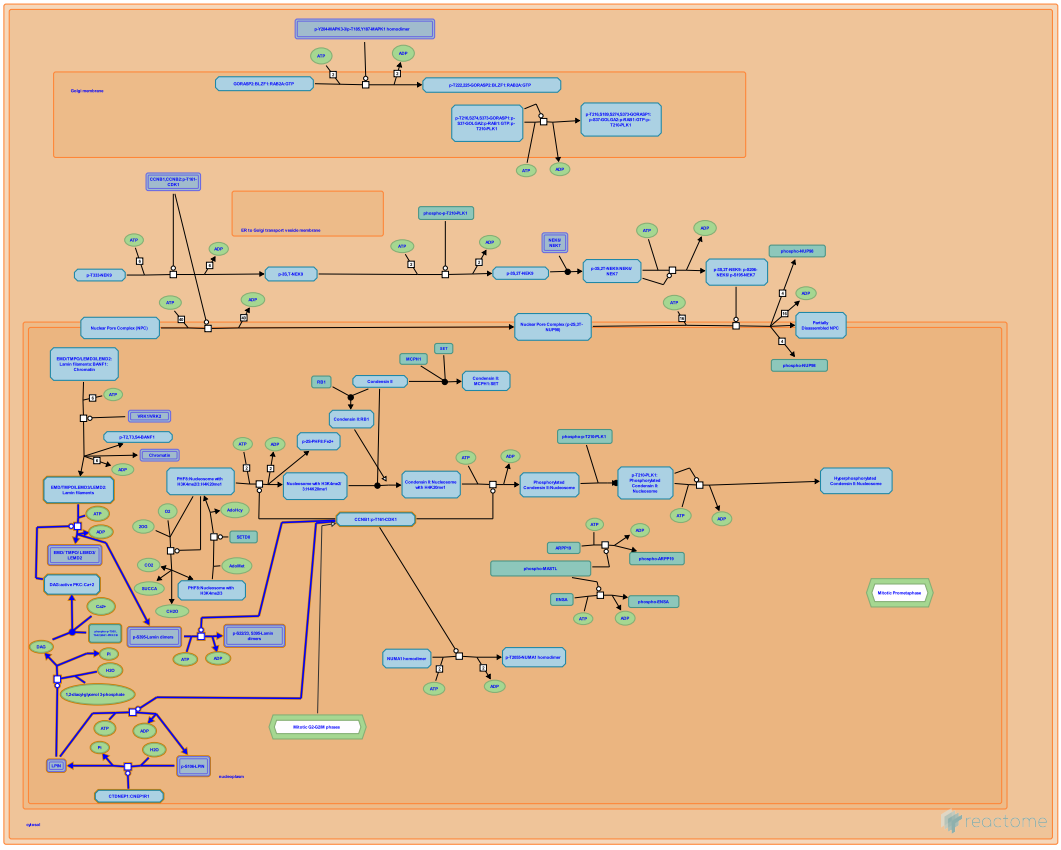
Depolymerization of the Nuclear Lamina



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

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.

