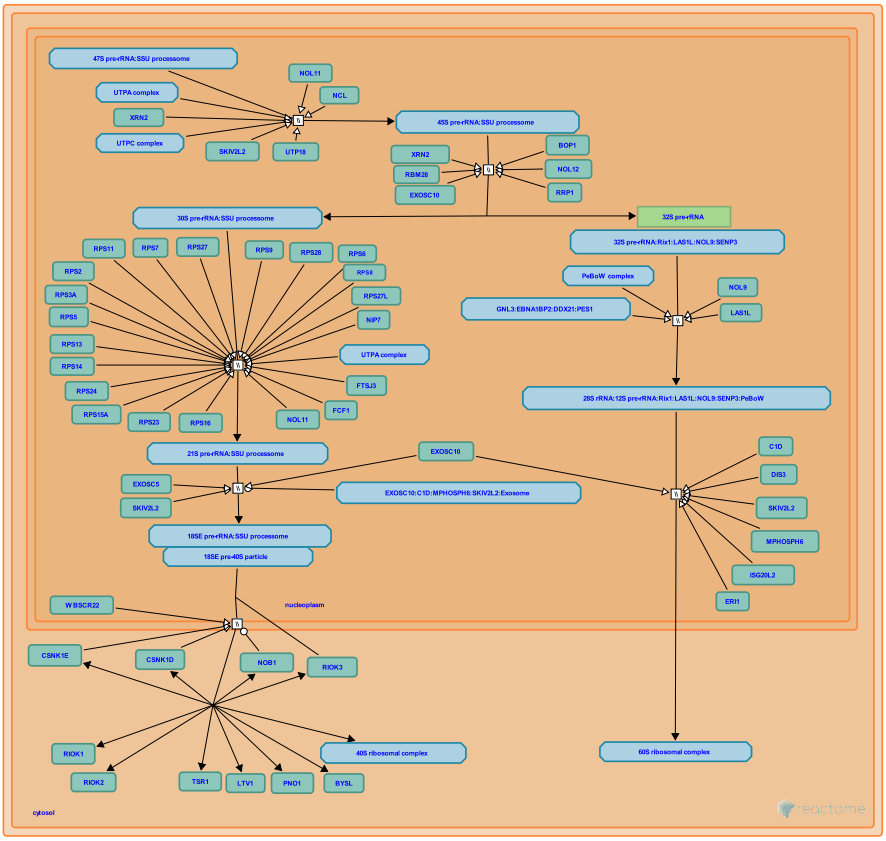
Major pathway of rRNA processing in the nucleolus and cytosol



May, B., Vincent, NG.

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

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.

08/10/2024

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. ↗

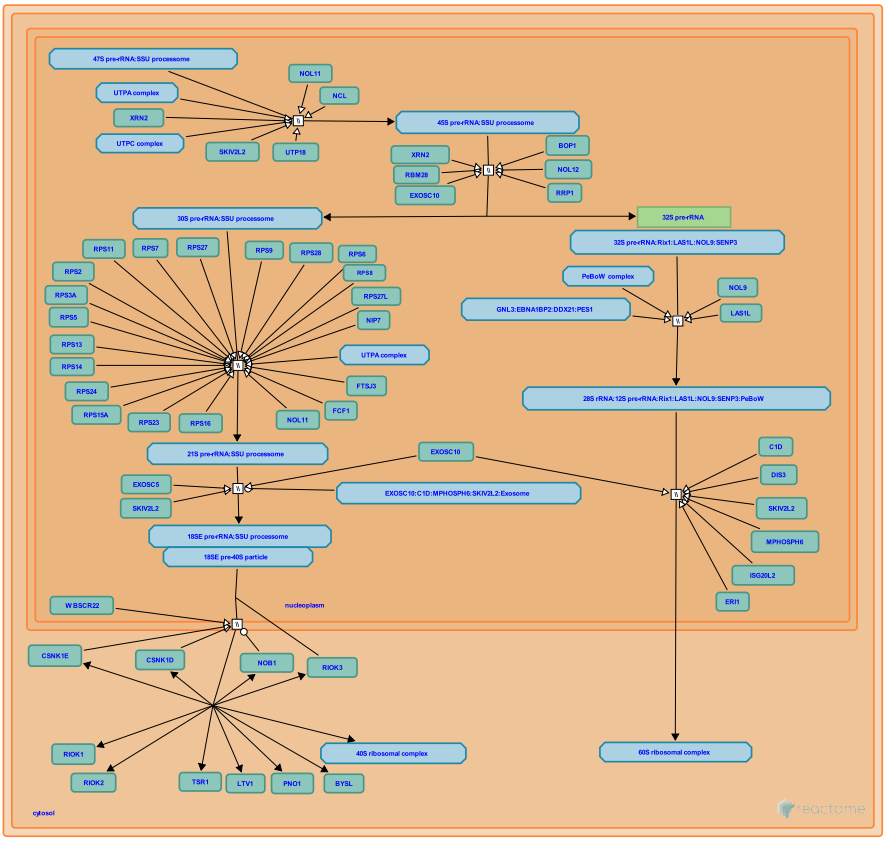
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Reactome database release: 90

