

Transport of the export-competent mRNP complex through the NPC

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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: 77

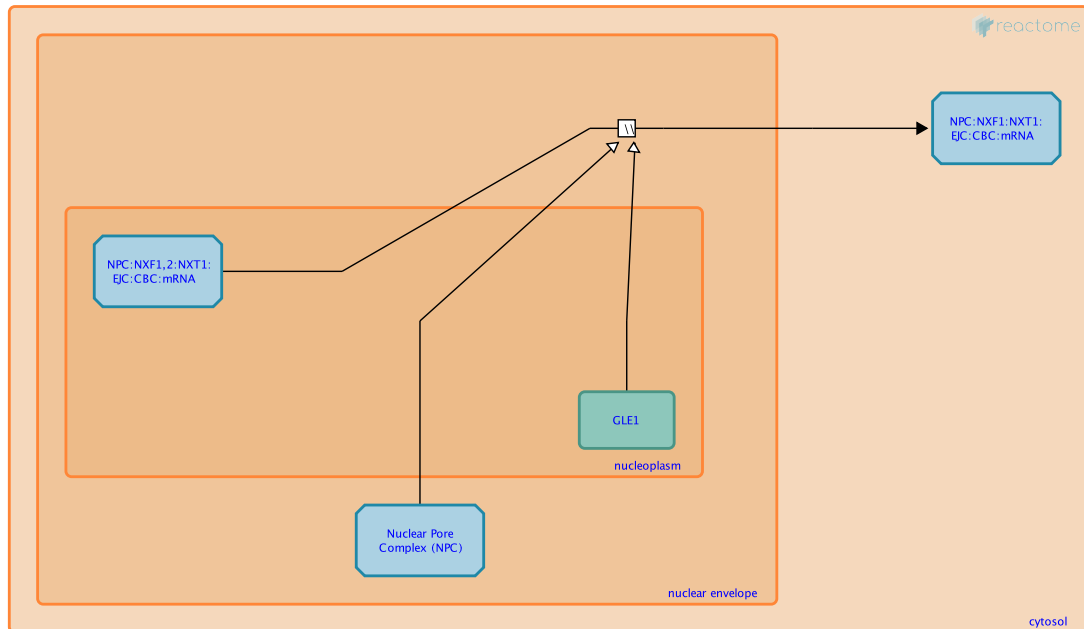
This document contains 1 reaction ([see Table of Contents](#))

Transport of the export-competent mRNP complex through the NPC ↗

Stable identifier: R-HSA-75097

Type: omitted

Compartments: nuclear envelope, cytosol, nucleoplasm



In this reaction, 1 molecule of 'Export Receptor bound mature mRNA Complex' is translocated from nucleoplasm to cytosol.

This reaction takes place in the 'nuclear envelope'.

Literature references

- Katahira, J., Strässer, K., Podtelejnikov, A., Mann, M., Jung, JU., Hurt, E. (1999). The Mex67p-mediated nuclear mRNA export pathway is conserved from yeast to human. *EMBO J.*, 18, 2593-609. ↗
- Wiegand, HL., Coburn, GA., Zeng, Y., Kang, Y., Bogerd, HP., Cullen, BR. (2002). Formation of Tap/NXT1 heterodimers activates Tap-dependent nuclear mRNA export by enhancing recruitment to nuclear pore complexes. *Mol. Cell. Biol.*, 22, 245-56. ↗
- Guzik, BW., Levesque, L., Prasad, S., Bor, YC., Black, BE., Paschal, BM. et al. (2001). NXT1 (p15) is a crucial cellular cofactor in TAP-dependent export of intron-containing RNA in mammalian cells. *Mol. Cell. Biol.*, 21, 2545-54. ↗
- Grüter, P., Taberner, C., von Kobbe, C., Schmitt, C., Saavedra, C., Bachi, A. et al. (1998). TAP, the human homolog of Mex67p, mediates CTE-dependent RNA export from the nucleus. *Mol. Cell*, 1, 649-59. ↗
- Lévesque, L., Guzik, B., Guan, T., Coyle, J., Black, BE., Rekosh, D. et al. (2001). RNA export mediated by tap involves NXT1-dependent interactions with the nuclear pore complex. *J. Biol. Chem.*, 276, 44953-62. ↗