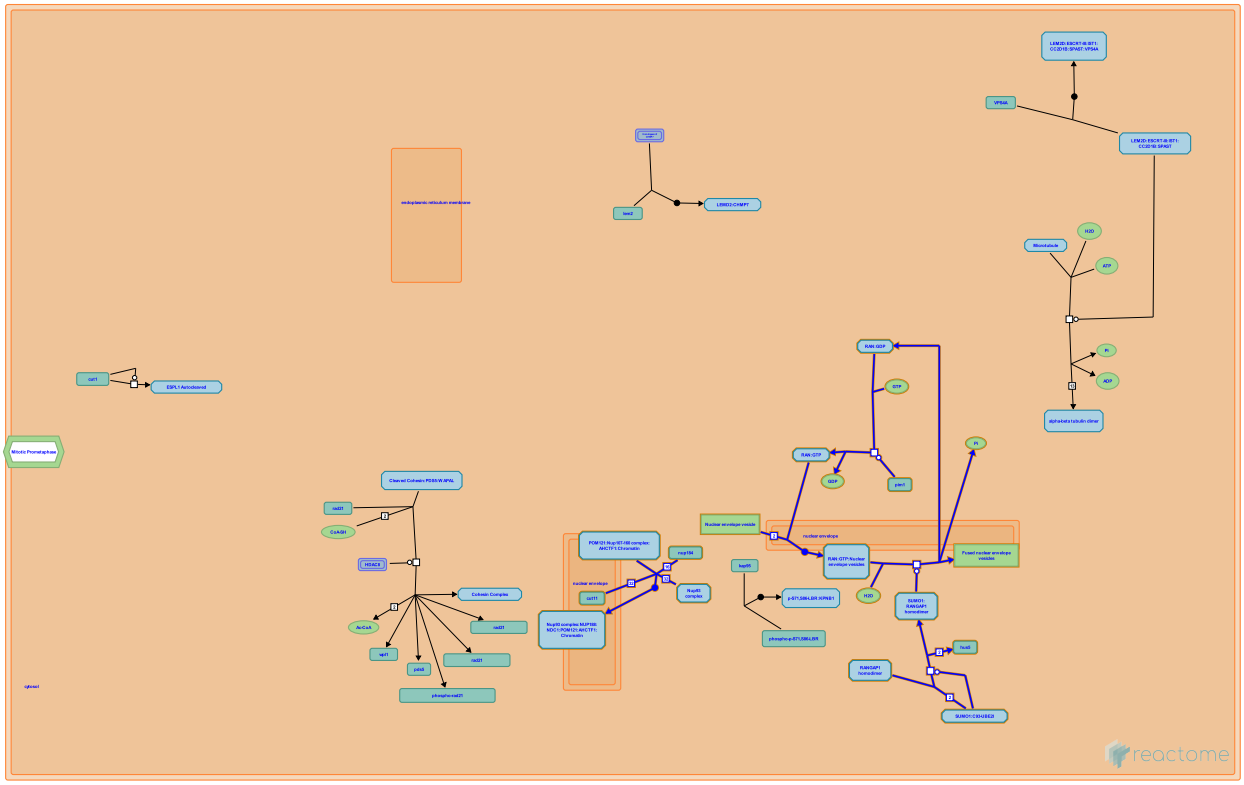
Postmitotic nuclear pore complex (NPC) reformation



