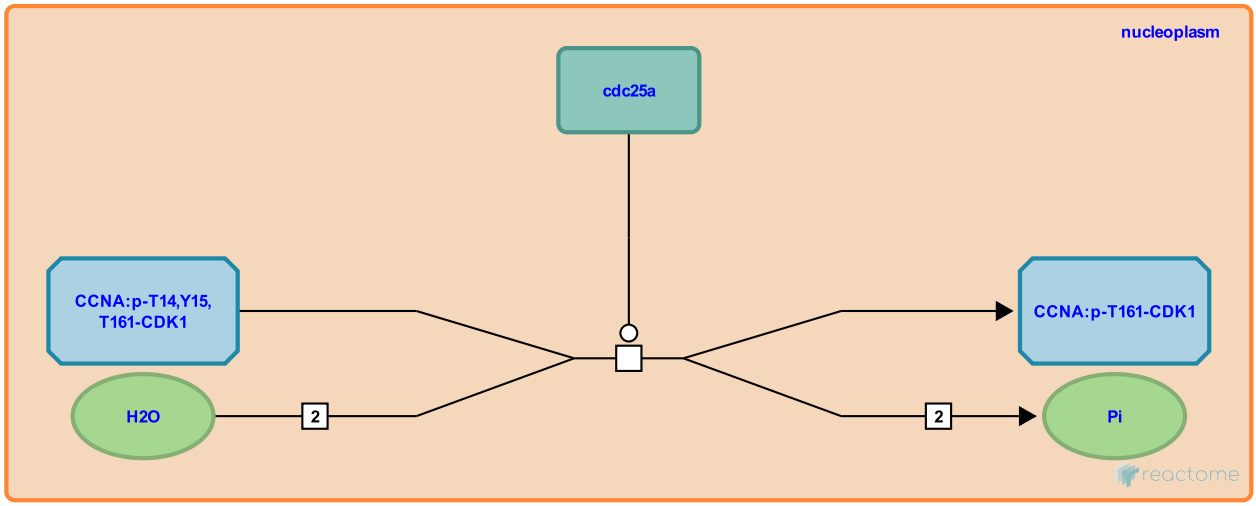
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170158

Type: transition

Compartments: nucleoplasm

Inferred from: Dephosphorylation of nuclear Cyclin A:phospho-Cdc2 complexes (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.

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Preceded by: Translocation of active Cdc25C to the nucleus

Formation of Cyclin B:Cdc2 complexes ↗

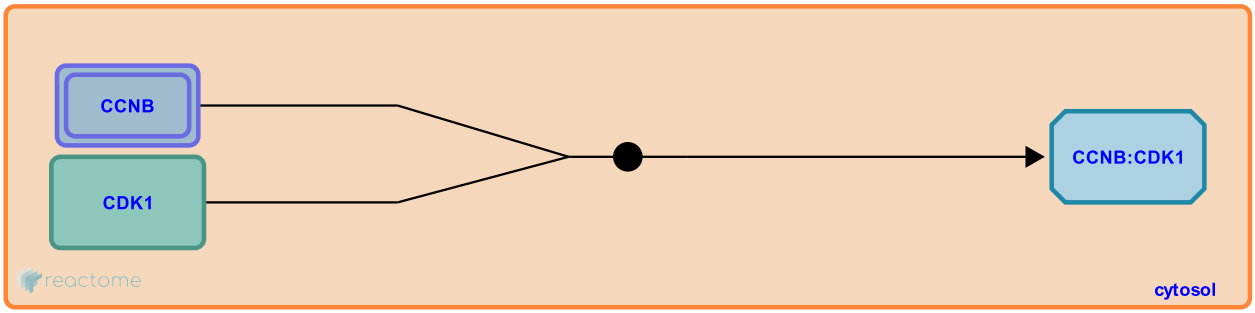
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170057

Type: binding

Compartments: cytosol

Inferred from: Formation of Cyclin B:Cdc2 complexes (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.

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Followed by: Myt-1 mediated phosphorylation of Cyclin B:Cdc2 complexes