07/05/2024

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. ↗

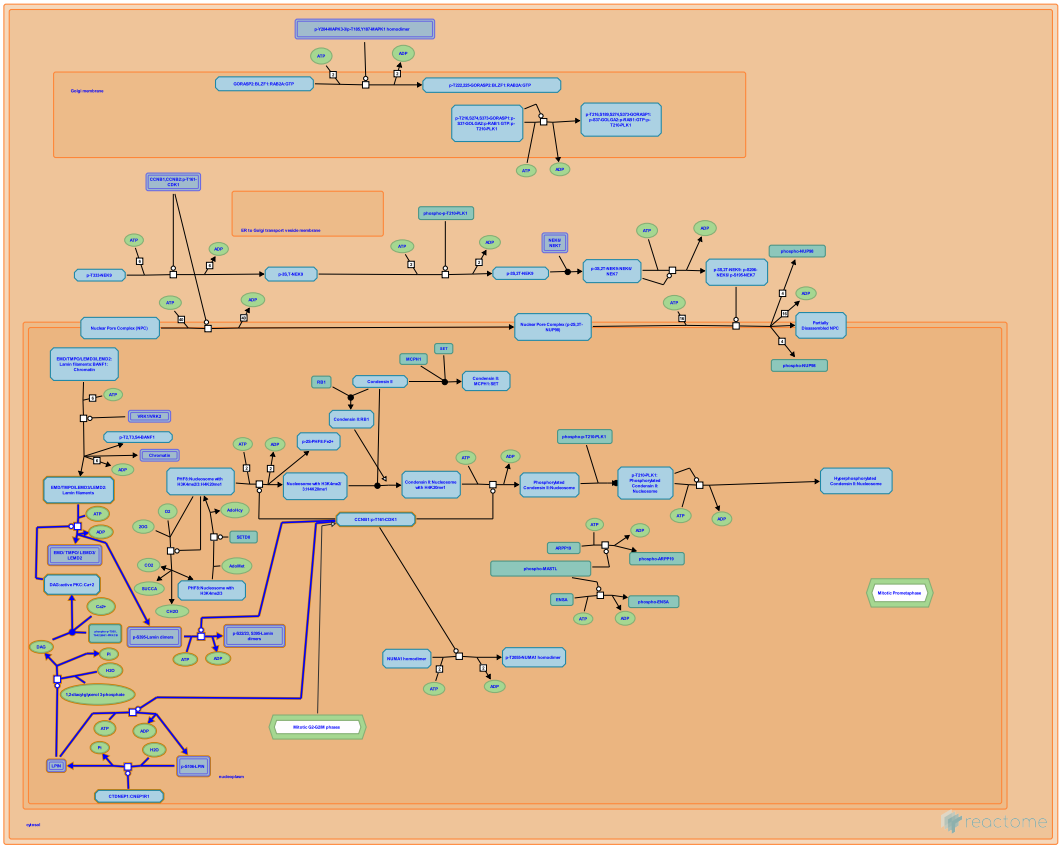
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Depolymerization of the Nuclear Lamina ↗

Stable identifier: R-BTA-4419969

Inferred from: Depolymerization of the Nuclear Lamina (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

CDK1 phosphorylates LPIN ↗

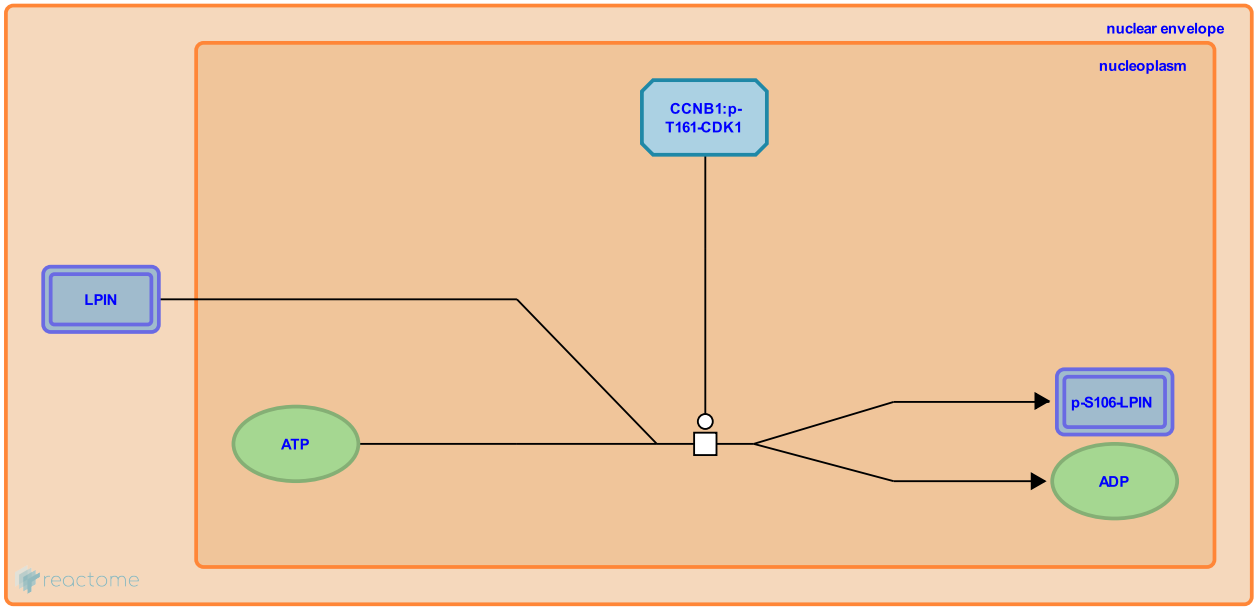
Location: Depolymerization of the Nuclear Lamina

Stable identifier: R-BTA-5195402

Type: transition

Compartments: nucleoplasm

Inferred from: CDK1 phosphorylates LPIN (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: CTDNEP1:CNEP1R1 dephosphorylates LPIN

