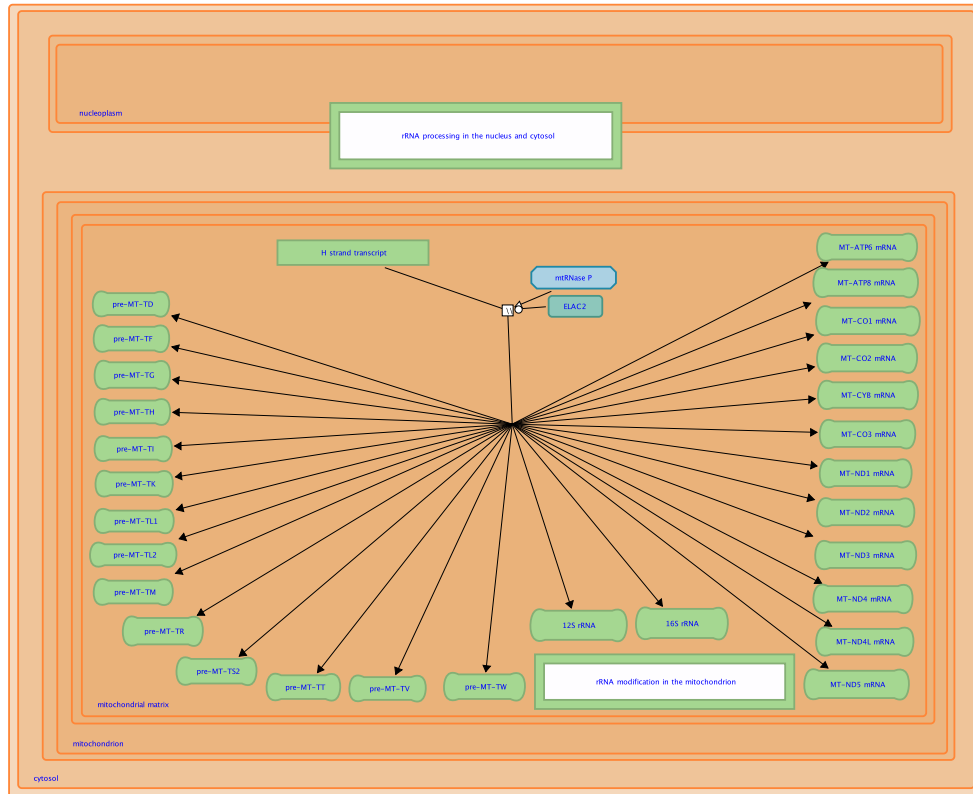


rRNA processing



Boghenagen, DF., Joshi-Tope, G., May, B., Vincent, NG.

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

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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