Myt-1 mediated phosphorylation of Cyclin B:Cdc2 complexes ↗

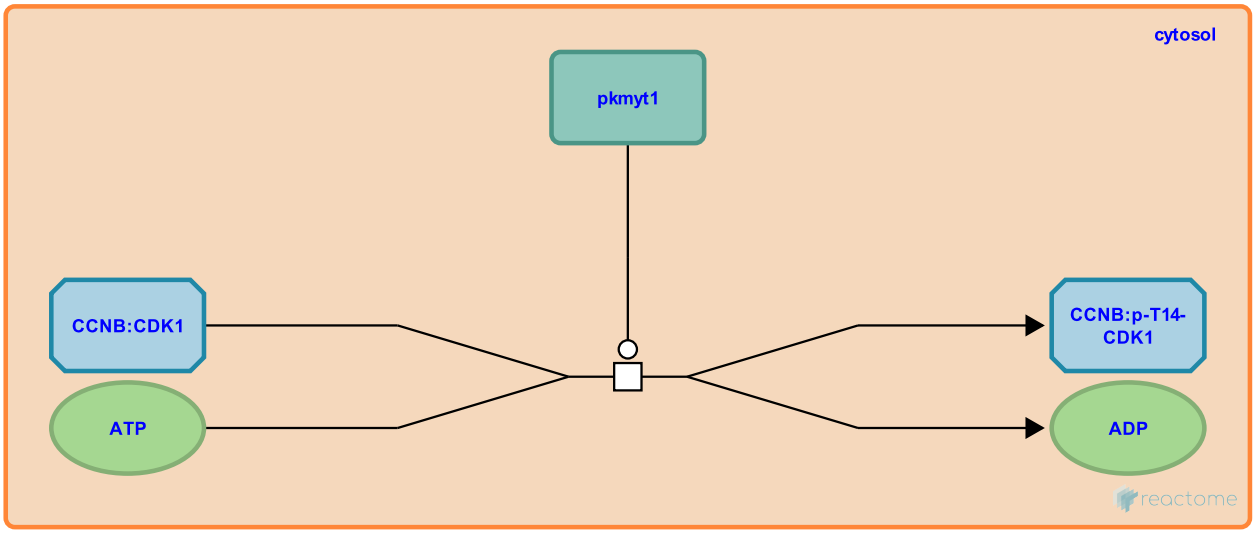
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170055

Type: transition

Compartments: cytosol

Inferred from: Myt-1 mediated phosphorylation of Cyclin B:Cdc2 complexes (Homo sapiens)



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

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Preceded by: Formation of Cyclin B:Cdc2 complexes

Followed by: Translocation of Cyclin B1:phospho-Cdc2 complexes to the nucleus

Translocation of Cyclin B1:phospho-Cdc2 complexes to the nucleus ↗

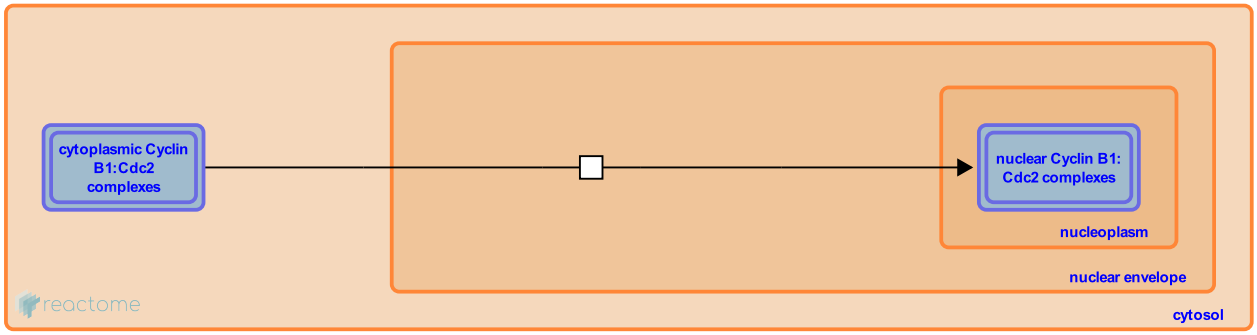
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170044

Type: transition

Compartments: nuclear envelope

Inferred from: Translocation of Cyclin B1:phospho-Cdc2 complexes to 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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: Myt-1 mediated phosphorylation of Cyclin B:Cdc2 complexes

