

SUPPLEMENTARY FIGURE S1: Current model for the ribosome biogenesis pathway from S. cerevisiae. The different predicted particles along the synthesis of both SSUs and LSUs are depicted. The first detected particle is called 90S pre-ribosomal particle or SSU processome. This particle is nucleolar and contains either the nascent pre-rRNA, which has been cleaved at site A₂ in the co-transcriptional pre-rRNA processing branch, or 35S pre-rRNA in the post-transcriptional processing branch (not shown). This pre-rRNA is transcribed by the RNA polymerase I (RNAP I), while pre-5S is transcribed by RNAP III. 90S particles contain about three dozens of trans-acting factors and many r-proteins from the SSU. Maturation of the 90S particle involves the dissociation of the early pre-40S particle from the bulk of these factors, except few of them. Pre-40S particles are termed, according to their position in the pathway, early (E), late (L) and cytoplasmic (C). Cleavage D occurs in the cytoplasm within a 80S-like complex that contains not only the pre-40S particle C but also a mature LSU (not shown). Pre-60S particles assemble on the remaining part of the nascent pre-rRNA transcript. Pre-60S particles are termed early (E), middle (M), late (L) and cytoplasmic (C). The pre-rRNA processing reactions that occur inside the particles as they travel from the nucleolus to the cytoplasm are depicted. About 20 placeholder trans-acting factors have been described so far. In the figure, we have highlighted the dynamics of association and dissociation of ribosomal-like factors and their r-protein counterparts. Note that only two factors, Mrt4 and Rlp24, harbour placeholding activity. See text for further details.

A

R

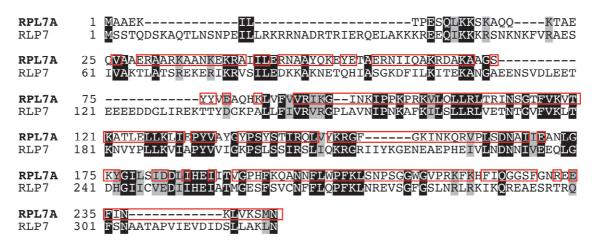
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RPL24A
1 MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFONSKSASLFKORKNPRRIAWTVLFRKHHK
RLP24 1 MRIYQCHFCSSPCYPGHGIMFVRNDAKEFRFCRSKCHKAFKQRRNPRKLKWTKAFRKAAG

RPL24A 61 KGITEEVA---KKRSRKTVKAQRPITGASLDLIKERRSLKPEVRKANREEKLKANKEK--
RLP24 61 KELAVDSTLTFAQRRNVPVRYNRELVATTLKAMARIEEIRQKRERAFYKNRMRGNKEKDF

RPL24A 116 ------KKAEKAARKAEKAKSAGTQSSKFSKQQ------AKG
RLP24 121 LRDKKLVESNPELLRIREVEIARKLAKEQERAESVSEQEESEEEEEDMEIDSDEEEEEQL

RPL24A 146 AFQKVAATSR------
RLP24 181 EKQKILLKNRRRNTKKIAF
```

C



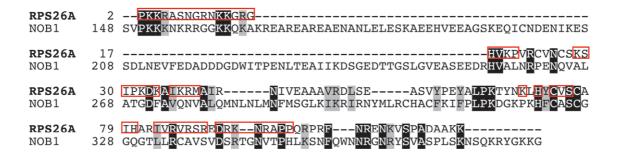
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RPS9A 1 MPRAPRTYSKTYSTPKR----PYESSRLDAELKLAGEFGLKNKKELYRISFOLSKIRRAA
IMP3 1 MVRKLKHHEQ--KLLKKVDFLEWKQDQGHRDTQVMRTYHIQNREDYHKYNRICGDIRRLA

RPS9A 57 RDLLTRDEKDPKRLFEGNAI IRRIVRYGVLSEDKKKLDYVLALKVEDFLERRLQTQVYKL
IMP3 59 NKLSLLPPTDPFRRKHEQLLLDKLYAMGVLTTKSKISDLENKVTVSAICRRRLPVIMHRL

RPS9A 117 GLAKSVHHARVLITORHIAVGKOIVNIPSFMVRLDSEKHIDFAPTSPFGGARPGRVARRN
IMP3 119 KMAETIQDAVKFIEOGHVRVGPNLINDPAYLVTRNMEDYVTWVDNSKI---KKTLLRYRN

RPS9A 177 AARKAEASGEAADEADEE
IMP3 176 ------QIDDFDFS
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E



SUPPLEMENTARY FIGURE S2: Alignment of distinct ribosomal proteins and their respective ribosomal-like protein counterpart from *S. cerevisiae*. Sequence alignments were performed using the slow and accurate version of MAFFT [1]. Alignments were visualised with Belvu [2]. Identical residues are marked by black boxes and similar amino acids are marked by grey boxes (BLOSUM62). Red boxes indicate residues of the ribosomal proteins situated at or closer than 5 Å from rRNA. Comparison of the amino acid sequences of yeast (A) P0 (uL10), Mrt4 and Mex67, (B) L24 (eL24) and Rlp24, (C) L7 (uL30) and Rlp7, (D) S9 (uS4) and Imp3, (E) S26 (eS26) and Nob1. All sequences were taken from the *Saccharomyces Genome Database* (http://www.yeastgenome.org/).

Supplementary references

- 1. Kazutaka, K, Standley, DM (2013). Multiple Sequence Alignment Software Version 7: improvements in performance and usability. **Mol Biol Evol** 30(4): 772-780. doi: 10.1093/molbev/mst010.
- 2. Sonnhammer, ELL, Hollich, V (2005). *Scoredist*: A simple and robust protein sequence distance estimator. **BMC Bioinformatics** 6: 108. doi: 10.1186/1471-2105-6-108.