



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: 88

This document contains 1 pathway and 5 reactions ([see Table of Contents](#))

47S pre-rRNA is nucleolytically processed at A' (01,A1), site A0, and site 02 (site 6) to yield 45S pre-rRNA ↗

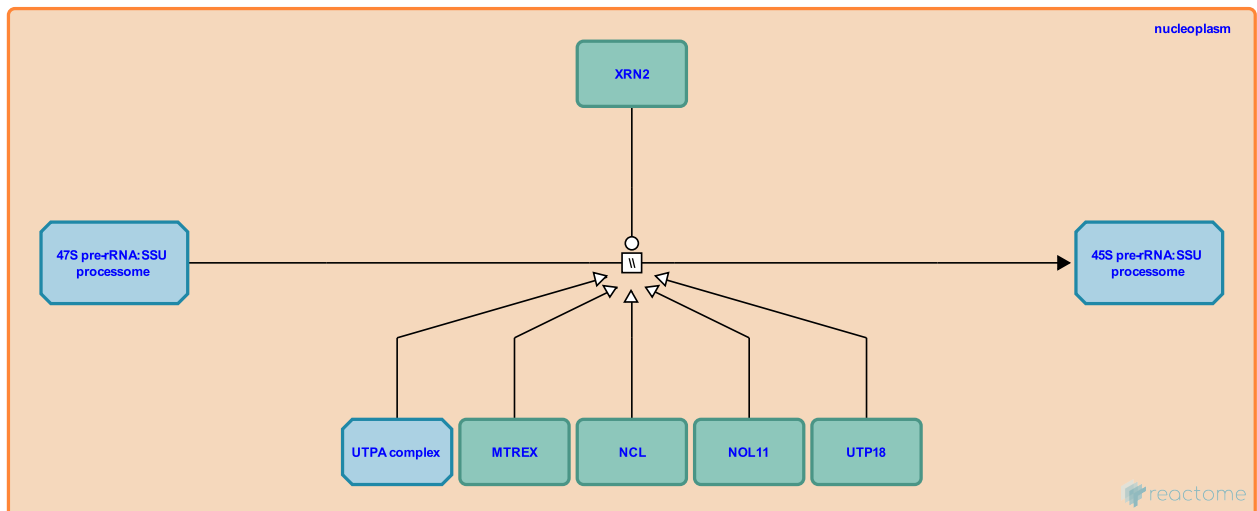
Location: Major pathway of rRNA processing in the nucleolus and cytosol

Stable identifier: R-CFA-6791227

Type: omitted

Compartments: nucleoplasm

Inferred from: 47S pre-rRNA is nucleolytically processed at A' (01,A1), site A0, and site 02 (site 6) to yield 45S pre-rRNA (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

30S pre-rRNA is nucleolytically processed at site 1 to yield 21S pre-rRNA ↗

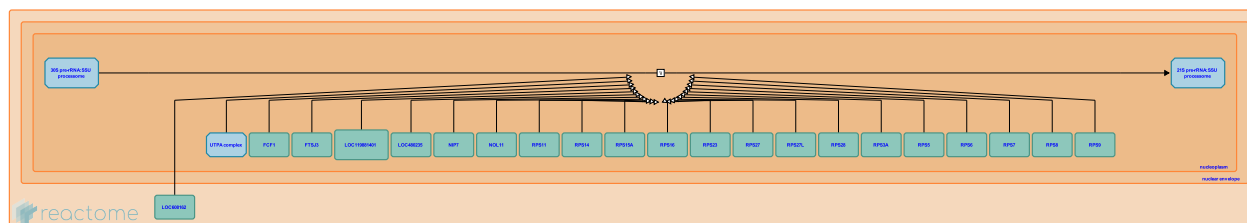
Location: Major pathway of rRNA processing in the nucleolus and cytosol

Stable identifier: R-CFA-6791221

Type: omitted

Compartments: nucleoplasm

Inferred from: 30S pre-rRNA is nucleolytically processed at site 1 to yield 21S pre-rRNA (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: 21S pre-rRNA is nucleolytically processed at site E (site2a) to yield 18SE pre-rRNA

21S pre-rRNA is nucleolytically processed at site E (site2a) to yield 18SE pre-rRNA ↗

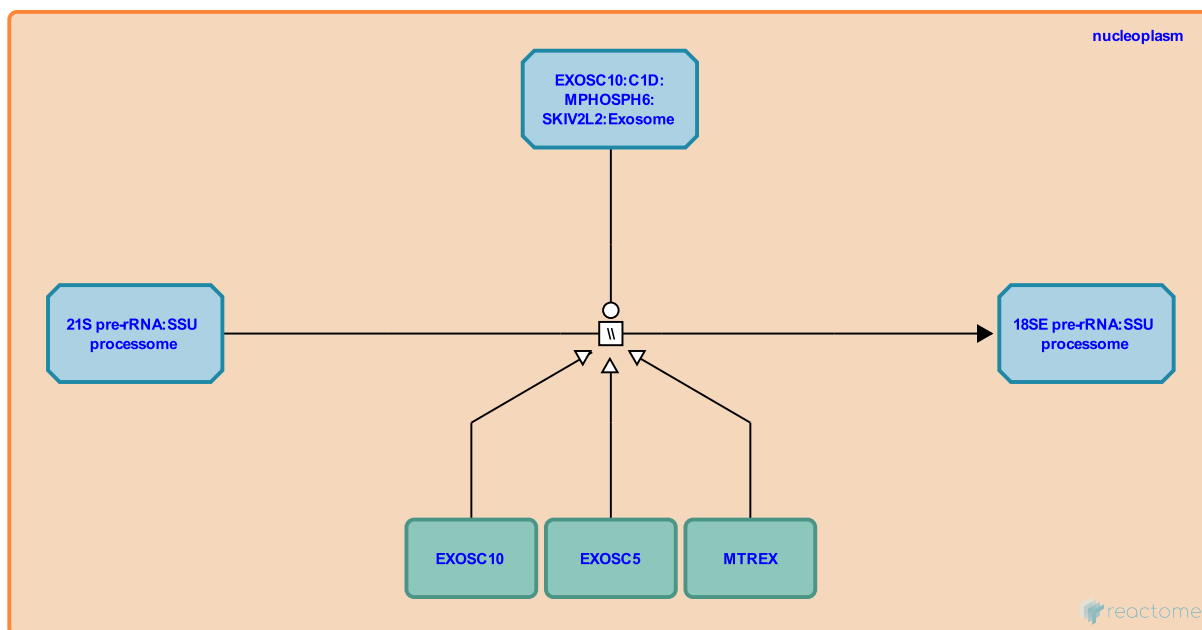
Location: Major pathway of rRNA processing in the nucleolus and cytosol

