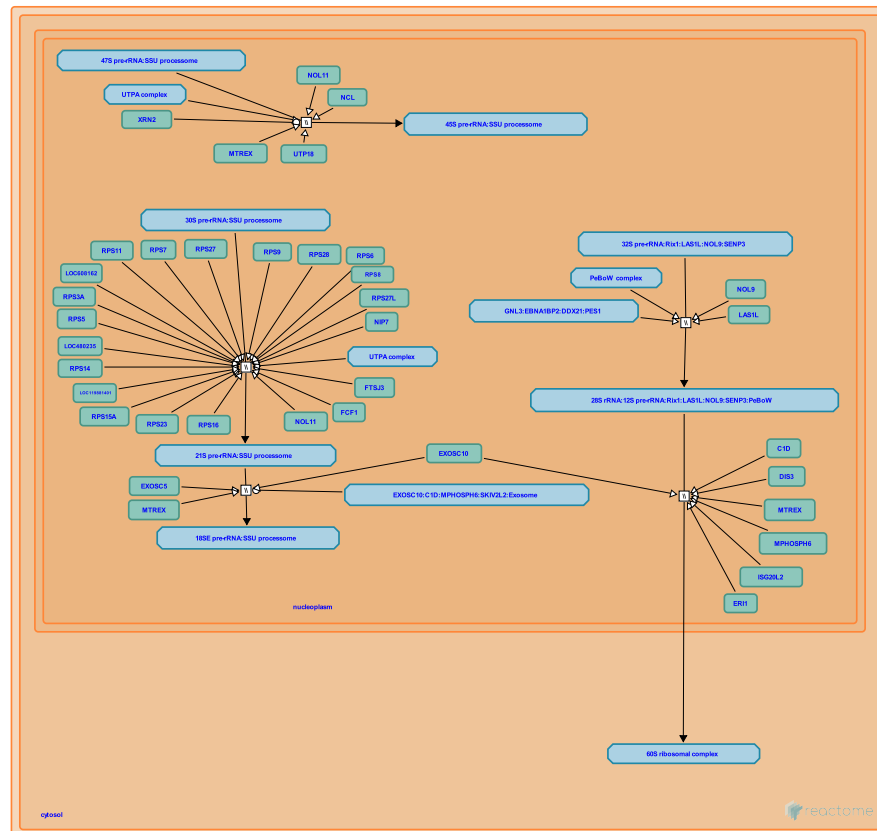


# Major pathway of rRNA processing in the nucleolus and cytosol



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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](https://creativecommons.org/licenses/by/4.0/). For more information see our [license](https://reactome.org/licenses/).

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](https://reactome.org/textbook/).

09/05/2024

## 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. [↗](#)

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 ↗**

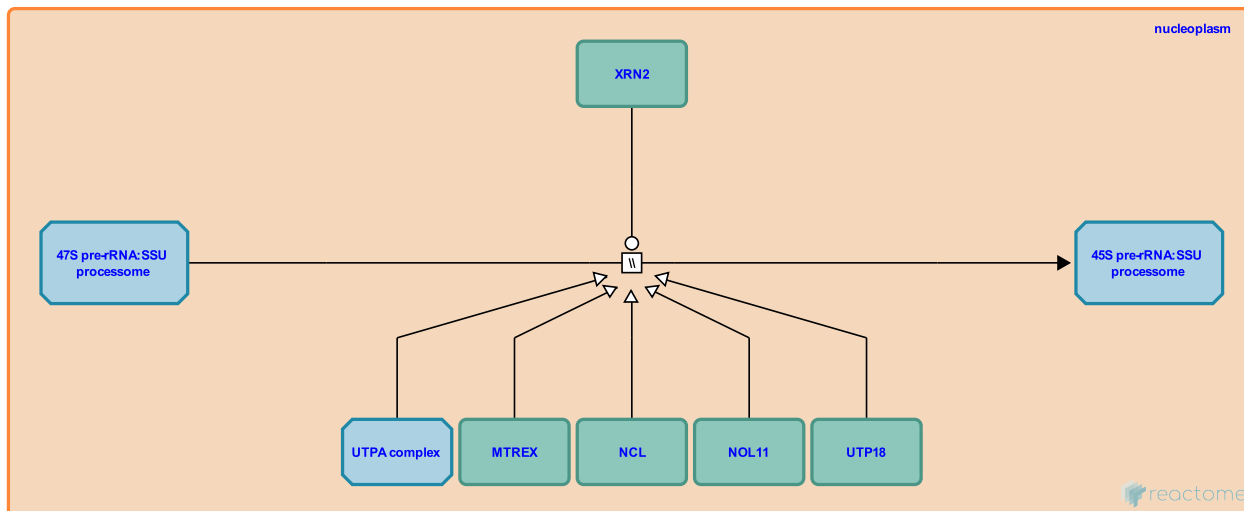
**Location:** Major pathway of rRNA processing in the nucleolus and cytosol