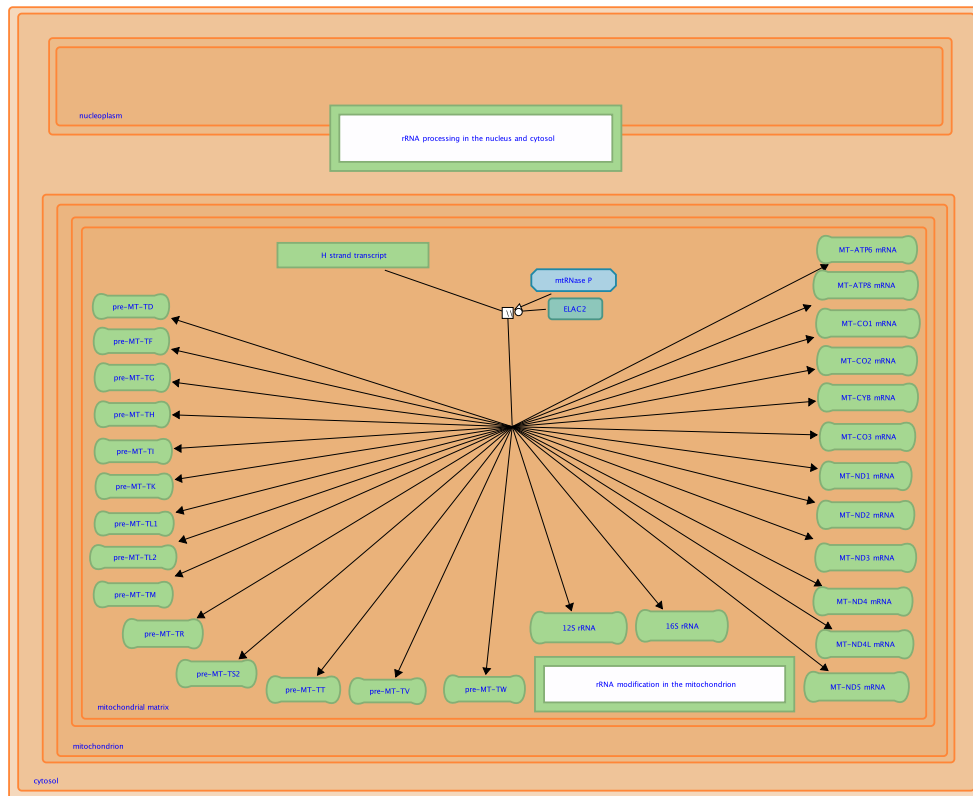
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Reactome database release: 77

This document contains 3 pathways ([see Table of Contents](#))

rRNA processing ↗

Stable identifier: R-HSA-72312



reactome

Each eukaryotic cytosolic ribosome contains 4 molecules of RNA: 28S rRNA (25S rRNA in yeast), 5.8S rRNA, and 5S rRNA in the 60S subunit and 18S rRNA in the 40S subunit. The 18S rRNA, 5.8S rRNA, and 28S rRNA are produced by endonucleolytic and exonucleolytic processing of a single 47S precursor (pre-rRNA) (reviewed in Henras et al. 2015). Transcription of ribosomal RNA genes, processing of pre-rRNA, and assembly of precursor 60S and 40S subunits occur in the nucleolus (reviewed in Hernandez-Verdun et al. 2010), with a few late reactions occurring in the cytosol. Within the nucleolus non-transcribed DNA and inactive polymerase complexes are located in the fibrillar center, active DNA polymerase I transcription occurs at the interface between the fibrillar center and the dense fibrillar component, early processing of pre-rRNA occurs in the dense fibrillar component, and late processing of pre-rRNA occurs in the granular component (Stanek et al. 2001).

Processed ribosomal RNA contains many modified nucleotides which are generated by enzymes acting on encoded nucleotides contained in the precursor rRNA (reviewed in Boschi-Muller and Motorin 2013). The most numerous modifications are pseudouridine residues and 2'-O-methylribonucleotides. Pseudouridylation is guided by base pairing between the precursor rRNA and a small nucleolar RNA (snoRNA) in a Box C/D snoRNP (reviewed in Henras et al 2004, Yu and Meier 2014). Similarly, 2'-O-methylation is guided by base pairing between the precursor rRNA and a snoRNA in a Box H/ACA snoRNP (reviewed in Henras et al. 2004, Hamma and Ferre-D'Amare 2010). Other modifications include N(1)-methylpseudouridine, 5-methylcytosine, 7-methylguanosine, 6-dimethyladenosine, and 4-acetylcytidine. Modification of nucleotides occur as the pre-rRNA is being cleaved. However, the order of cleavage and modification steps is not clear so these two processes are presented separately here. Defects in ribosome biogenesis factors can cause disease (reviewed in Freed et al. 2010).