CTDNEP1:CNEP1R1 dephosphorylates LPIN ↗

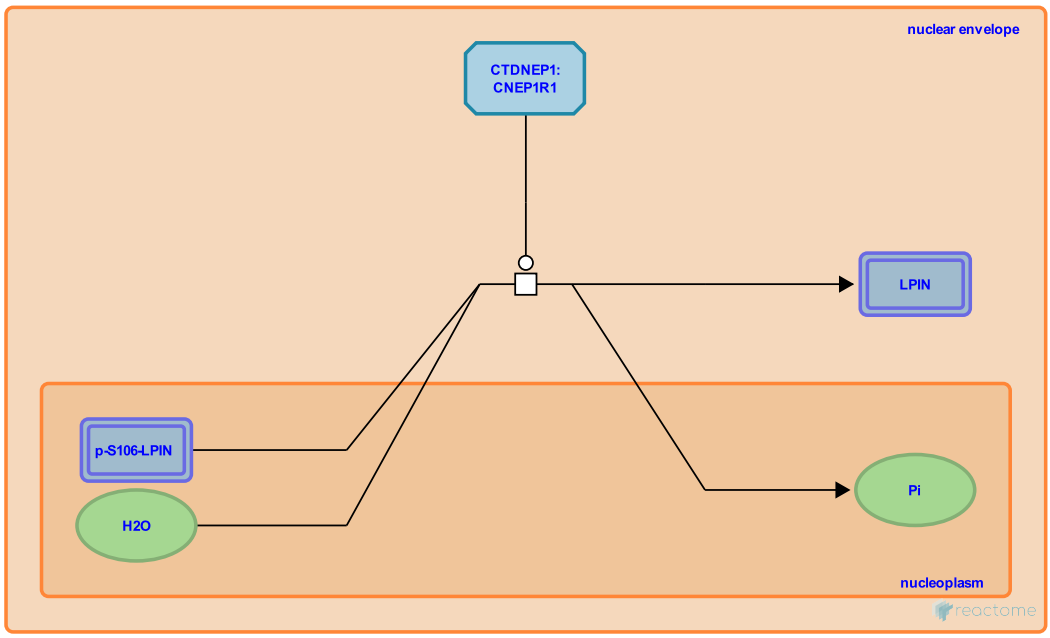
Location: Depolymerization of the Nuclear Lamina

Stable identifier: R-BTA-4419948

Type: transition

Compartments: nuclear envelope, nucleoplasm

Inferred from: CTDNEP1:CNEP1R1 dephosphorylates LPIN (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: CDK1 phosphorylates LPIN

Followed by: LPIN catalyzes conversion of phosphatidic acid to diacylglycerol

LPIN catalyzes conversion of phosphatidic acid to diacylglycerol ↗

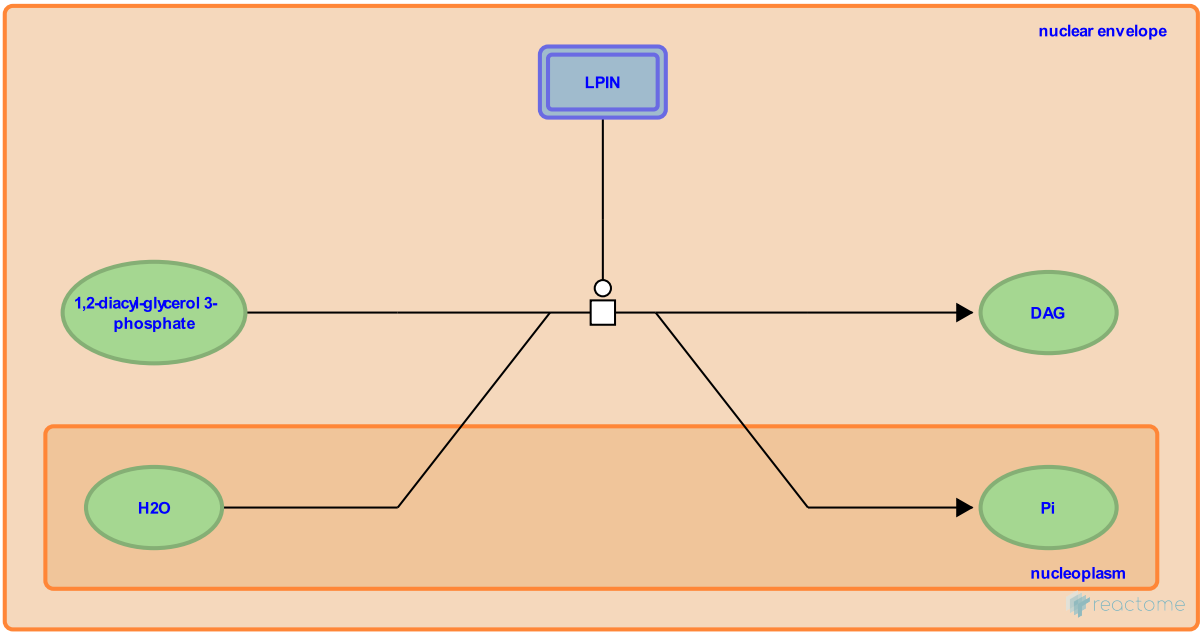
Location: Depolymerization of the Nuclear Lamina