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

03/02/2023

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. ↗

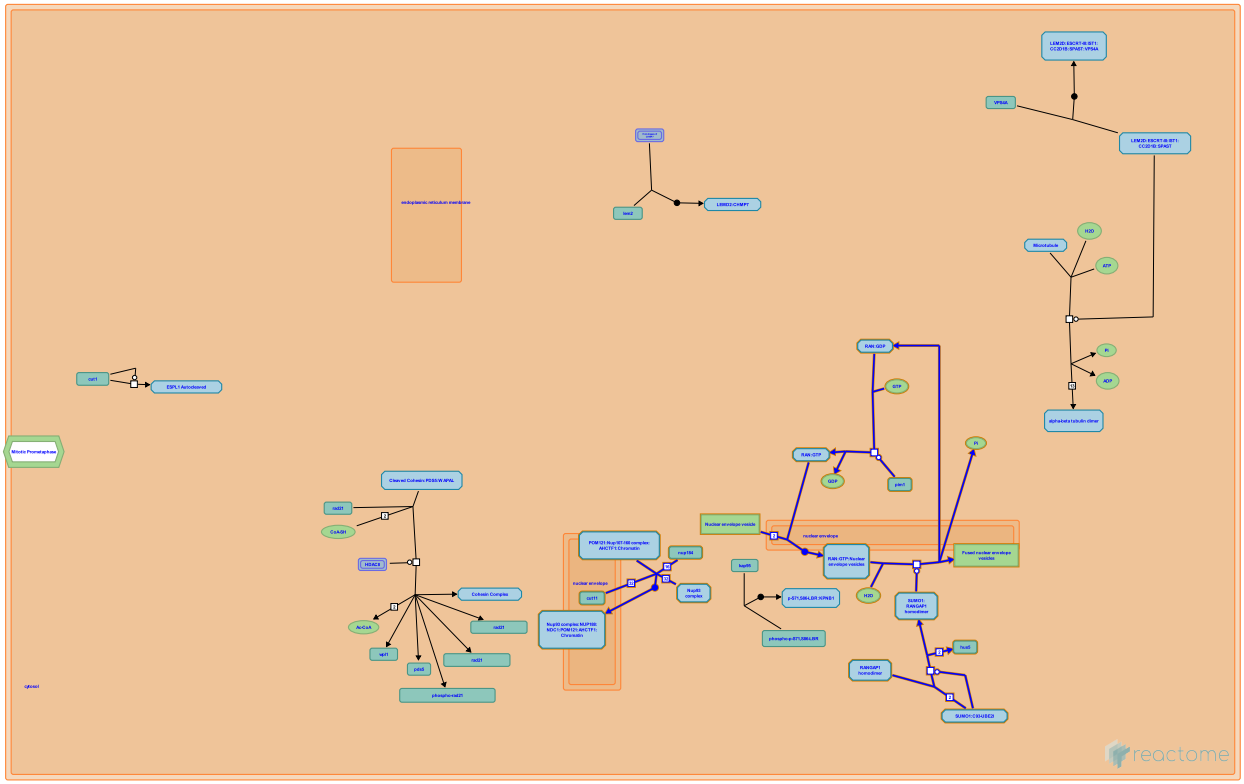
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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. ↗

Postmitotic nuclear pore complex (NPC) reformation ↗

Stable identifier: R-SPO-9615933

Inferred from: Postmitotic nuclear pore complex (NPC) reformation (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