Mitochondrial ribosomes are completely distinct from cytoplasmic ribosomes, having different protein subunits and 12S rRNA and 16S rRNA. The mitochondrial rRNAs are encoded in the mitochondrial gen-

ome and are produced by processing of a long H strand transcript. Specific residues in the rRNAs are modified by enzymes to yield 5 different types of modified nucleotides:

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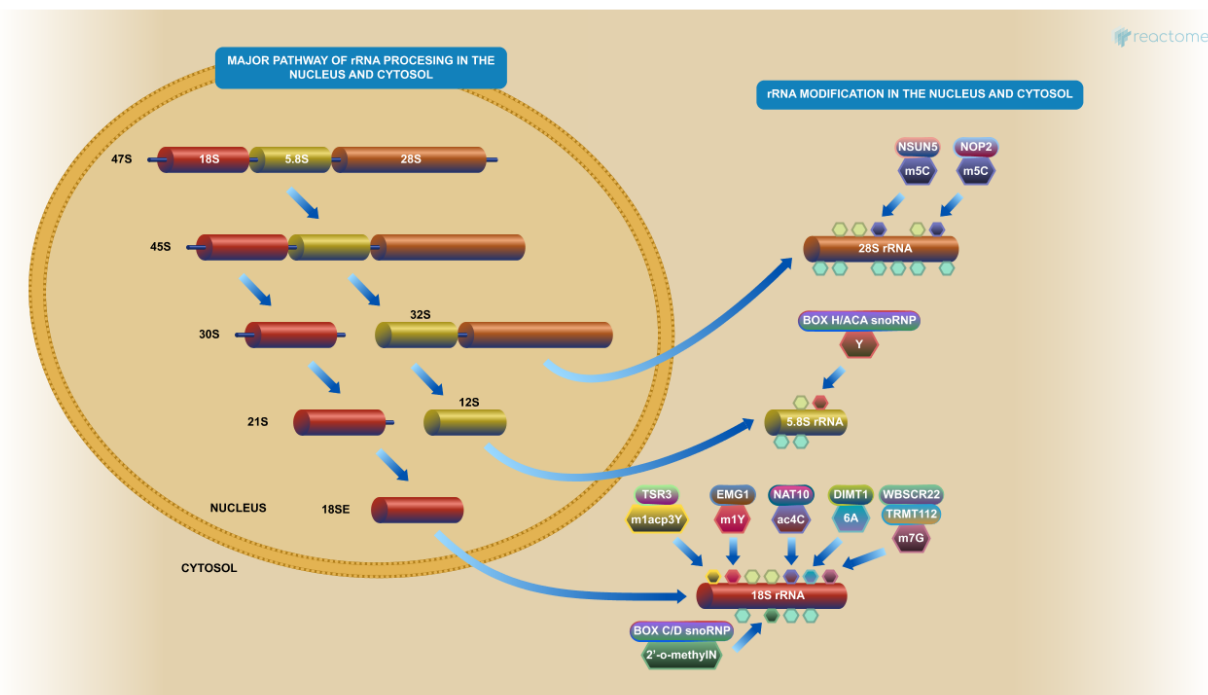
Editions

2003-07-15	Authored	Joshi-Tope, G.
2015-08-12	Authored, Edited	May, B.
2016-01-30	Reviewed	Vincent, NG.

rRNA processing in the nucleus and cytosol ↗

Location: [rRNA processing](#)

Stable identifier: R-HSA-8868773



Each eukaryotic cytosolic ribosome contains 4 molecules of RNA: 28S rRNA (25S rRNA in yeast), 5.8S rRNA, and 5S rRNA in the 60S subunit and 18S rRNA in the 40S subunit. The 18S rRNA, 5.8S rRNA, and 28S rRNA are produced by endonucleolytic and exonucleolytic processing of a single 47S precursor (pre-rRNA) (reviewed in Henras et al. 2015). Transcription of ribosomal RNA genes, processing of pre-rRNA, modification of nucleotide residues within the rRNA, and assembly of precursor 60S and 40S subunits occur predominantly in the nucleolus (reviewed in Hernandez-Verdun et al. 2010, Boschi-Muller and Motorin 2013), with a few late reactions occurring in the cytosol.