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

Major pathway of rRNA processing in the nucleolus and cytosol ↗

Stable identifier: R-HSA-6791226



In humans, a 47S precursor rRNA (pre-rRNA) is transcribed by RNA polymerase I from rRNA-encoding genes (rDNA) at the boundary of the fibrillar center and the dense fibrillar components of the nucleolus (Stanek et al. 2001). The 47S precursor is processed over the course of about 5-8 minutes (Popov et al. 2013) by endoribonucleases and exoribonucleases to yield the 28S rRNA and 5.8S rRNA of the 60S subunit and the 18S rRNA of the 40S subunit (reviewed in Mullineus and Lafontaine 2012, Henras et al. 2015). As the pre-rRNA is being transcribed, a large protein complex, the small subunit (SSU) processome, assembles in the region of the 18S rRNA sequence, forming terminal knobs on the pre-rRNA (reviewed in Phipps et al. 2011, inferred from yeast in Dragon et al. 2002). The SSU processome contains both ribosomal proteins of the small subunit and processing factors which process the pre-rRNA and modify nucleotides. Through addition of subunits the SSU processome appears to be converted into the larger 90S pre-ribosome (inferred from yeast in Grandi et al. 2002). An analogous large subunit processome (LSU) assembles in the region of the 28S rRNA, however the LSU is less well characterized (inferred from yeast in McCann et al. 2015).
Following cleavage of the pre-rRNA within internal transcribed spacer 1 (ITS1), the pre-ribosomal particle separates into a pre-60S subunit and a pre-40S subunit in the nucleolus (reviewed in Hernandez-Verdun et al. 2010, Phipps et al. 2011). The pre-60S and pre-40S ribosomal particles are then exported from the nucleus to the cytoplasm where the processing factors dissociate and recycle back to the nucleus
Nuclease digestions of the 47S pre-rRNA can follow several paths. In the major pathway, the ends of the 47S pre-rRNA are trimmed to yield the 45S pre-rRNA. Digestion at site 2 (also called site 2b in mouse, see Henras et al. 2015 for nomenclature) cleaves the 45S pre-rRNA to yield the 30S pre-rRNA containing the 18S rRNA of the small subunit and the 32S pre-rRNA containing the 5.8S rRNA and the 28S rRNA of the large subunit. The 32S pre-rRNA is digested in the nucleus to yield the 5.8S rRNA and the 28S rRNA while the 30S pre-rRNA is digested in the nucleus to yield the 18SE pre-rRNA which is then processed in the nucleus and cytosol to yield the 18S rRNA. At least 286 human proteins, 74 of which have no yeast homolog, are required for efficient processing of pre-rRNA in the nucleus (Tafforeau et al. 2013)

Literature references

Stanek, D., Pliss, A., Malínský, J., Risueño, MC., Raska, I., Masata, M. et al. (2001). Non-isotopic mapping of ribosomal RNA synthesis and processing in the nucleolus. *Chromosoma, 110*, 460-70. ↗

Popov, A., Raska, I., Raška, O., Kováčik, L., Hagen, G., Stixová, L. et al. (2013). Duration of the first steps of the human rRNA processing. *Nucleus, 4*, 134-41. ↗

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Mullineux, ST., Lafontaine, DL. (2012). Mapping the cleavage sites on mammalian pre-rRNAs: where do we stand?. *Biochimie, 94*, 1521-32. ↗

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

Editions

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2016-01-30	Reviewed	Vincent, NG.