**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 ↗

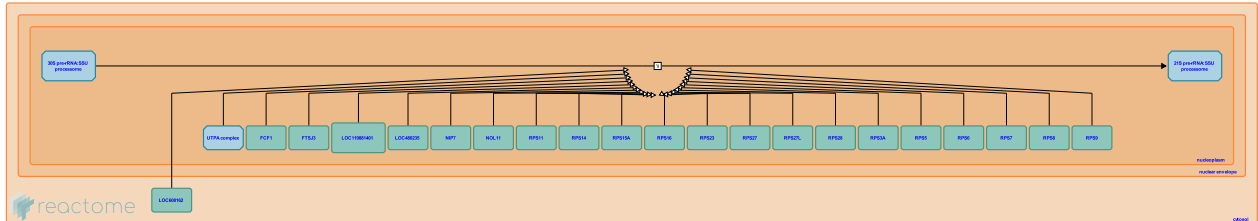
**Location:** Major pathway of rRNA processing in the nucleolus and cytosol

**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 ↗

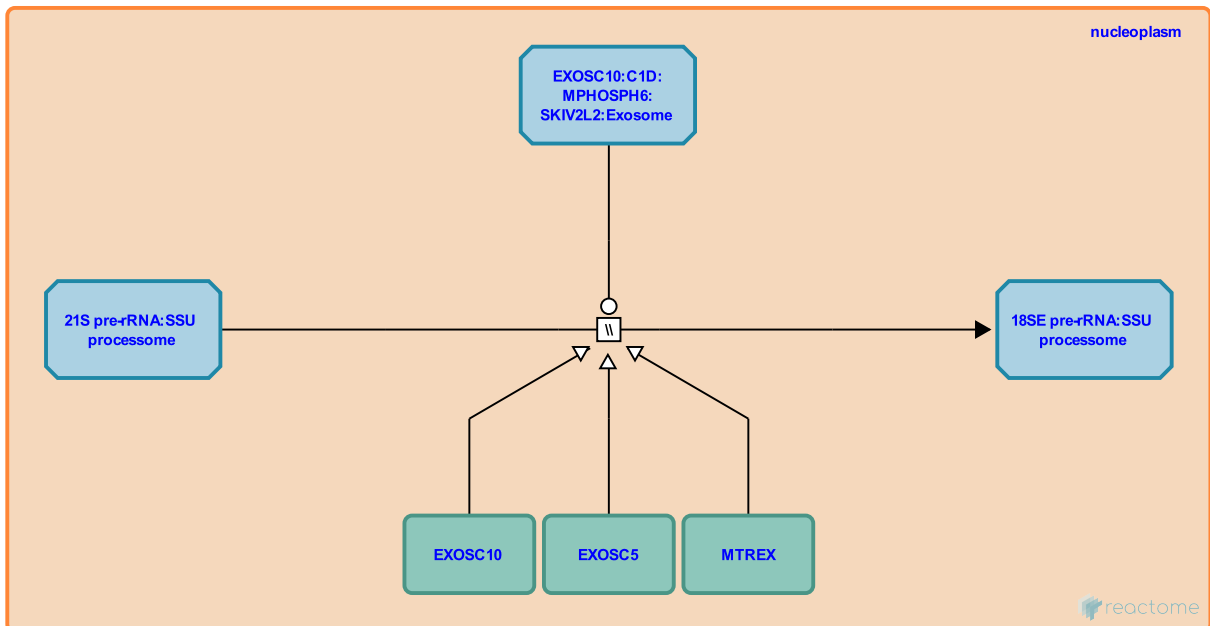
**Location:** Major pathway of rRNA processing in the nucleolus and cytosol