Followed by: CAK-mediated phosphorylation of Cyclin B1:Cdc2 complexes

CAK-mediated phosphorylation of Cyclin B1:Cdc2 complexes ↗

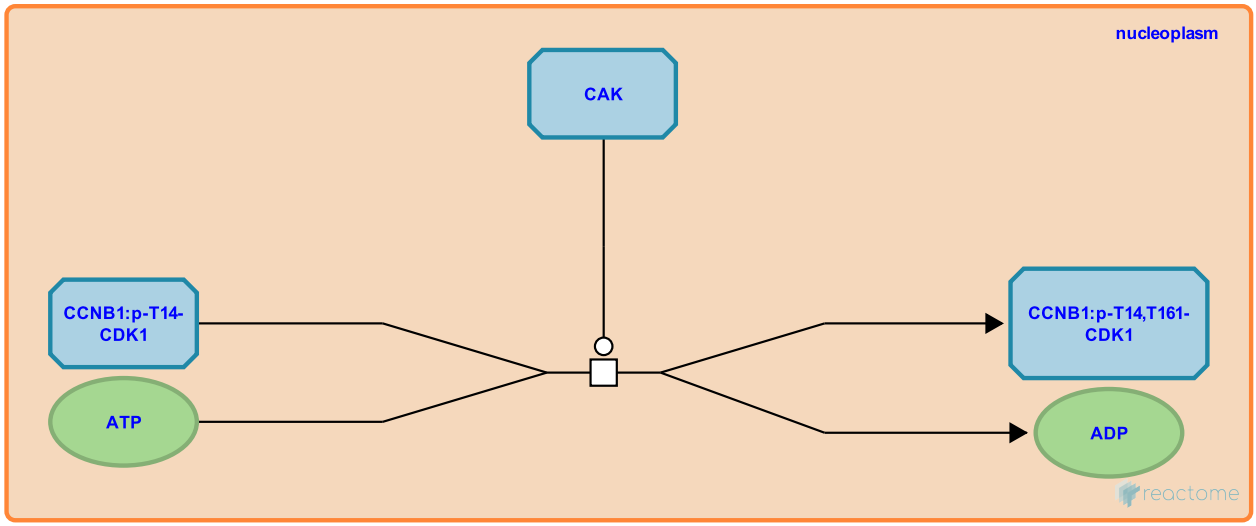
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170076

Type: transition

Compartments: nucleoplasm

Inferred from: CAK-mediated phosphorylation of Cyclin B1:Cdc2 complexes (Homo sapiens)



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

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Preceded by: Translocation of Cyclin B1:phospho-Cdc2 complexes to the nucleus

Followed by: Phosphorylation of Cyclin B1 in the CRS domain

Translocation of Cyclin B1:phospho-Cdc2 to the cytoplasm ↗

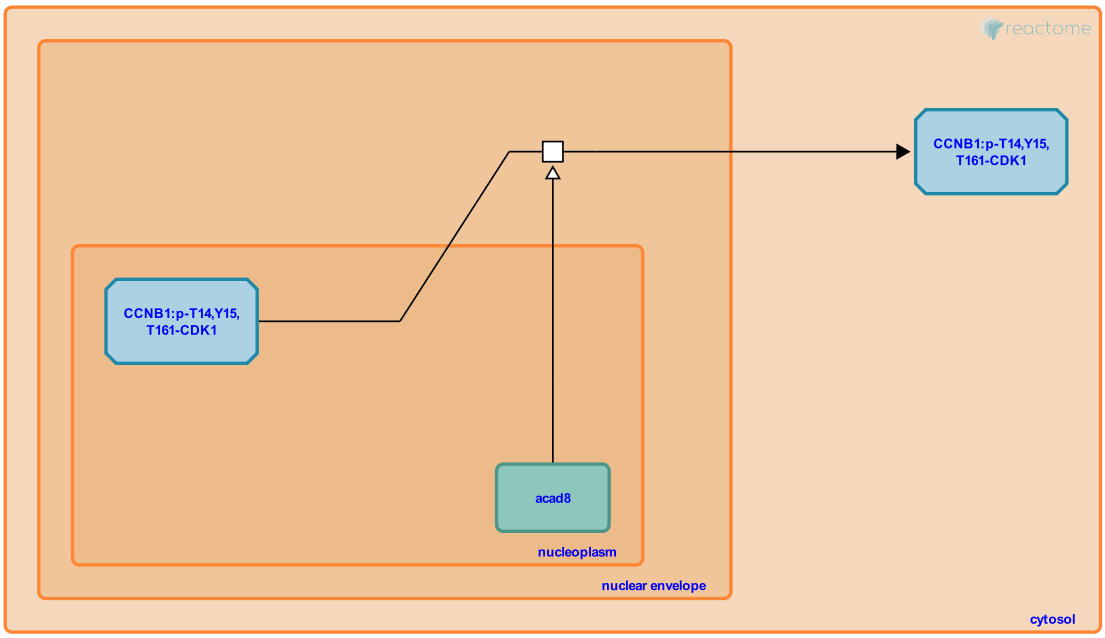
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170072

Type: transition

Compartments: nuclear envelope

Inferred from: Translocation of Cyclin B1:phospho-Cdc2 to the cytoplasm (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Followed by: Dephosphorylation of cytoplasmic Cyclin B1/B2:phospho-Cdc2 (Thr 14, Tyr 15) complexes by CDC25B