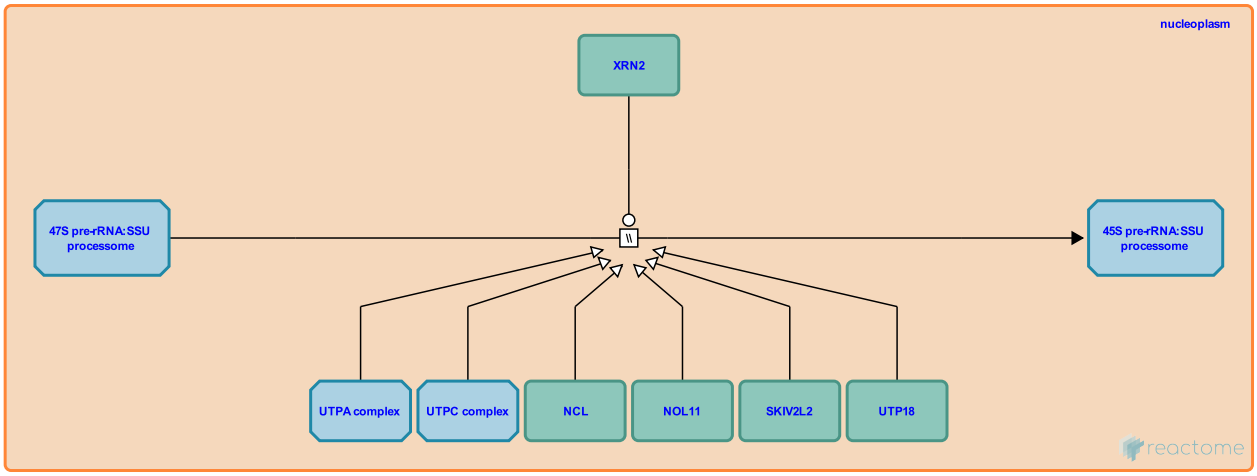
47S pre-rRNA is nucleolytically processed at A' (01,A1), site A0, and site 02 (site 6) to yield 45S pre-rRNA ↗

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

Stable identifier: R-HSA-6791227

Type: omitted

Compartments: nucleoplasm



Unknown nucleases concomitantly cleave the 47S precursor rRNA (pre-rRNA) at the A' site (also known as the 01 site or the A1 site), the A0 site in the 5' external transcribed spacer (5' ETS), and site 02 (also known as site 6 in mouse) in the 3' ETS (Sloan et al. 2014). Cleavage occurs when the pre-rRNA is complexed with the small subunit processome (SSU processome) complex, a large protein complex that binds the 5' region of the pre-rRNA after transcription commences (Kass and Sollner-Webb 1990, Sloan et al. 2014, inferred from yeast in Dragon et al. 2002). The UTP-A subcomplex of the SSU processome and SKIV2L2 (MTR4) are required for cleavage at the A' site while the UTP-B subcomplex and U3 snoRNP (Sloan et al. 2014) and RRP36 of the UTPC subcomplex of the SSU processome (Gerus et al. 2010) improve efficiency of cleavage. UTP18 is required for cleavage of the 5' ETS (Holzel et al. 2010). Nucleolin (NCL) interacts with the 47S pre-rRNA (Yanagida et al. 2001, inferred from mouse in Ginisty et al. 1998) and is involved in cleavage at the A' site (inferred from mouse in Ginisty et al. 1998) but its association with the SSU processome is transitory (Turner et al. 2009). NOL11, a component of the SSU processome which interacts with UTP4, increases the efficiency of processing at A', but is not strictly required (Freed et al. 2012). XRN2 exonucleolytically degrades the 5' 01 fragment (Sloan et al. 2013, inferred from mouse homologs in Wang and Pestov 2011).

Followed by: 45S pre-rRNA is nucleolytically processed at site 2 (site 2b) to yield 30S pre-rRNA and 32S pre-rRNA

Literature references

Prieto, JL., McStay, B., Baserga, SJ., McCann, KL., Freed, EF. (2012). NOL11, implicated in the pathogenesis of North American Indian childhood cirrhosis, is required for pre-rRNA transcription and processing. *PLoS Genet., 8*, e1002892. ↗

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Lebaron, S., Sloan, KE., Mattijssen, S., Pruijn, GJ., Tollervey, D., Watkins, NJ. (2013). Both endonucleolytic and exonucleolytic cleavage mediate ITS1 removal during human ribosomal RNA processing. *J. Cell Biol., 200*, 577-88. ↗

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Editions

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2016-01-30	Reviewed	Vincent, NG.

