**Supporting Information**

Armache et al. 10.1073/pnas.1009999107

![Fourier shell correlation (FSC) curve](image)

Fig. S1. Fourier shell correlation (FSC) curve for the cryo-EM reconstruction of the *Triticum aestivum* 80S ribosome-nascent chain complex, with resolution of 5.5 Å according to a cut-off of the FSC at 0.5.
Fig. S2. Secondary structure diagram for the small subunit (18S) rRNA of *Triticum aestivum*, modified from ref. 1. Green regions indicated de novo modeled regions, gray regions are expansion segments, whereas orange nucleotides were not modeled.

Fig. S3. Secondary structure diagram for the small subunit (18S) rRNA of Saccharomyces cerevisiae modified from ref. 1. Gray regions indicate expansion segments, whereas orange nucleotides were not modeled.

BMC Bioinformatics 3:2.
Fig. S4. Secondary structure diagram for the 5′ region of the large subunit rRNAs (5.8S and 28S) of *Triticum aestivum* modified from ref. 1. Green regions indicated de novo modeled regions, gray regions are expansion segments, whereas orange nucleotides were not modeled.

Fig. S5. Secondary structure diagram for the 3′ region of the large subunit rRNAs (5S and 28S) of *Triticum aestivum* modified from ref. 1. Green regions indicated de novo modeled regions, gray regions are expansion segments, whereas orange nucleotides were not modeled.

Fig. S6. Secondary structure diagram for the 5′ region of the large subunit rRNAs (5.8S and 25S) of Saccharomyces cerevisiae modified from ref. 1. Gray regions are expansion segments, whereas orange nucleotides were not modeled.

Fig. S7. Secondary structure diagram for the 3′ region of the large subunit rRNAs (5S and 25S) of *Saccharomyces cerevisiae* modified from ref. 1. Gray regions are expansion segments, whereas orange nucleotides were not modeled.

**Fig. S8.** Visualization of density for (A–C) *Saccharomyces cerevisiae* ES7^a^ (yellow) and (D–F) *Triticum aestivum* ES27^a^, int (blue) at different contour levels. (A–C) In the *S. cerevisiae* 80S reconstruction, density for ES7^a^ is observed at lower thresholds (C). R-protein L6e (green) interacts with ES7^b^, c. (D–F) In the *T. aestivum* 80S reconstruction, density for ES27^a^ is observed at lower thresholds, where interaction with r-protein L38e (red) with ES27^b^ is evident (F).
**Fig. S9.** Comparison of fit of yeast models in *Thermomyces lanuginosus* and *Saccharomyces cerevisiae* 80S cryo-EM maps. (Left) Protein Data Bank (PDB) 3JYV, 3JYW, 3JYX in the associated cryo-EM map of *T. lanuginosus* 80S ribosome from Taylor et al. (1). The fit of the yeast model (this paper) into cryo-EM map of *T. lanuginosus* 80S ribosome from Taylor et al. (1) and into the yeast 80S ribosome from Becker et al. (2) is shown in the center and right panels, respectively.