**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 ↗

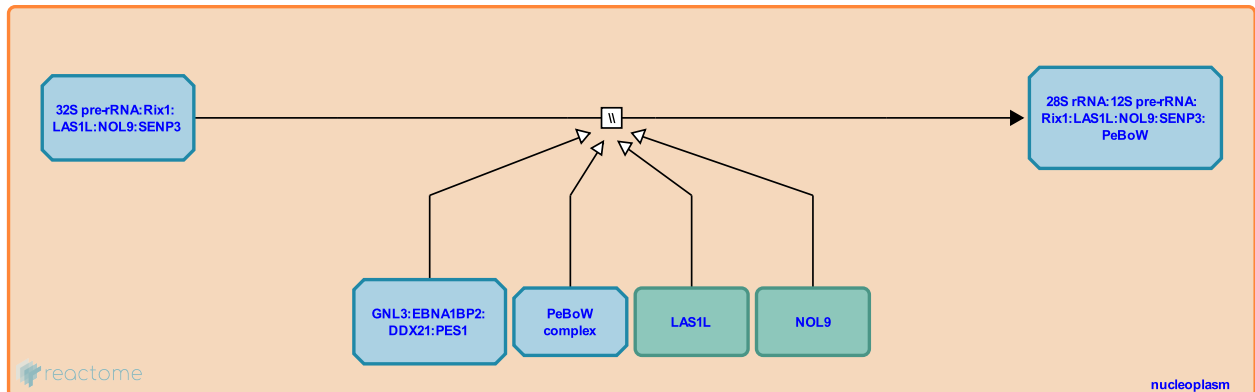
**Location:** Major pathway of rRNA processing in the nucleolus and cytosol

**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 ↗

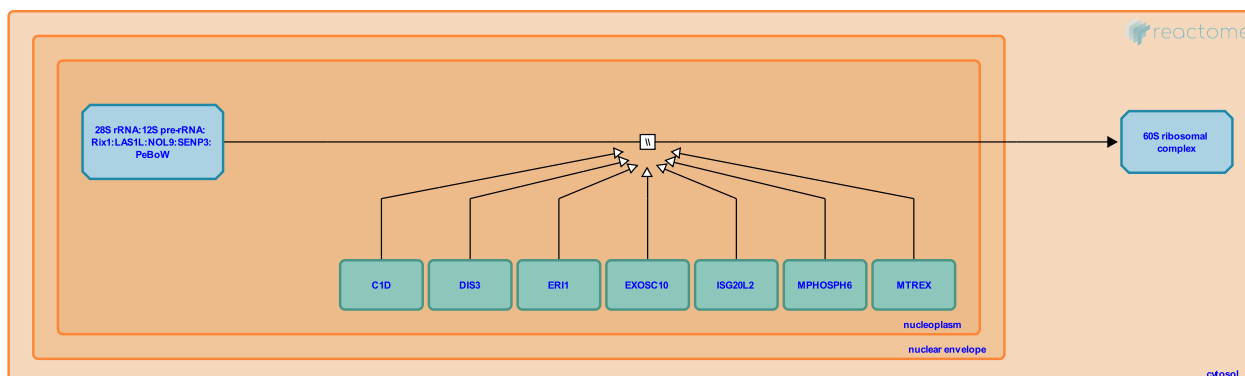
**Location:** Major pathway of rRNA processing in the nucleolus and cytosol

**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



# Table of Contents

Introduction	1
Major pathway of rRNA processing in the nucleolus and cytosol	2
47S pre-rRNA is nucleolytically processed at A' (01,A1), site A0, and site 02 (site 6) to yield 45S pre-rRNA	3
30S pre-rRNA is nucleolytically processed at site 1 to yield 21S pre-rRNA	4
21S pre-rRNA is nucleolytically processed at site E (site2a) to yield 18SE pre-rRNA	5
32S pre-rRNA is nucleolytically processed at site 4 (4a) to yield 12S pre-rRNA and 28S rRNA	6
12S pre-rRNA is nucleolytically processed to yield 5.8S rRNA	7
Table of Contents	8