



## 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. [↗](#)
- 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. [↗](#)

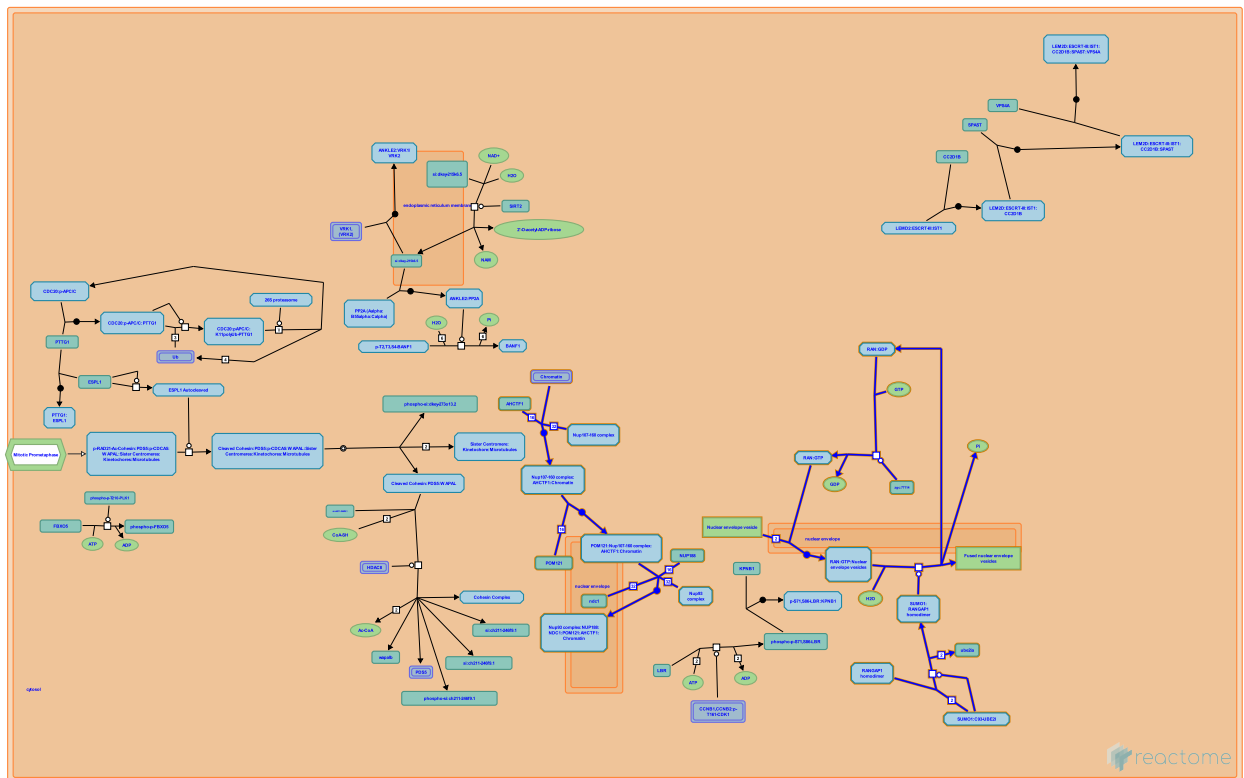
Reactome database release: 83

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

## Postmitotic nuclear pore complex (NPC) reformation ↗

Stable identifier: R-DRE-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.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