Translocation of Cdc25B to the cytoplasm ↗

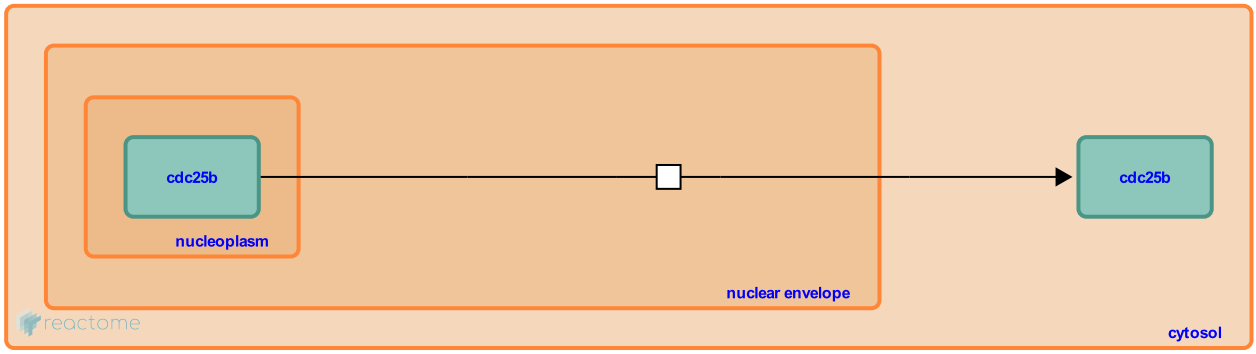
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170120

Type: transition

Compartments: nuclear envelope

Inferred from: Translocation of Cdc25B to the cytoplasm (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Followed by: Dephosphorylation of cytoplasmic Cyclin B1/B2:phospho-Cdc2 (Thr 14, Tyr 15) complexes by CDC25B

Dephosphorylation of cytoplasmic Cyclin B1/B2:phospho-Cdc2 (Thr 14, Tyr 15) complexes by CDC25B ↗

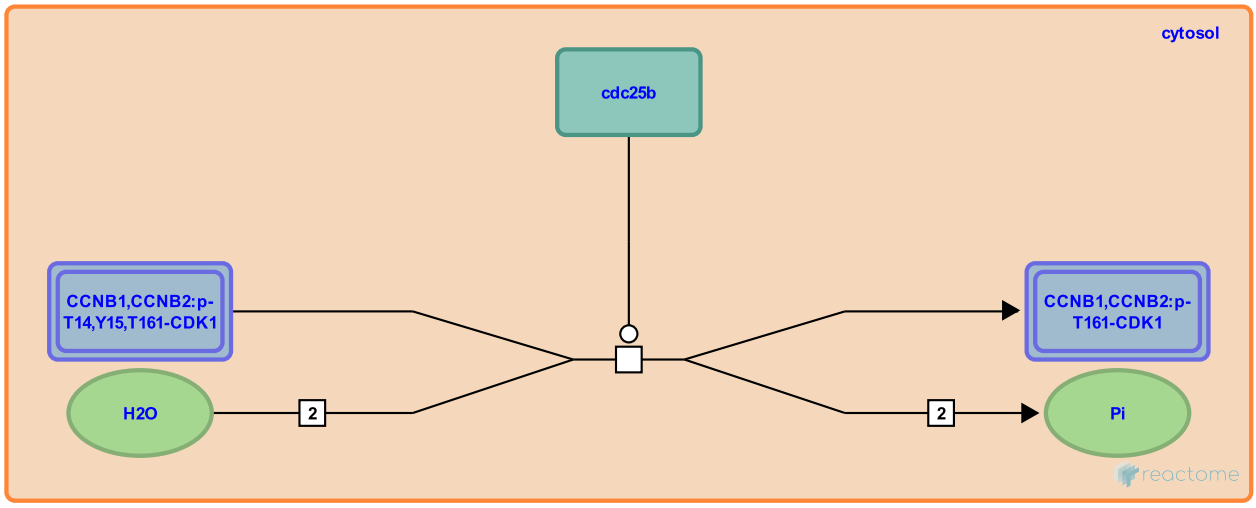
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170161

Type: transition

Compartments: cytosol

Inferred from: Dephosphorylation of cytoplasmic Cyclin B1/B2:phospho-Cdc2 (Thr 14, Tyr 15) complexes by CDC25B (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.