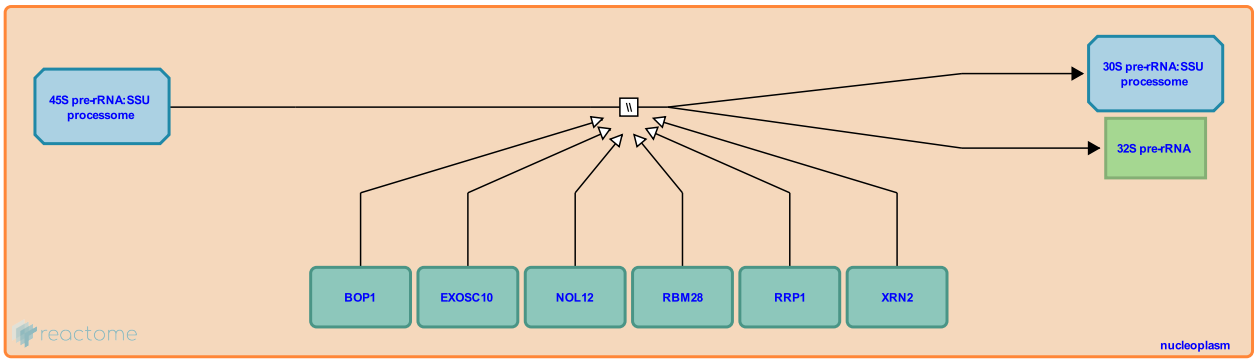
45S pre-rRNA is nucleolytically processed at site 2 (site 2b) to yield 30S pre-rRNA and 32S pre-rRNA ↗

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

Stable identifier: R-HSA-6791228

Type: omitted

Compartments: nucleoplasm



An unknown endonuclease cleaves at site 2 (also called site 2b in mouse) in the internal transcribed spacer 1 (ITS1) between the 18S rRNA and the 5.8S rRNA in the 45S precursor rRNA (pre-rRNA) while the pre-rRNA is contained in a 90S particle containing ribosomal proteins and assembly factors (Sloan et al. 2013). (The 90S particle is believed to be produced by addition of further subunits to the complex containing the pre-RNA and the small subunit (SSU) processome (inferred from yeast in Grandi et al. 2002).) The products are a 30S pre-rRNA which contains the 18S rRNA and a 32S pre-rRNA containing the 5.8S rRNA and the 28S rRNA. The cleavage splits the 90S particle into a pre-40S particle and a pre-60S particle and is believed to occur while the 5' region of the 45S rRNA is bound by the SSU processome. BOP1 (a subunit of the PeBoW complex), RBM28, NOL12 and RRP1 (NOP52) also participate in the cleavage (Sloan et al. 2013, Yoshikawa et al. 2015). Exonucleases including XRN2 and EXOSC10 (RRP6) of the exosome complex then remove further nucleotides from the end of the ITS (Sloan et al. 2013).

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

Followed by: 32S pre-rRNA is nucleolytically processed at site 4 (4a) to yield 12S pre-rRNA and 28S rRNA, 30S pre-rRNA is nucleolytically processed at site 1 to yield 21S pre-rRNA

Literature references

Lebaron, S., Sloan, KE., Mattijssen, S., Pruijn, GJ., Tollervey, D., Watkins, NJ. (2013). Both endonucleolytic and exonucleolytic cleavage mediate ITS1 removal during human ribosomal RNA processing. *J. Cell Biol., 200,* 577-88. ↗

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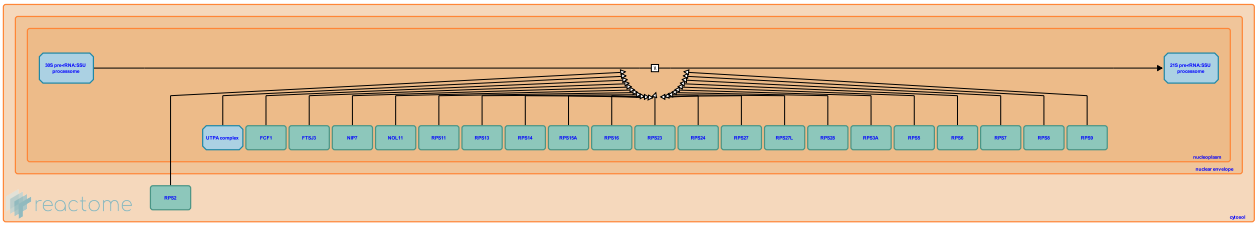
30S pre-rRNA is nucleolytically processed at site 1 to yield 21S pre-rRNA ↗

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

Stable identifier: R-HSA-6791221

Type: omitted

Compartments: nucleoplasm



An unknown endonuclease cleaves site 1 (also called site A1), removing the remainder of the 5' external transcribed spacer (5' ETS) from 30S pre-rRNA containing the 18S rRNA (Freed et al. 2012, Tomecki et al. 2015). Sixteen proteins of the small ribosomal subunit are required for processing sequences flanking the 18S rRNA in the 30S pre-rRNA (O'Donohue et al. 2010) presumably due to their assembly onto pre-rRNA as processing proceeds. Additionally, FCF1 (hUTP24, part of the SSU processome) is required for cleavage at site 1 (Tomecki et al. 2015) and NOL11 and CIRH1A (Cirhin, part of the UTPA complex) interact and are required for cleavage at site 1 and other sites (A', A0, and 2) (Freed et al. 2012). FTSJ3 and NIP7 interact and are required for processing at sites 1, 2, and A0 (Morello et al. 2011).