Stable identifier: R-CFA-6791222

Type: omitted

Compartments: nucleoplasm

Inferred from: 21S pre-rRNA is nucleolytically processed at site E (site2a) to yield 18SE pre-rRNA (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: 30S pre-rRNA is nucleolytically processed at site 1 to yield 21S pre-rRNA

32S pre-rRNA is nucleolytically processed at site 4 (4a) to yield 12S pre-rRNA and 28S rRNA ↗

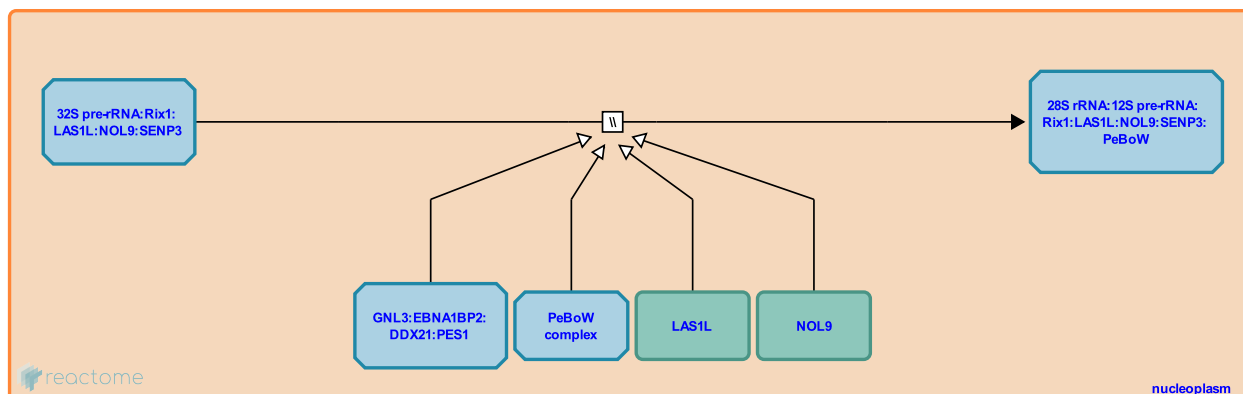
Location: Major pathway of rRNA processing in the nucleolus and cytosol

Stable identifier: R-CFA-6791219

Type: omitted

Compartments: nucleoplasm

Inferred from: 32S pre-rRNA is nucleolytically processed at site 4 (4a) to yield 12S pre-rRNA and 28S rRNA (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: 12S pre-rRNA is nucleolytically processed to yield 5.8S rRNA

12S pre-rRNA is nucleolytically processed to yield 5.8S rRNA ↗

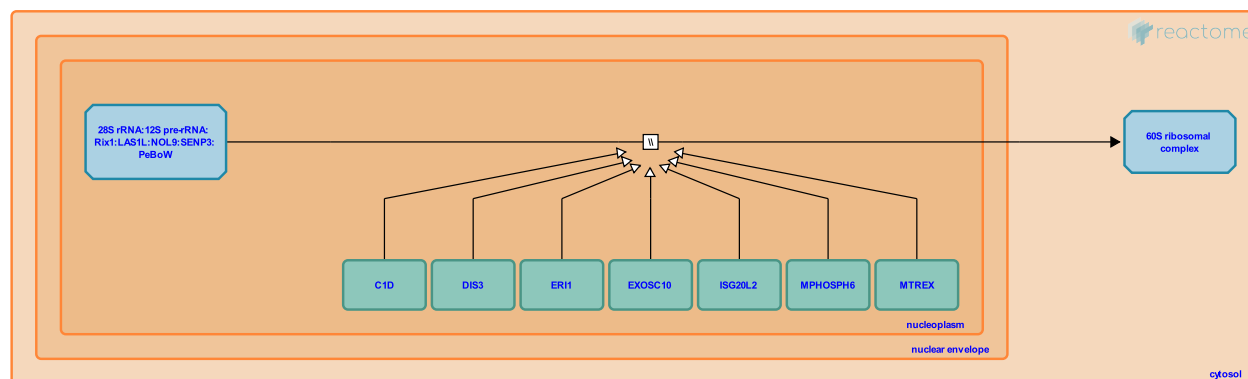
Location: Major pathway of rRNA processing in the nucleolus and cytosol

Stable identifier: R-CFA-6791218

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: 12S pre-rRNA is nucleolytically processed to yield 5.8S rRNA (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.](http://www.pantherdb.org/about.jsp) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: 32S pre-rRNA is nucleolytically processed at site 4 (4a) to yield 12S pre-rRNA and 28S rRNA

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