## RCC1 stimulates GDP to GTP exchange on RAN ↗

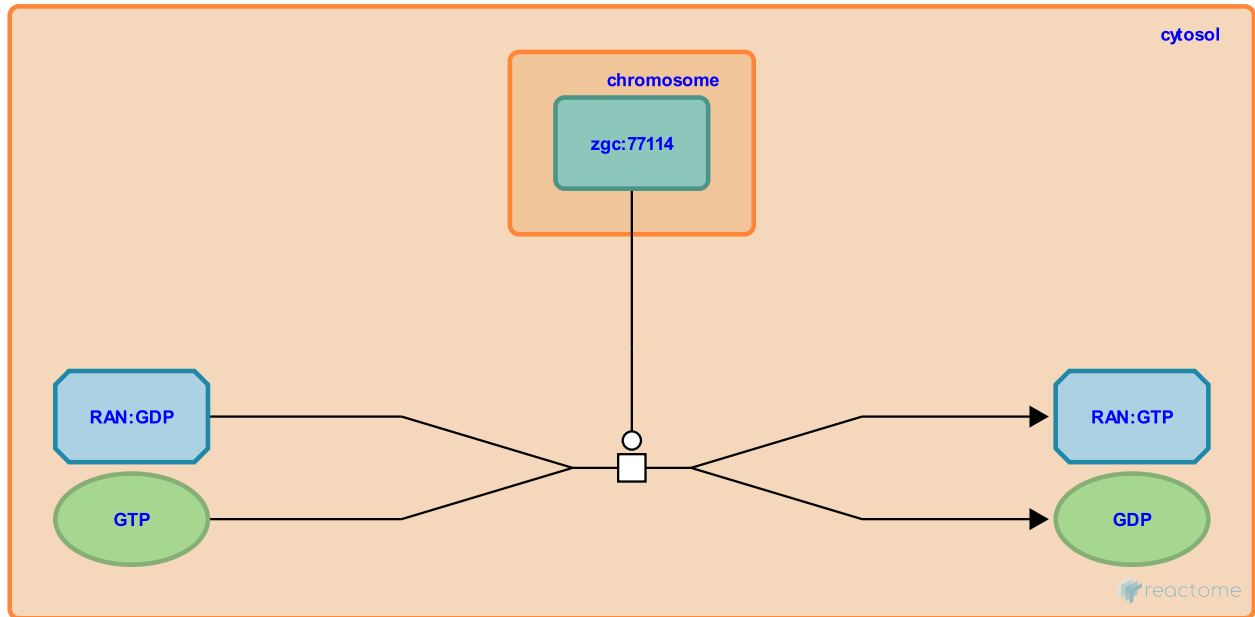
**Location:** [Postmitotic nuclear pore complex \(NPC\) reformation](#)

**Stable identifier:** R-DRE-9624845

**Type:** transition

**Compartments:** cytosol, chromosome

**Inferred from:** [RCC1 stimulates GDP to GTP exchange on RAN \(Homo sapiens\)](#)



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:** [RAN:GTP recruits nuclear envelope \(NE\) membranes](#)

## AHCTF1 (ELYS) binds chromatin and Nup107-Nup160 complex ↗

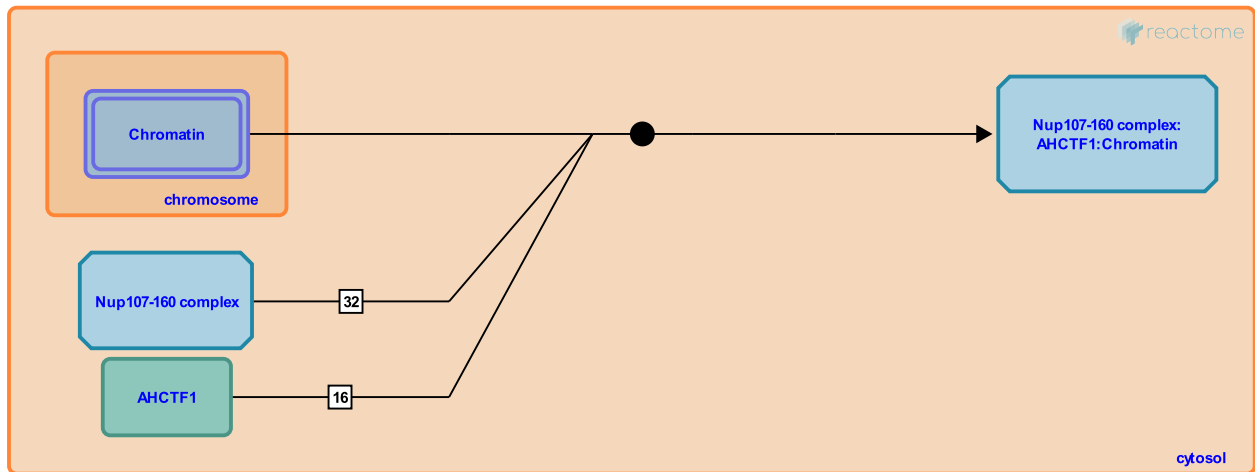
**Location:** Postmitotic nuclear pore complex (NPC) reformation

**Stable identifier:** R-DRE-9615901

**Type:** binding

**Compartments:** cytosol

**Inferred from:** AHCTF1 (ELYS) binds chromatin and Nup107-Nup160 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.

