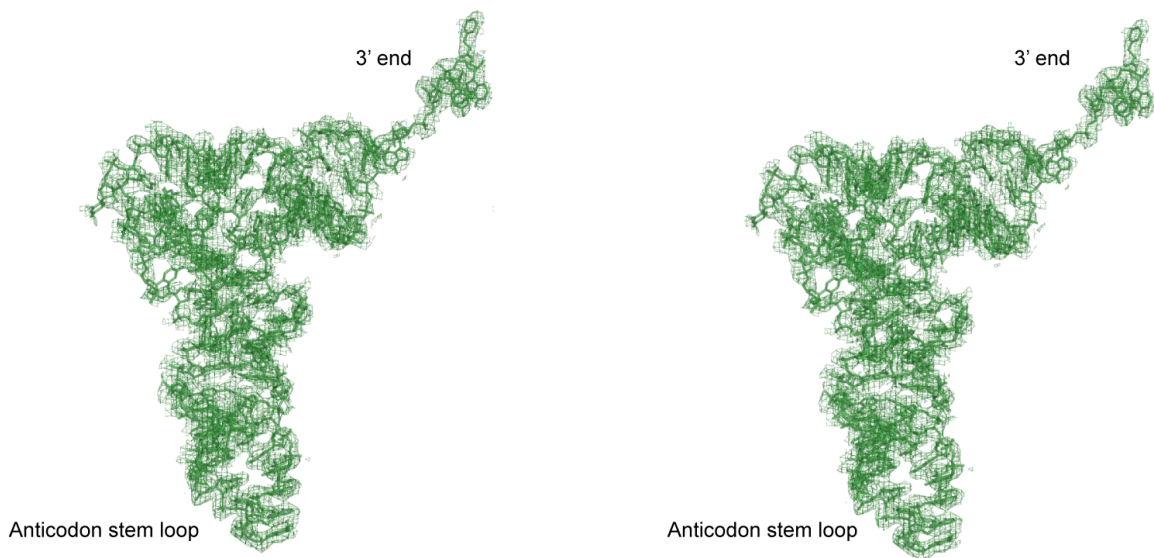


Insights into substrate stabilization from snapshots of the peptidyl transferase center of the intact 70S ribosome.