Preceded by: 45S pre-rRNA is nucleolytically processed at site 2 (site 2b) to yield 30S pre-rRNA and 32S pre-rRNA

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

Literature references

Prieto, JL., McStay, B., Baserga, SJ., McCann, KL., Freed, EF. (2012). NOL11, implicated in the pathogenesis of North American Indian childhood cirrhosis, is required for pre-rRNA transcription and processing. *PLoS Genet., 8*, e1002892. ↗

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Zanchin, NI., Nickerson, JA., Singh, G., Silva, TC., Coltri, PP., Quaresma, AJ. et al. (2011). The human nucleolar protein FTSJ3 associates with NIP7 and functions in pre-rRNA processing. *PLoS ONE, 6*, e29174. ↗

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2016-01-30	Reviewed	Vincent, NG.

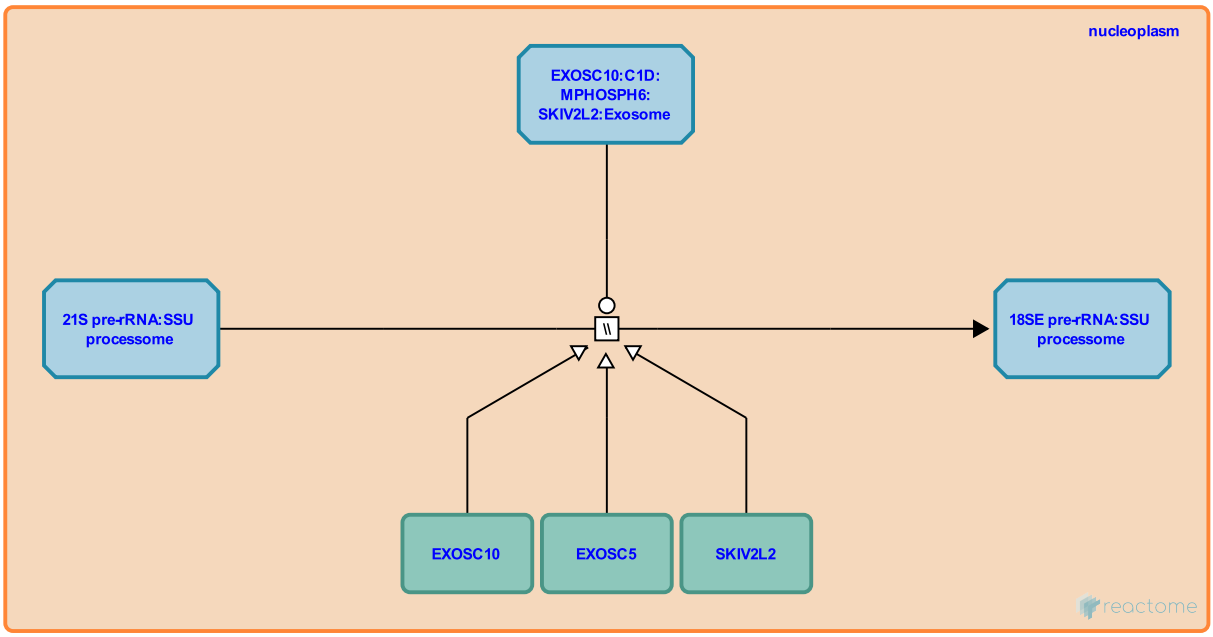
21S pre-rRNA is nucleolytically processed at site E (site2a) to yield 18SE pre-rRNA ↗

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

Stable identifier: R-HSA-6791222

Type: omitted

Compartments: nucleoplasm



An unknown endonuclease in the nucleolus cleaves at site E (site 2a in mouse) of 21S pre-rRNA, yielding 18SE pre-rRNA (Preti et al. 2013, Sloan et al. 2013). Evidence also indicates that 18SE may also be produced by an exonucleolytic pathway (Carron et al. 2011, Sloan et al. 2013). BYSL (Bystin, ENG1), SKIV2L2 (MTR4), and the exonuclease activity of EXOSC10 (RRP6), all associated with the exosome, are required for formation of 18SE by the exonucleolytic pathway (Sloan et al. 2013). Sequencing indicates that 18SE molecules can have variable ends, presumably due to exonuclease activity (Preti et al. 2013).

