Supplemental Figure Legends

Supp. Fig. S1, Supp. Fig. S2 and Supp. Fig. S3 – The amino-acid sequences of r-proteins L7, L8 and L35, respectively, from *S. cerevisiae* are shown. The gray boxes under each residue mark the extent of conservation in eukaryotes. The disorder consensus and RNA and/or protein binding site predictions were conducted using Disorder Prediction Meta Server (DisMeta). The disordered binding regions are based on the prediction server ANCHOR.

Supp. Fig. S4 – The mature conformations of ribosomal proteins L7 (green), L35 (magenta) and L8 (cyan) and surrounding rRNA (yellow) (PDB 3U5H and 3U5I) are superimposed with the conformations of the same proteins (black) and rRNA (gray) from the cryo-EM structure of Nog2-associated pre-ribosomes (PDB 3JCT).

Supp. Table 1 – Summary of results. Informative results are shaded.

Supp. Fig. S5- Pre-rRNA processing pathway of yeast ribosomes

Supp. Fig. S6- Growth of yeast expressing plasmid-borne wild-type L21 or mutant L21 in glucose-containing medium at 30°C. A strain containing the plasmid vector only is included as a negative control for growth.

Supp. Fig. S7- Protein composition of pre-60S particles in wild-type yeast (GAL) and *L8Δ1-70* mutant strains (GLU). TAP-tagged Rpf2 was used as the bait to affinity-purify pre-ribosomes. Western blotting was conducted to investigate the levels of assembly factors in pre-ribosomes that diminish when L8 was depleted. Levels of all tested assembly factors remained the same in the absence of the N-terminal extension of L8.

Supp. Fig. S8 – **(A)** Northern blot hybridization showing the accumulation of 7S pre-rRNA and decreased levels of mature 5.8S rRNA when Sda1 is depleted. U3 snoRNA was used as the loading control (strain obtained from D. Kellogg). **(B)** Pre-ribosomes were purified using Nog2 as the bait protein. The protein profile was assayed by SDS-PAGE, followed by silver staining.