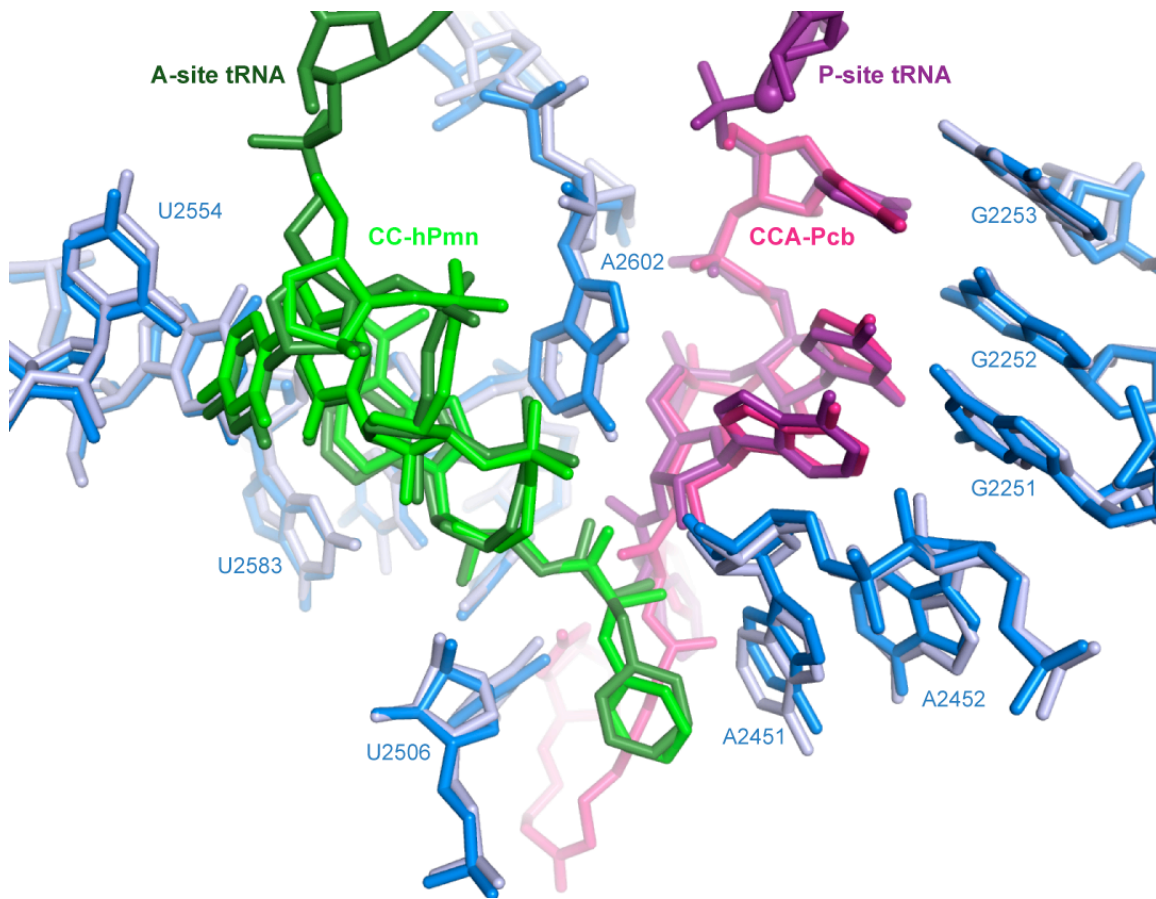
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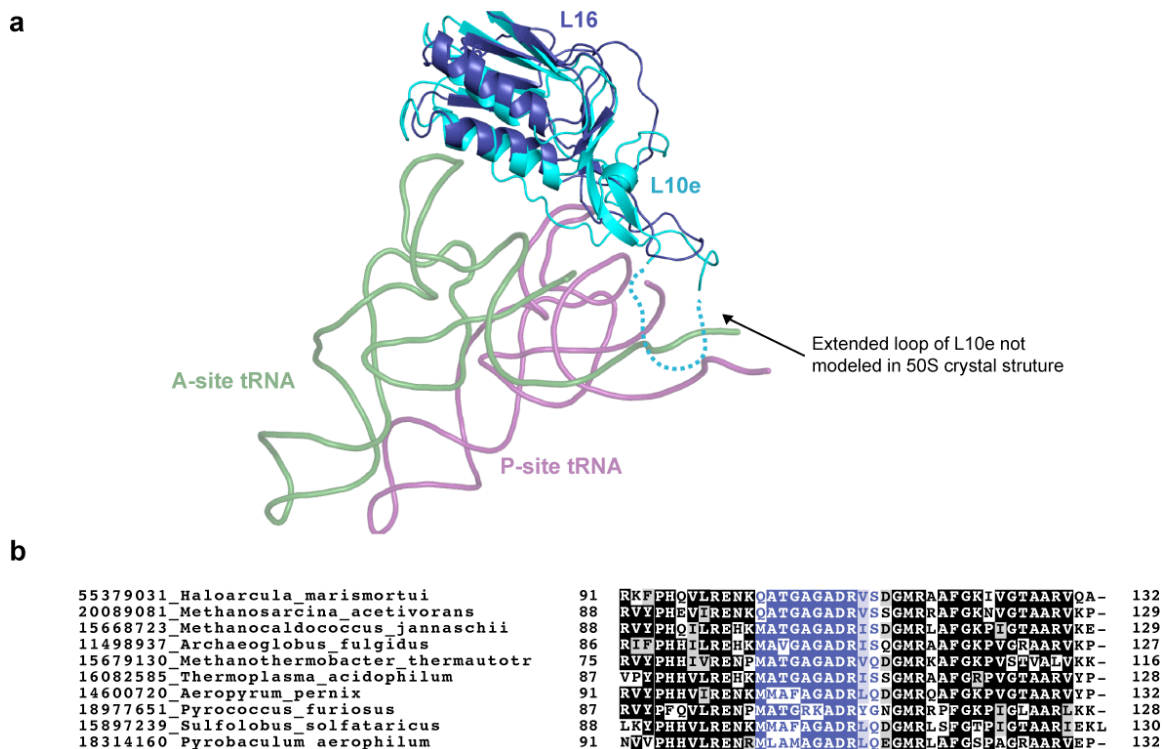
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Supplementary Figure 1. Representative electron density for the A-site tRNA. Wall-eyed stereo image of the $3F_o-2F_c$ data for the A-site tRNA shown in green, from the pre-peptidyl transfer structure reported here. Note that while the 3' CCA tail and anticodon stem loop are well-resolved, regions surrounding the elbow of the tRNA are likely dynamic and thus not as well-ordered.



Supplementary Figure 2. Comparison of the PTC from the 50S subunit alone with that of the intact 70S ribosome. Superposition of several 23S RNA residues within the PTC from the structure of the 50S subunit of *Haloarcula marismortui* (1VQN)² with that from the pre-peptidyl transfer structure of the 70S ribosome reported here. The 50S structure is displayed in the lighter shade throughout: A-site substrates are shown in green, P-site substrates in purple, and 23S RNA in blue. Note the similarity between the two structures, demonstrating that the PTC between the 50S subunit and intact 70S ribosome are very similar.



Supplementary Figure 3. Conservation of an extended loop of ribosomal protein L10e. a) Structural alignment of protein L10e from Ban *et al.*³ with L16 from the pre-peptidyl transfer structure, shown in cyan and dark blue, respectively. A conserved 11-residue loop of L10e was disordered in the crystal structure, though it is expected to extend between the acceptor arms of A- and P-site tRNA. A hypothetical model of this loop region is represented here with a dashed line. b) Sequence alignment of protein L10e from ten archaeal genomes representative of a diverse cross-section of the archaeal sub-kingdoms. In blue are those amino acids that correlate to the 11-residue loop of L10e that was disordered in initial structures of the 50S subunit from *Haloarcula marismortui*³. From the sequence alignment, it is clear that this portion of the loop is highly conserved across archaea in both length and sequence.

References

1. Selmer, M. et al. Structure of the 70S ribosome complexed with mRNA and tRNA. *Science* **313**, 1935-1942 (2006).
2. Schmeing, T.M., Huang, K.S., Strobel, S.A. & Steitz, T.A. An induced-fit mechanism to promote peptide bond formation and exclude hydrolysis of peptidyl-tRNA. *Nature* **438**, 520-524 (2005).
3. Ban, N., Nissen, P., Hansen, J., Moore, P.B., and Steitz, T.A. The complete atomic structure of the large ribosomal subunit at 2.4 Å resolution. *Science* **289**, 905-920 (2000).