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Preceded by: Translocation of Cdc25B to the cytoplasm, Translocation of Cyclin B1:phospho-Cdc2 to the cytoplasm

Followed by: Phosphorylation of Cyclin B1 in the CRS domain

Phosphorylation of Cyclin B1 in the CRS domain ↗

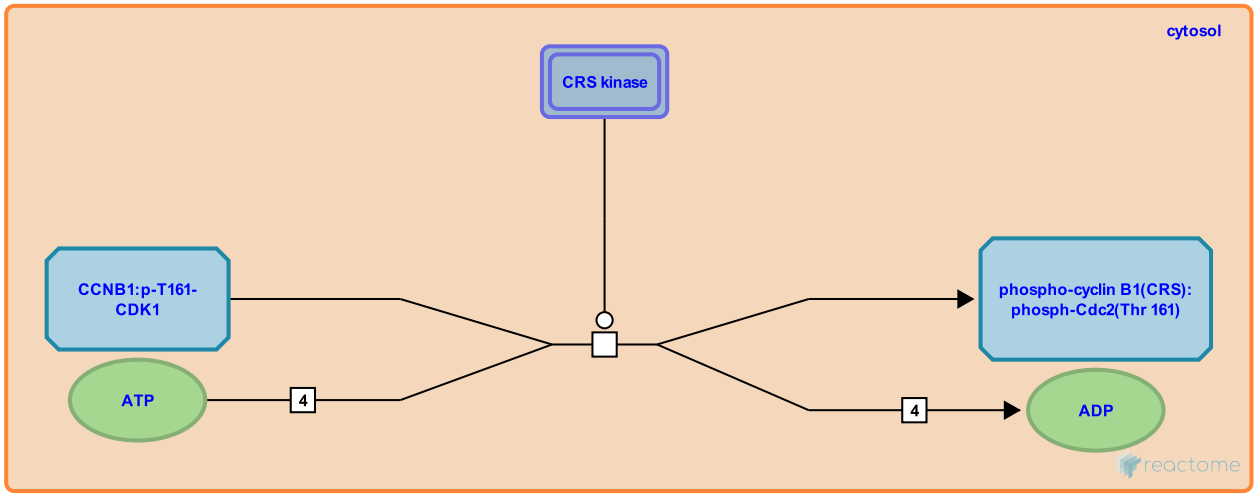
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170126

Type: transition

Compartments: cytosol

Inferred from: Phosphorylation of Cyclin B1 in the CRS domain (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.

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Preceded by: CAK-mediated phosphorylation of Cyclin B1:Cdc2 complexes, Dephosphorylation of cytoplasmic Cyclin B1/B2:phospho-Cdc2 (Thr 14, Tyr 15) complexes by CDC25B

Followed by: Translocation of CRS phosphorylated Cyclin B1:Cdc2 complexes

Translocation of CRS phosphorylated Cyclin B1:Cdc2 complexes ↗

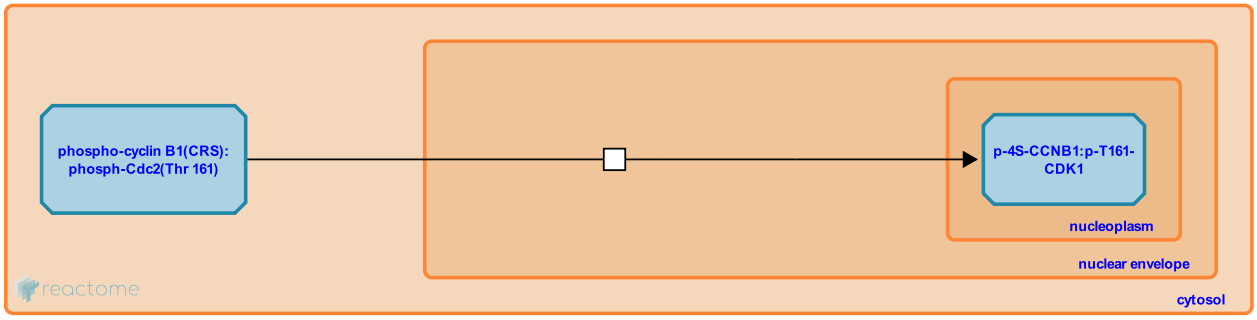
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170131

Type: transition

Compartments: nuclear envelope

Inferred from: Translocation of CRS phosphorylated Cyclin B1:Cdc2 complexes (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.

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Preceded by: Phosphorylation of Cyclin B1 in the CRS domain

Followed by: Dephosphorylation of nuclear Cyclin B1:phospho-Cdc2 (Thr 14, Tyr15) complexes by Cdc25 phosphatases