Literature references

- Henras, AK., Plisson-Chastang, C., O'Donohue, MF., Chakraborty, A., Gleizes, PE. (2015). An overview of pre-ribosomal RNA processing in eukaryotes. *Wiley Interdiscip Rev RNA*, 6, 225-42. ↗
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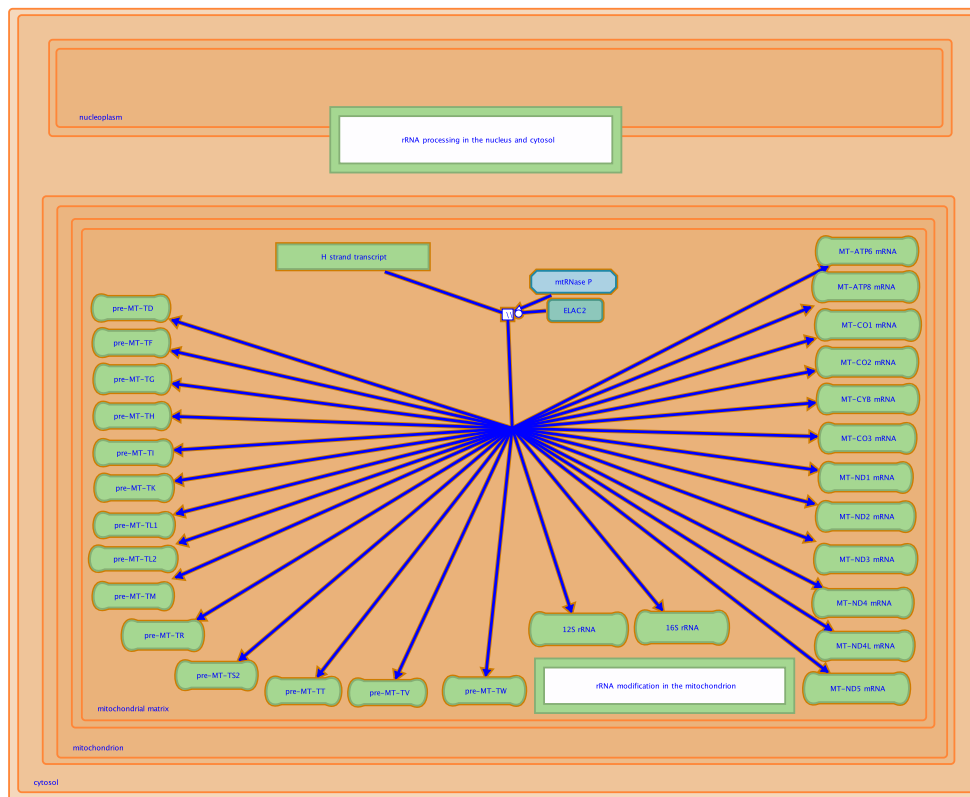
Editions

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2016-04-25	Authored, Edited	May, B.

rRNA processing in the mitochondrion ↗

Location: rRNA processing

Stable identifier: R-HSA-8868766



reactome

Mitochondrial ribosomes contain 16S rRNA (large subunit) and 12S rRNA (small subunit) that are encoded in the mitochondrial genome and produced by processing of a long H strand transcript (reviewed in Van Haute et al. 2015). Enzymes encoded in the nucleus and acting in the mitochondrial matrix modify 5 nucleotides in the 12S RNA and 4 nucleotides in the 16S rRNA (reviewed in Van Haute et al. 2015).

Literature references

Van Haute, L., Pearce, SF., Powell, CA., D'Souza, AR., Nicholls, TJ., Minczuk, M. (2015). Mitochondrial transcript maturation and its disorders. *J. Inherit. Metab. Dis.*, 38, 655-80. ↗

Editions

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2016-04-25	Authored, Edited	May, B.

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