RCC1 stimulates GDP to GTP exchange on RAN ↗

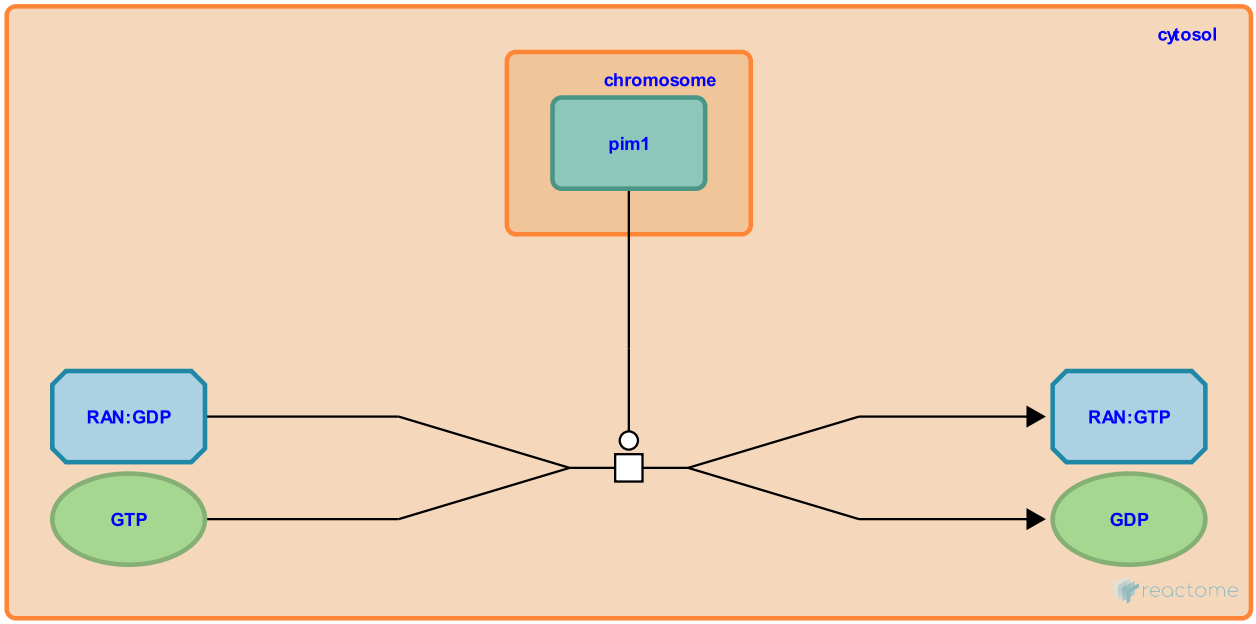
Location: Postmitotic nuclear pore complex (NPC) reformation

Stable identifier: R-SPO-9624845

Type: transition

Compartments: cytosol, chromosome

Inferred from: RCC1 stimulates GDP to GTP exchange on RAN (Homo sapiens)



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Followed by: RAN:GTP recruits nuclear envelope (NE) membranes

POM121 and NDC1 bind the Nup93 complex ↗

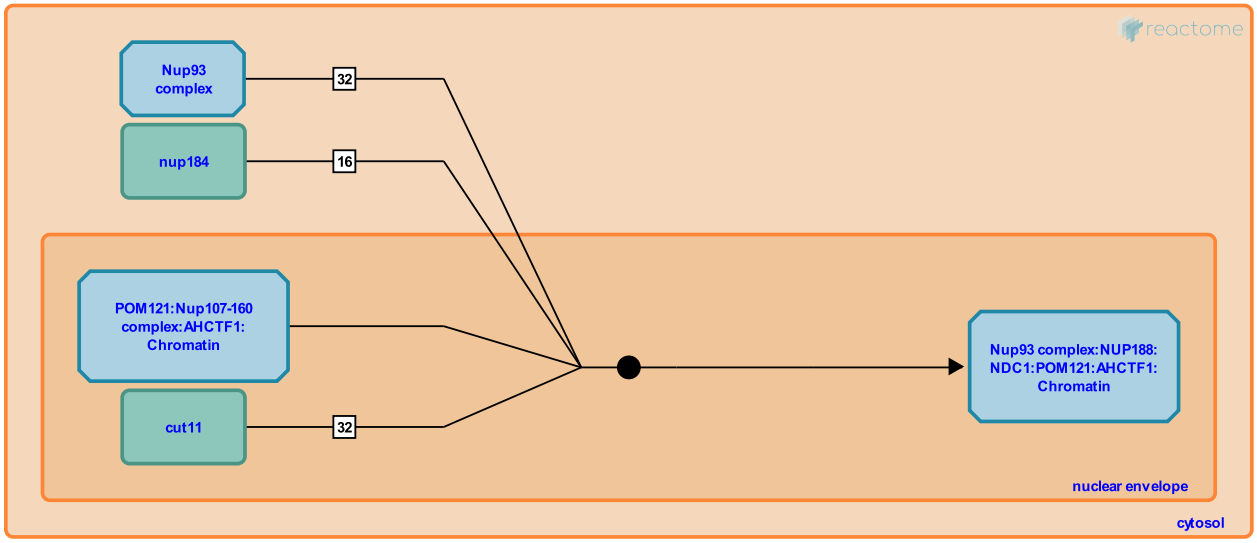
Location: Postmitotic nuclear pore complex (NPC) reformation