Stable identifier: R-BTA-5221130

Type: transition

Compartments: nuclear envelope, nucleoplasm

Inferred from: LPIN catalyzes conversion of phosphatidic acid to diacylglycerol (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: CTDNEP1:CNEP1R1 dephosphorylates LPIN

Followed by: DAG and Ca+2 bind to PKC and tether it to membrane

DAG and Ca+2 bind to PKC and tether it to membrane ↗

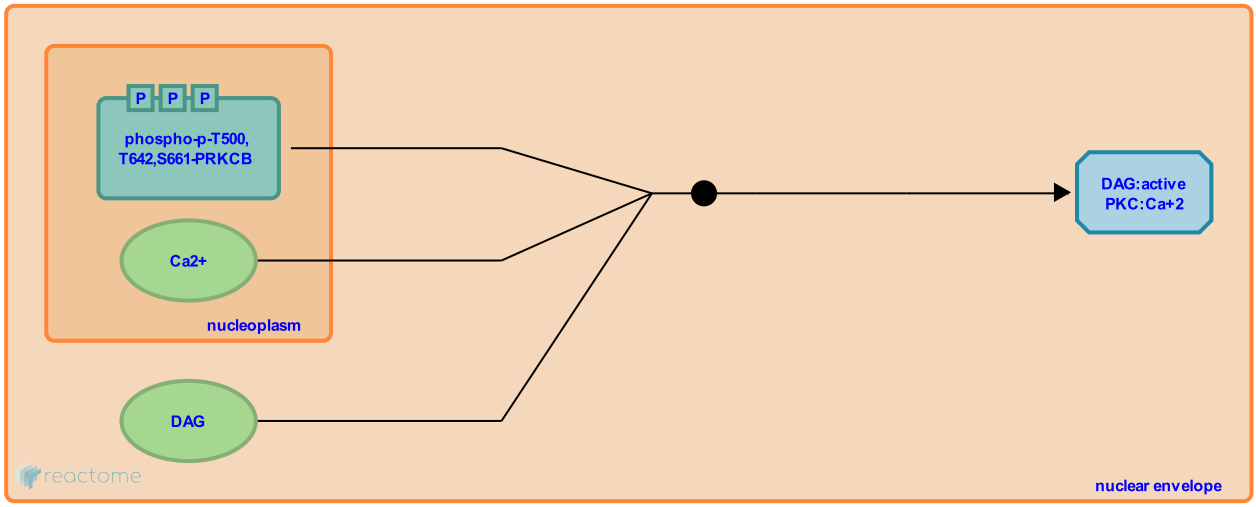
Location: Depolymerization of the Nuclear Lamina

Stable identifier: R-BTA-5223304

Type: binding

Compartments: nuclear envelope, nucleoplasm

Inferred from: DAG and Ca+2 bind to PKC and tether it to membrane (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: LPIN catalyzes conversion of phosphatidic acid to diacylglycerol

Followed by: Depolymerization of lamin filaments after PKC-mediated phosphorylation