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**Followed by:** [POM121 binds the Nup107-Nup160 complex](#)

## POM121 binds the Nup107-Nup160 complex ↗

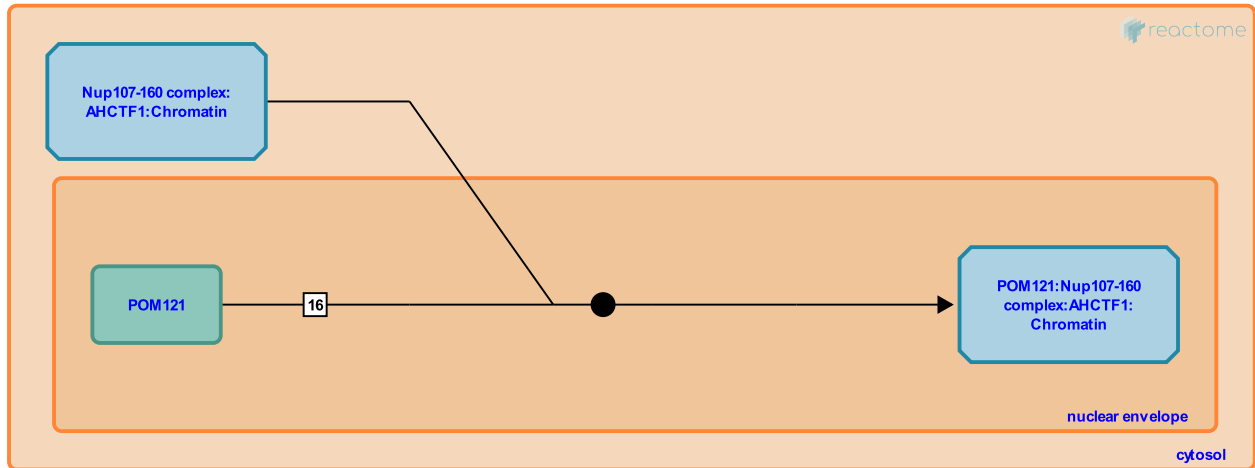
**Location:** [Postmitotic nuclear pore complex \(NPC\) reformation](#)

**Stable identifier:** R-DRE-9618378

**Type:** binding

**Compartments:** nuclear envelope, cytosol

**Inferred from:** [POM121 binds the Nup107-Nup160 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.

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**Preceded by:** [AHCTF1 \(ELYS\) binds chromatin and Nup107-Nup160 complex](#)

**Followed by:** [POM121 and NDC1 bind the Nup93 complex](#)

## POM121 and NDC1 bind the Nup93 complex ↗

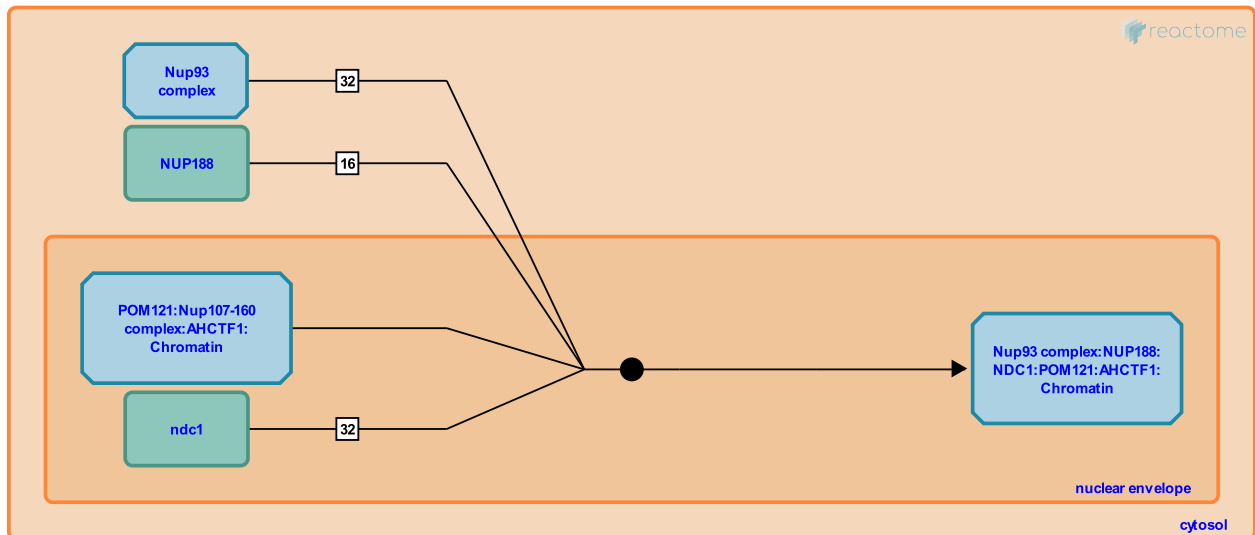
**Location:** [Postmitotic nuclear pore complex \(NPC\) reformation](#)