Stable identifier: R-SPO-9634169

Type: binding

Compartments: nuclear envelope, cytosol

Inferred from: POM121 and NDC1 bind the Nup93 complex (Homo sapiens)



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RAN:GTP recruits nuclear envelope (NE) membranes ↗

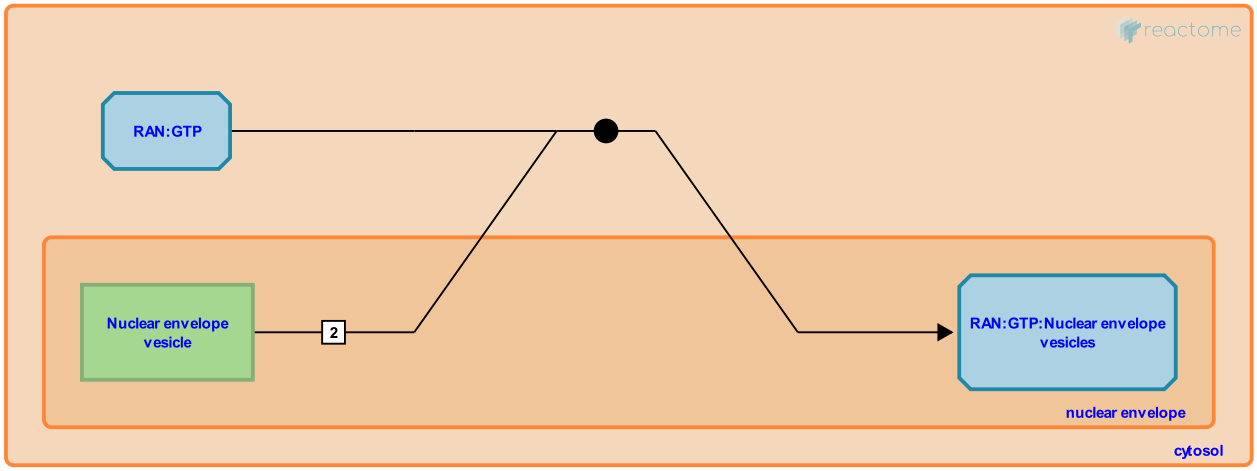
Location: Postmitotic nuclear pore complex (NPC) reformation

Stable identifier: R-SPO-9624876

Type: binding

Compartments: cytosol

Inferred from: RAN:GTP recruits nuclear envelope (NE) membranes (Homo sapiens)



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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: RCC1 stimulates GDP to GTP exchange on RAN

Followed by: RAN stimulates fusion of nuclear envelope (NE) membranes

UBC9 (UBE2I) SUMOylates RANGAP1 with SUMO, which targets RANGAP1 to RANBP2 ↗

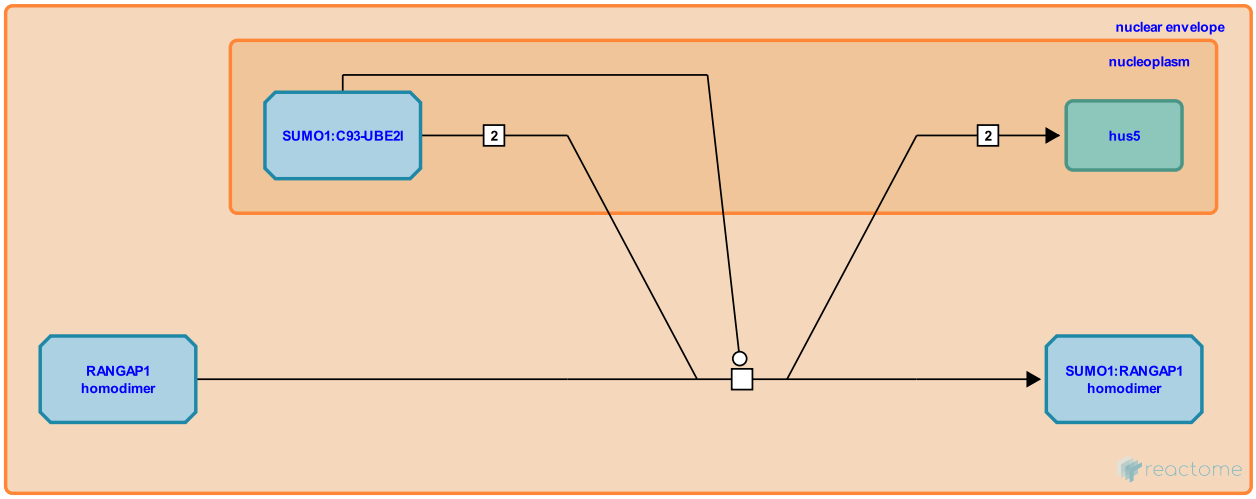
Location: Postmitotic nuclear pore complex (NPC) reformation