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

Followed by: 18SE pre-rRNA in pre-40S particles is nucleolytically processed during translocation from the nucleus to the cytosol

Literature references

O'Donohue, MF., Carron, C., Faubladier, M., Choesmel, V., Gleizes, PE. (2011). Analysis of two human pre-ribosomal factors, bystin and hTsr1, highlights differences in evolution of ribosome biogenesis between yeast and mammals. *Nucleic Acids Res., 39*, 280-91. ↗

Lebaron, S., Sloan, KE., Mattijssen, S., Pruijn, GJ., Tollervey, D., Watkins, NJ. (2013). Both endonucleolytic and exonucleolytic cleavage mediate ITS1 removal during human ribosomal RNA processing. *J. Cell Biol., 200*, 577-88. ↗

Preti, M., O'Donohue, MF., Bortolin-Cavaillé, ML., Choesmel, V., Gleizes, PE., Montel-Lehry, N. (2013). Gradual processing of the ITS1 from the nucleolus to the cytoplasm during synthesis of the human 18S rRNA. *Nucleic Acids Res., 41*, 4709-23. ↗

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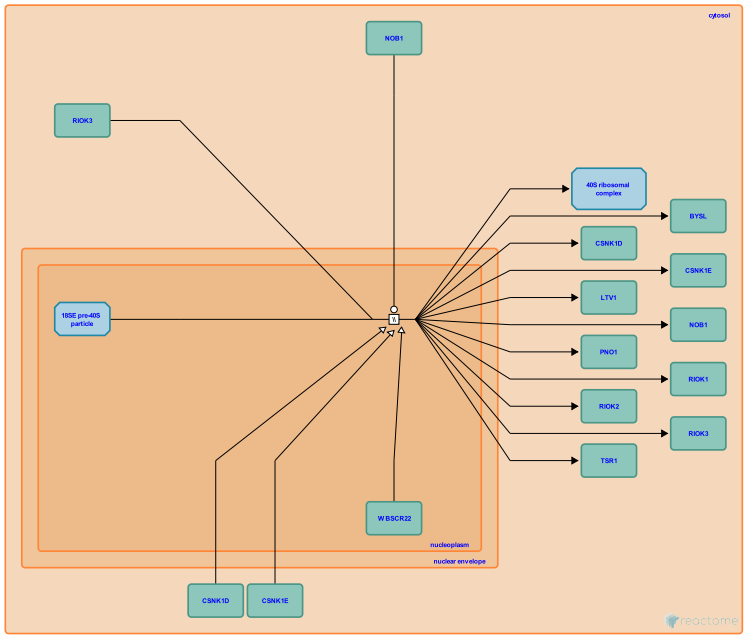
18SE pre-rRNA in pre-40S particles is nucleolytically processed during translocation from the nucleus to the cytosol ↗

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

Stable identifier: R-HSA-6791223

Type: omitted

Compartments: nucleoplasm, cytosol



Exonuclease activity of the exosome (Preti et al. 2013) and endonuclease activity of NOB1 (inferred from yeast, Pertschy et al. 2009) process the 3' end of precursor rRNA (pre-rRNA) 18SE to yield mature 18S rRNA. During the processing, pre-rRNA 18SE is bound in the pre-40S ribosome subunit, which contains ribosomal proteins and processing factors such as NOB1 and BYSL. The pre-40S subunit is exported from the nucleus to the cytosol where processing factors are released and recycled back to the nucleus. The kinases RIOK1, RIOK2, CSNK1D and CSNK1E are associated with the pre-40S rRNA subunit in both the nucleus and cytosol and their kinase activity is required for recycling of processing factors back to the nucleus (Zemp et al. 2009, Zemp et al. 2014). RIOK1 and RIOK2 are also required for 18SE processing (Widmann et al. 2012, Zemp et al. 2009). RIOK3 (RIO3) is a cytosolic kinase that associates with the pre-40S ribosomal particle after export from the nucleus and is required for release of processing factors (Baumas et al. 2012).