Translocation of Cdc25 to the nucleus ↗

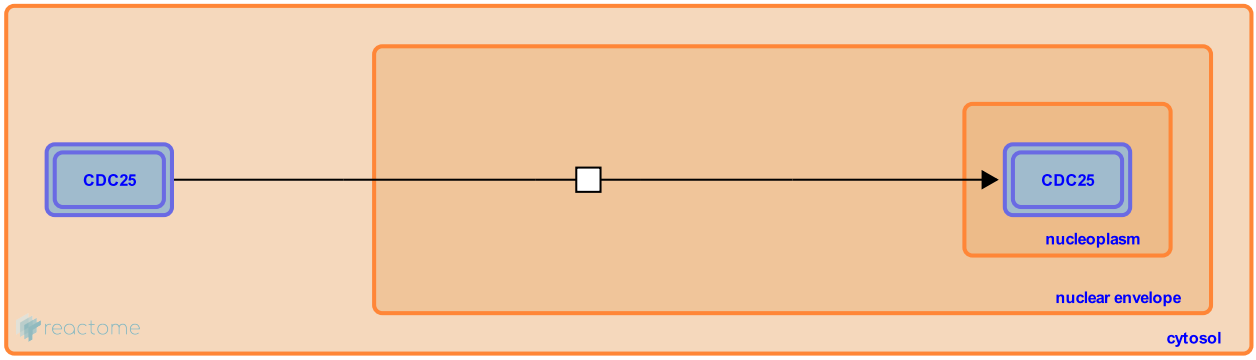
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170159

Type: transition

Compartments: nuclear envelope

Inferred from: Translocation of Cdc25 to 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.

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Followed by: Dephosphorylation of nuclear Cyclin B1:phospho-Cdc2 (Thr 14, Tyr15) complexes by Cdc25 phosphatases

Dephosphorylation of nuclear Cyclin B1:phospho-Cdc2 (Thr 14, Tyr15) complexes by Cdc25 phosphatases ↗

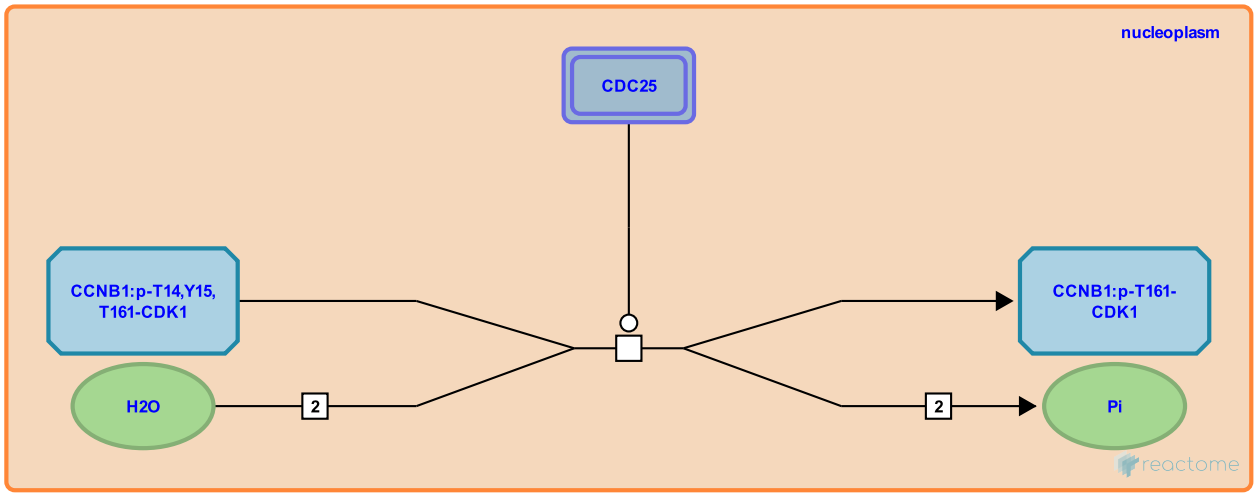
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-170153

Type: transition

Compartments: nucleoplasm

Inferred from: Dephosphorylation of nuclear Cyclin B1:phospho-Cdc2 (Thr 14, Tyr15) complexes by Cdc25 phosphatases (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.

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Preceded by: Translocation of Cdc25 to the nucleus, Translocation of CRS phosphorylated Cyclin B1:Cdc2 complexes