**Stable identifier:** R-DRE-9634169

**Type:** binding

**Compartments:** nuclear envelope, cytosol

**Inferred from:** [POM121 and NDC1 bind the Nup93 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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**Preceded by:** [POM121 binds the Nup107-Nup160 complex](#)

## RAN:GTP recruits nuclear envelope (NE) membranes ↗

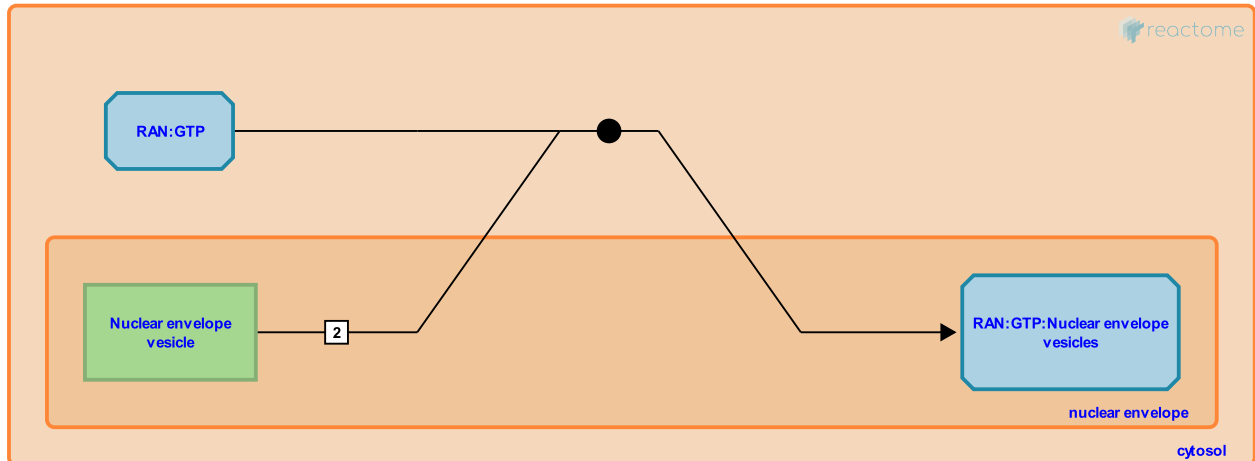
**Location:** Postmitotic nuclear pore complex (NPC) reformation

**Stable identifier:** R-DRE-9624876

**Type:** binding

**Compartments:** cytosol

**Inferred from:** RAN:GTP recruits nuclear envelope (NE) membranes (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