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

Literature references

Widmann, B., Pfannstiel, J., Badertscher, L., Wandrey, F., Wyler, E., Zemp, I. et al. (2012). The kinase activity of human Rio1 is required for final steps of cytoplasmic maturation of 40S subunits. *Mol. Biol. Cell, 23*, 22-35. ↗

Tollervey, D., Gnädig, M., Schneider, C., Hurt, E., Pertschy, B., Schäfer, T. (2009). RNA helicase Prp43 and its co-factor Pfa1 promote 20 to 18 S rRNA processing catalyzed by the endonuclease Nob1. *J. Biol. Chem., 284*, 35079-91. ↗

Rouquette, J., Choesmel, V., Gleizes, PE. (2005). Nuclear export and cytoplasmic processing of precursors to the 40S ribosomal subunits in mammalian cells. *EMBO J., 24*, 2862-72. ↗

O'Donohue, MF., Carron, C., Faubladier, M., Choesmel, V., Gleizes, PE. (2011). Analysis of two human pre-ribosomal factors, bystin and hTsr1, highlights differences in evolution of ribosome biogenesis between yeast and mammals. *Nucleic Acids Res., 39*, 280-91. ↗

Haag, S., Kretschmer, J., Bohnsack, MT. (2015). WBSCR22/Merm1 is required for late nuclear pre-ribosomal RNA processing and mediates N7-methylation of G1639 in human 18S rRNA. *RNA, 21*, 180-7. ↗

Editions

2015-08-16	Authored, Edited	May, B.
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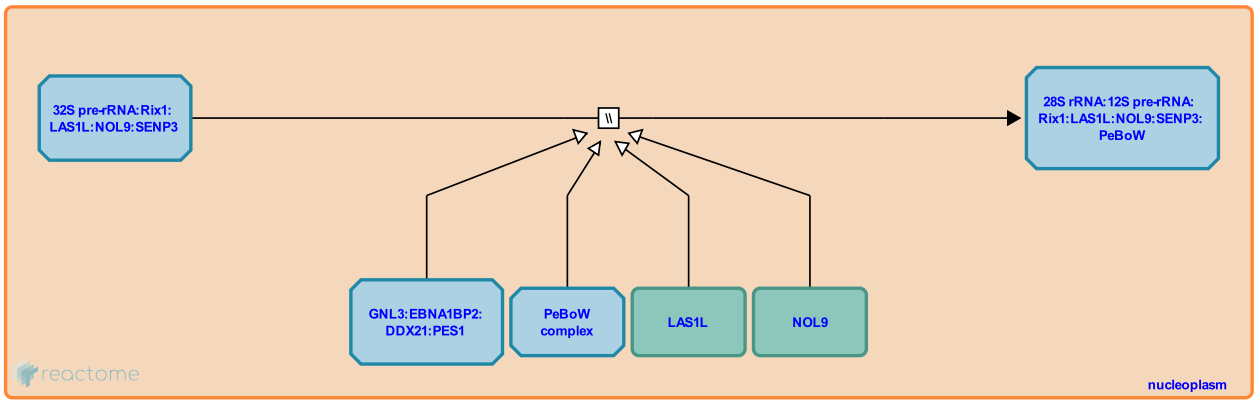
32S pre-rRNA is nucleolytically processed at site 4 (4a) to yield 12S pre-rRNA and 28S rRNA ↗

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

Stable identifier: R-HSA-6791219

Type: omitted

Compartments: nucleoplasm



Unknown nucleases process the 32S precursor rRNA (pre-rRNA) at site 4, yielding the 28S rRNA and the 12S pre-RNA that will be further processed to the mature 5.8S rRNA. Processing occurs in precursor 60S ribosomal (pre-60S) subunits that contain ribosomal proteins and processing factors. The PES1:BOP1:WDR12 complex (PeBoW complex) associates with pre-60S subunits in both the nucleus and cytosol where it is involved in processing 32S rRNA and recycling pre-60S subunit processing factors. Perturbation of the PeBoW complex prevents processing of the 32S pre-rRNA (Holzel et al. 2005, Grimm et al. 2006, Holzel et al 2007, Rohrmoser et al. 2007). The polynucleotide kinase activity of NOL9, which is associated with pre-60s subunits, is also required for processing of pre-32S rRNA (Heindl and Martinez 2010). LAS1L interacts with PELP1:TEX10:WDR18, NOL9, and SENP3 in pre-60S subunits where it is required for processing of the internal transcribed spacer 2 (ITS2) in pre-32S rRNA (Castle et al. 2012). The PELP1:TEX10:WDR18 complex is the mammalian homolog of the yeast Rix1 complex (Castle et al. 2012). A complex containing GNL3 (Nucleostemin), EBNA1BP2, DDX21, and PES1 is also required for processing 32S rRNA to 28S rRNA (Romanova et al. 2009). Both the Nucleostemin complex and the PeBoW complex both contain PES1 and therefore may be part of a single larger complex.