CCNA:CDK1/2 complexes and CCNB1:CDK1 complexes phosphorylate FOXM1 ↗

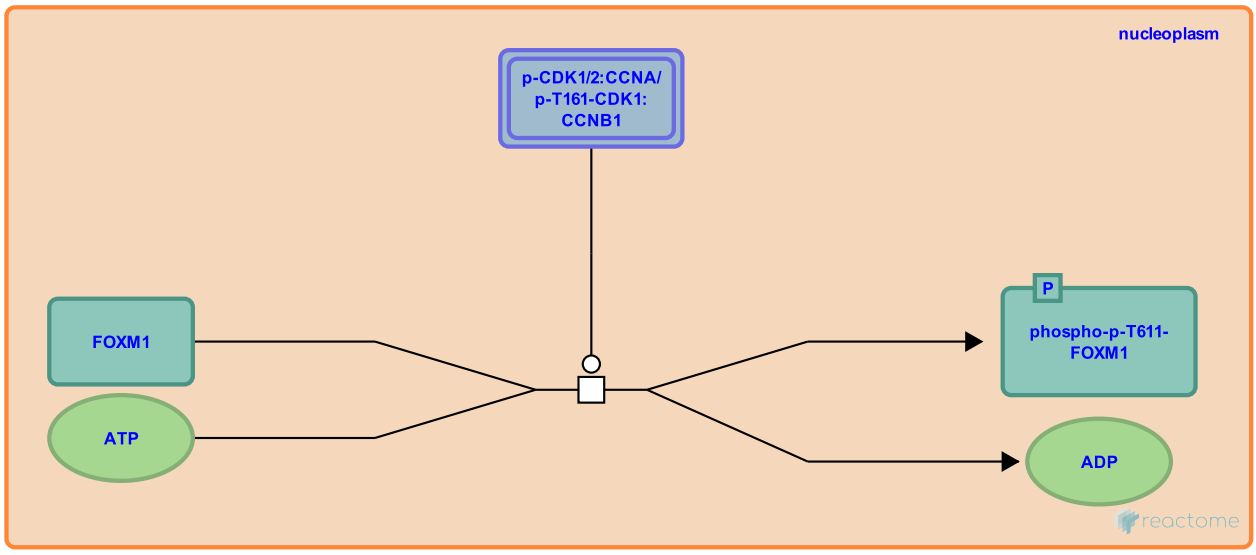
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-4088024

Type: transition

Compartments: nucleoplasm

Inferred from: CCNA:CDK1/2 complexes and CCNB1:CDK1 complexes phosphorylate FOXM1 (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Followed by: PP2A-PPP2R2A dephosphorylates FOXM1

PP2A-PPP2R2A dephosphorylates FOXM1 ↗

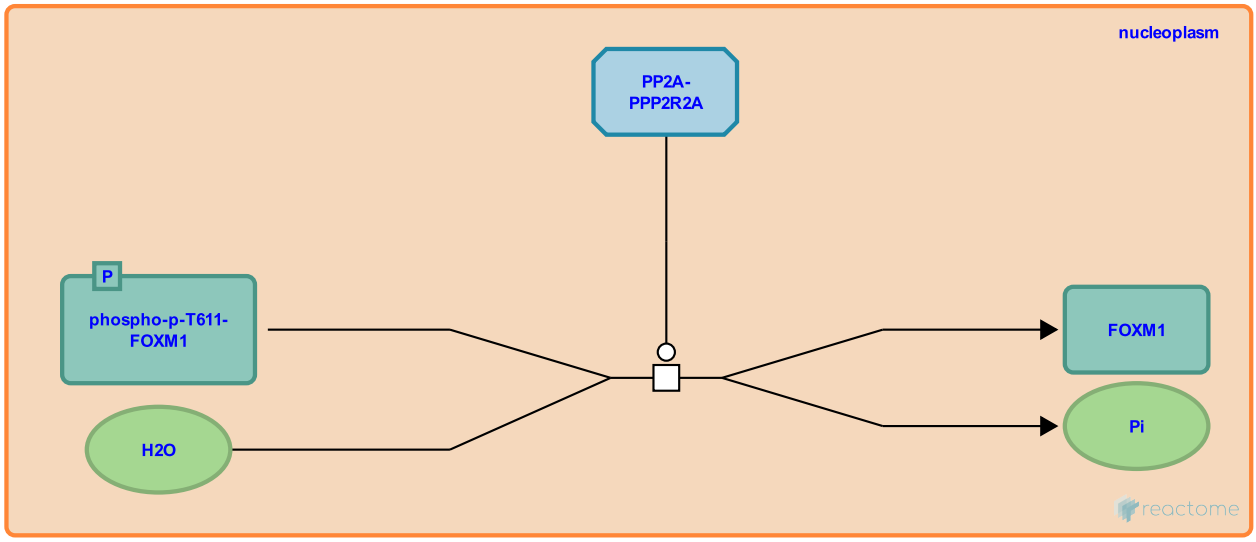
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-4088141

Type: transition

Compartments: nucleoplasm

Inferred from: PP2A-PPP2R2A dephosphorylates FOXM1 (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