Depolymerization of lamin filaments after PKC-mediated phosphorylation ↗

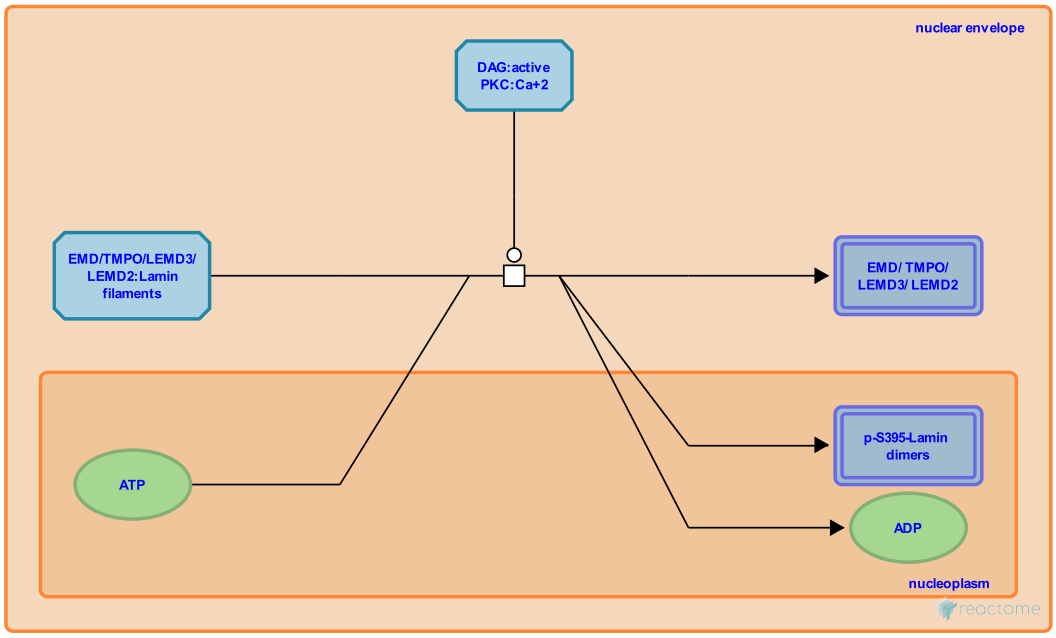
Location: Depolymerization of the Nuclear Lamina

Stable identifier: R-BTA-5229194

Type: transition

Compartments: nuclear envelope, nucleoplasm

Inferred from: Depolymerization of lamin filaments after PKC-mediated phosphorylation (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: DAG and Ca+2 bind to PKC and tether it to membrane

Followed by: CDK1 phosphorylates lamins and facilitates depolymerization of lamin filaments

CDK1 phosphorylates lamins and facilitates depolymerization of lamin filaments ↗

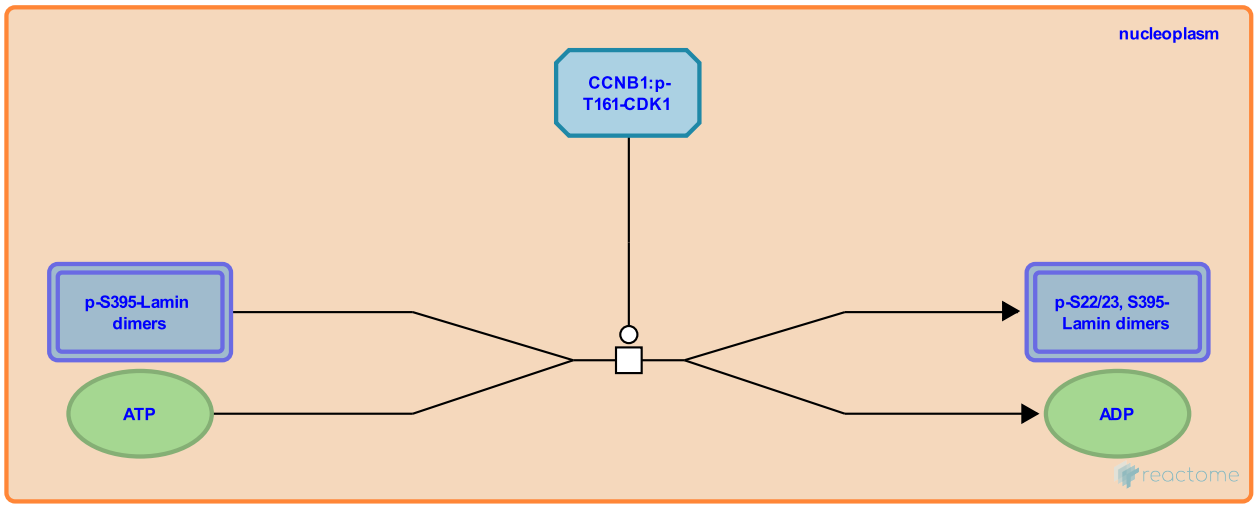
Location: Depolymerization of the Nuclear Lamina

Stable identifier: R-BTA-5244669

Type: transition

Compartments: nucleoplasm

Inferred from: CDK1 phosphorylates lamins and facilitates depolymerization of lamin filaments (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: Depolymerization of lamin filaments after PKC-mediated phosphorylation

Table of Contents