Stable identifier: R-SPO-3000449

Type: transition

Compartments: nuclear envelope, nucleoplasm

Inferred from: UBC9 (UBE2I) SUMOylates RANGAP1 with SUMO, which targets RANGAP1 to RANBP2 (Homo sapiens)



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

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Followed by: RAN stimulates fusion of nuclear envelope (NE) membranes

RAN stimulates fusion of nuclear envelope (NE) membranes ↗

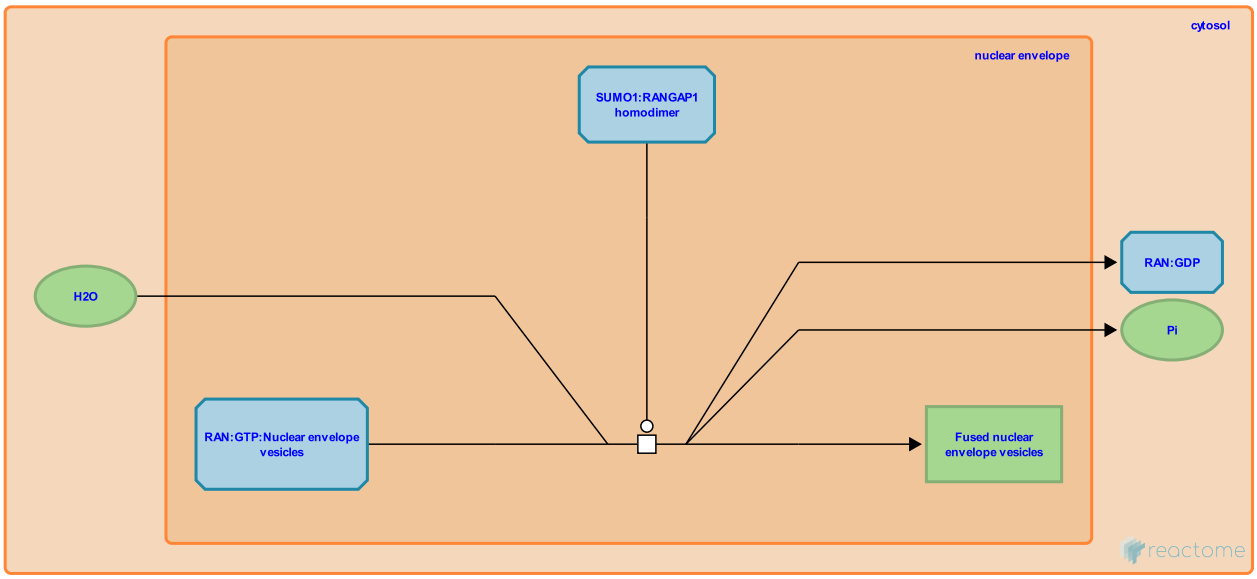
Location: Postmitotic nuclear pore complex (NPC) reformation

Stable identifier: R-SPO-9624893

Type: transition

Compartments: nuclear envelope, cytosol

Inferred from: RAN stimulates fusion of nuclear envelope (NE) membranes (Homo sapiens)



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Preceded by: RAN:GTP recruits nuclear envelope (NE) membranes, UBC9 (UBE2I) SUMOylates RANGAP1 with SUMO, which targets RANGAP1 to RANBP2

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