Preceded by: CCNA:CDK1/2 complexes and CCNB1:CDK1 complexes phosphorylate FOXM1

PP2A methylation by LCMT1 ↗

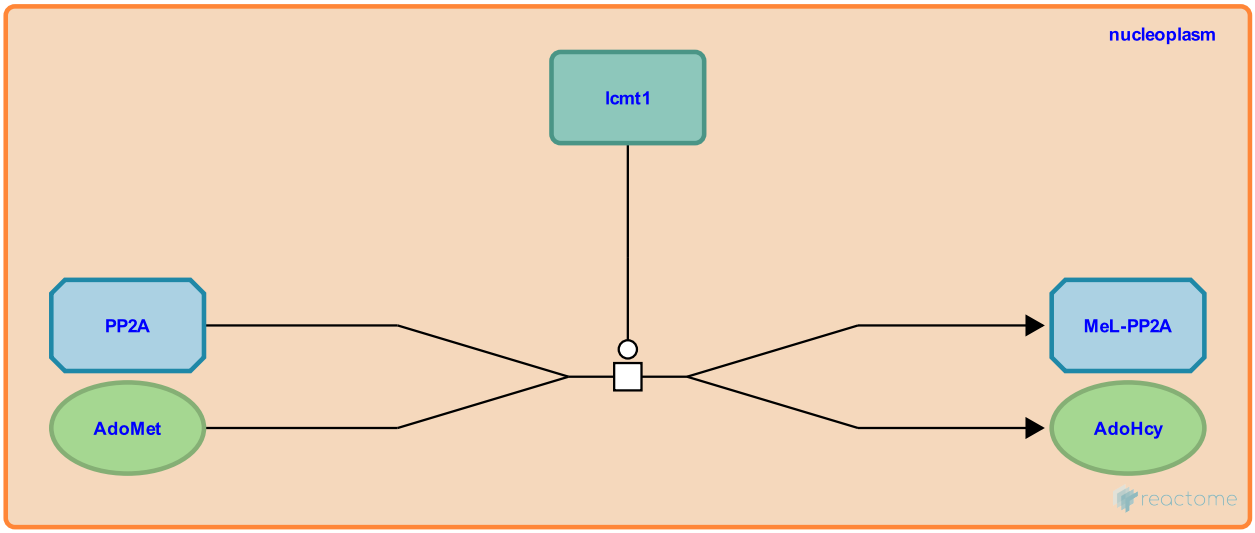
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-8856945

Type: transition

Compartments: nucleoplasm

Inferred from: PP2A methylation by LCMT1 (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

PP2A demethylation by PPME1 ↗

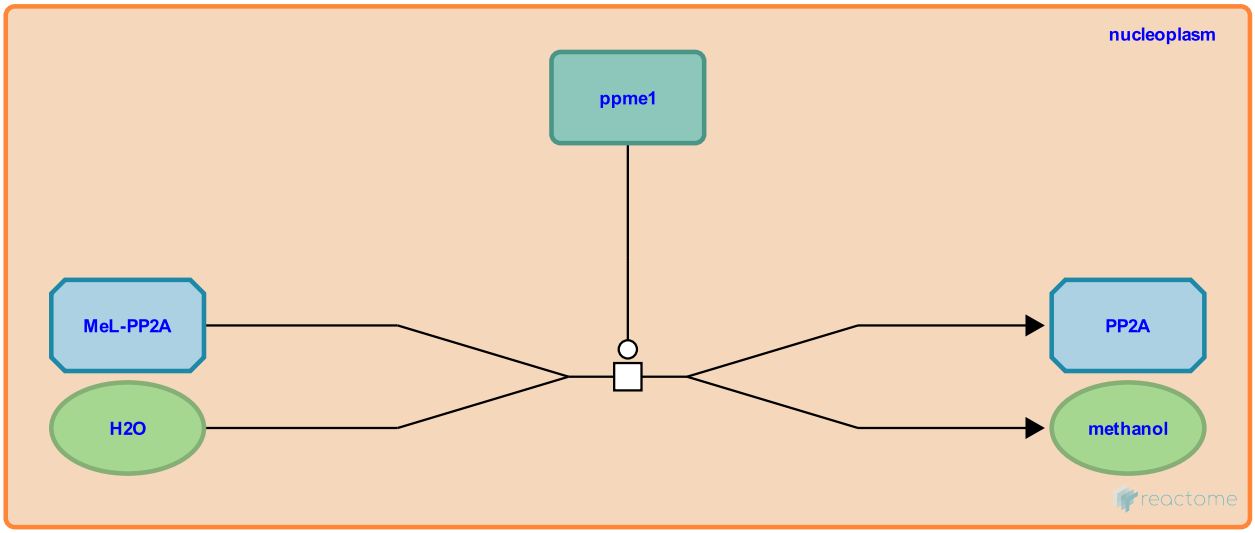
Location: Cyclin A/B1/B2 associated events during G2/M transition

Stable identifier: R-XTR-8856951

Type: transition

Compartments: nucleoplasm

Inferred from: PP2A demethylation by PPME1 (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.

<a href='/electronic_inference_compara.html' target = 'NEW'>More details and caveats of the event inference in Reactome. For details on PANTHER see also: <a href='http://www.pantherdb.org/about.jsp' target='NEW'>http://www.pantherdb.org/about.jsp

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