Preceded by: 45S pre-rRNA is nucleolytically processed at site 2 (site 2b) to yield 30S pre-rRNA and 32S pre-rRNA

Followed by: 12S pre-rRNA is nucleolytically processed to yield 5.8S rRNA

Literature references

Gruber-Eber, A., Harasim, T., Grimm, T., Malamoussi, A., Eick, D., Orban, M. et al. (2007). Interdependence of Pes1, Bop1, and WDR12 controls nucleolar localization and assembly of the PeBoW complex required for maturation of the 60S ribosomal subunit. *Mol. Cell. Biol., 27*, 3682-94. ↗

Gruber-Eber, A., Harasim, T., Grimm, T., Malamoussi, A., Eick, D., Rohrmoser, M. et al. (2006). Dominant-negative Pes1 mutants inhibit ribosomal RNA processing and cell proliferation via incorporation into the PeBoW-complex . *Nucleic Acids Res., 34*, 3030-43. ↗

Martinez, J., Heindl, K. (2010). Nol9 is a novel polynucleotide 5'-kinase involved in ribosomal RNA processing. *EMBO J., 29*, 4161-71. ↗

Gruber-Eber, A., Schlee, M., Harasim, T., Grimm, T., Malamoussi, A., Eick, D. et al. (2005). Mammalian WDR12 is a novel member of the Pes1-Bop1 complex and is required for ribosome biogenesis and cell proliferation. *J. Cell Biol., 170*, 367-78. ↗

Gruber-Eber, A., Harasim, T., Grimm, T., Malamoussi, A., Eick, D., Rohrmoser, M. et al. (2007). The BRCT domain of mammalian Pes1 is crucial for nucleolar localization and rRNA processing. *Nucleic Acids Res., 35*, 789-800. ↗

Editions

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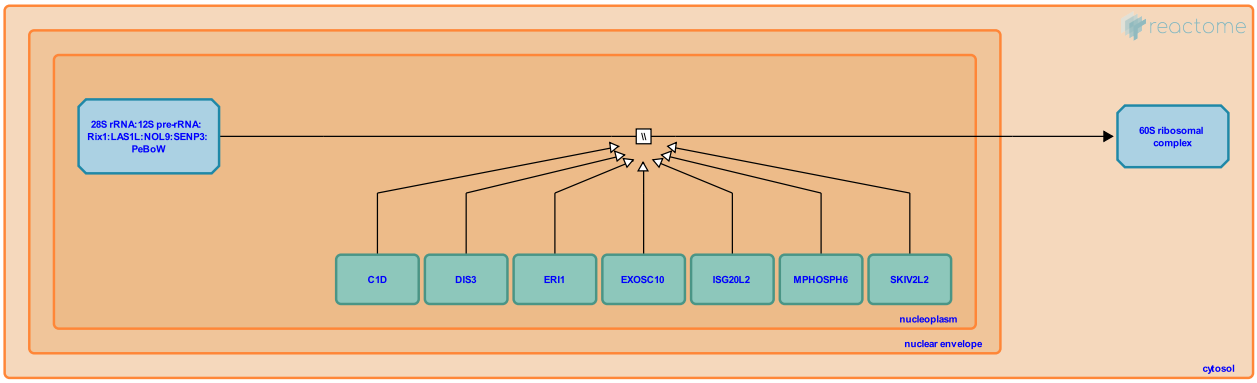
12S pre-rRNA is nucleolytically processed to yield 5.8S rRNA ↗

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

Stable identifier: R-HSA-6791218

Type: omitted

Compartments: nucleoplasm, cytosol



The 12S pre-rRNA is nucleolytically cleaved to yield 5.8S rRNA. C1D, MPHOSPH6 (MPP6), and EXOSC10 (Pm/Scl-100) of the exosome associate and, together with SKIV2L2 (MTR4), are required for 3' processing of mature 5.8S rRNA therefore the exonuclease activity of the exosome seems to be involved (Schilders et al. 2007). Similarly, the DIS3 subunit of the nuclear exosome is required for production of 5.8S rRNA (Tomecki et al. 2010) and the 3'-5' exoribonuclease ISG20L2 (Coute et al. 2008) are also required for production of 5.8S rRNA from 12S pre-rRNA. As inferred from the mouse homolog, the 3'-5' exonuclease ERI1 also plays a role in trimming the 3' end of pre-5.8S rRNA (Ansel et al. 2008).

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

Literature references

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