**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 ↗

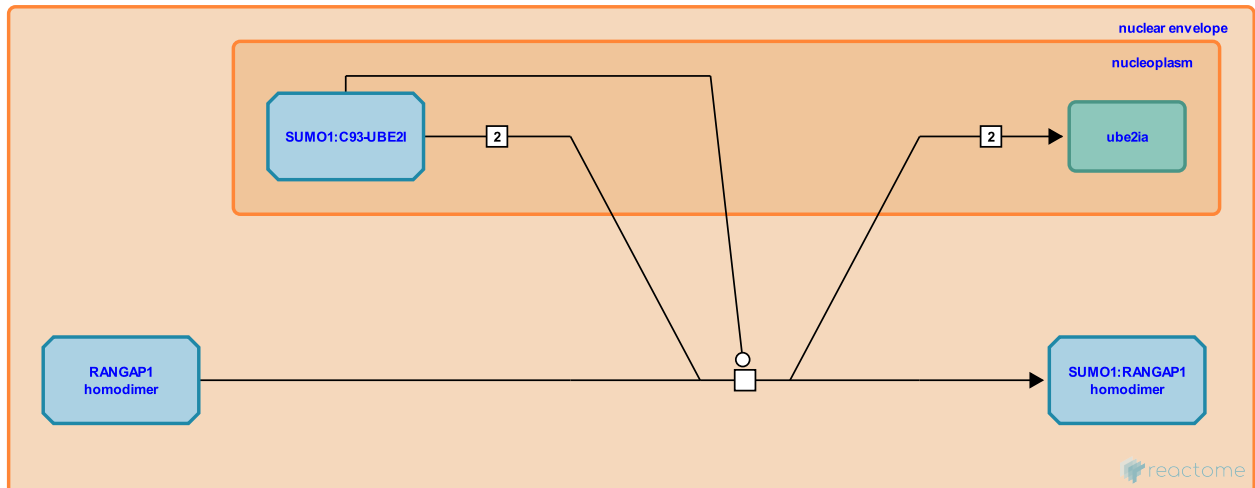
**Location:** Postmitotic nuclear pore complex (NPC) reformation

**Stable identifier:** R-DRE-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.

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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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

## RAN stimulates fusion of nuclear envelope (NE) membranes [↗](#)

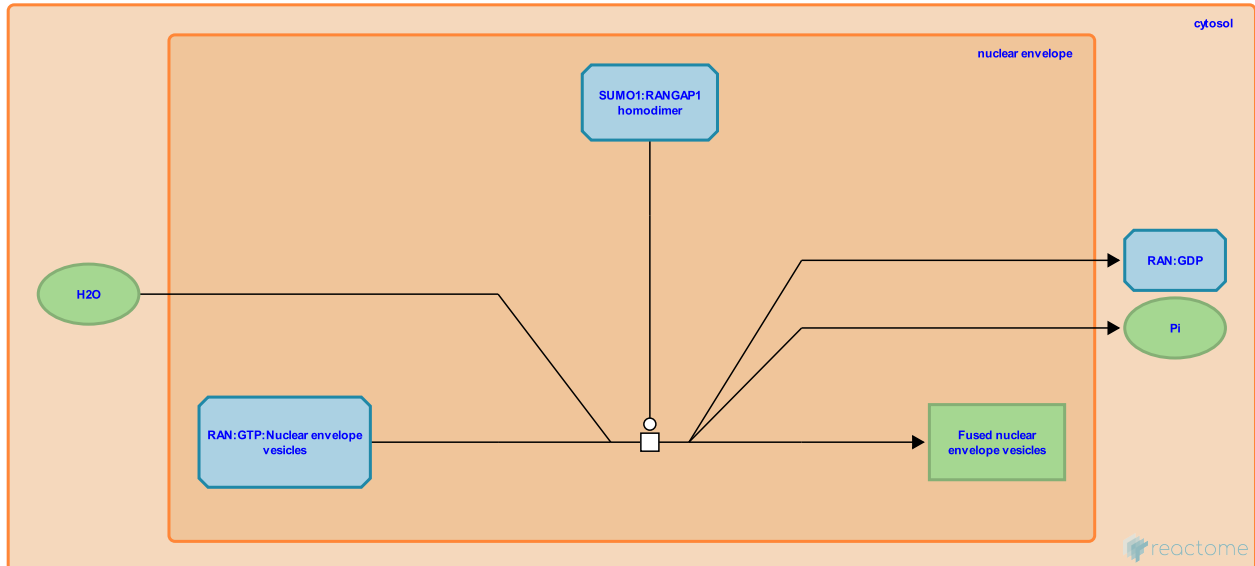
**Location:** Postmitotic nuclear pore complex (NPC) reformation

**Stable identifier:** R-DRE-9624893

**Type:** transition

**Compartments:** nuclear envelope, cytosol

**Inferred from:** RAN stimulates fusion of nuclear envelope (NE) membranes (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.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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

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