s8a.m3.o1 **The structure of the 50S ribosomal subunit at 2.7 Å resolution.** *P. Nissen (1), *N. Ban (1), J. Hansen (1), P.B. Moore (1,2) and T.A. Steitz (1,2,3). *Department of Molecular Biophysics & Biochemistry and (2) Department of Chemistry, Yale University and (3) Howard Hughes Medical Institute, New Haven, CT 06520-8114*
Keywords: protein biosynthesis.

The first X-ray crystallographic electron density map of a ribosomal subunit showing recognizable molecular features was of the *Haloarcula marismortui* 50S published at 9 Å resolution (Ban et al., 1998) and showed rods of density corresponding to duplex RNA crisscrossing the subunit. Extension of phasing to 5 Å resolution allowed the fitting of known protein and RNA structures but not extensive tracing of the RNA backbone (Ban et al., 1999). The resolution of an experimentally phased electron density map of the Haloarcula marismortui 50 S ribosomal subunit has now been extended to 2.7 Å resolution using heavy atom derivative data to 3.2 Å resolution and density modification procedures. A complete model of the approximately 3,000 nucleotides of the 23S and 5S RNAs has been constructed and partially refined against the experimental diffraction amplitudes and experimental phases to give a free R-factor of 0.35 at 2.7 Å resolution. Positioning of the substrate analogue CCdA-puromycin into this model shows that the ribosome is a ribozyme, since there is no protein electron density closer than about 18 Å from the bond being synthesized.

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Ban N., Nissen P., Hansen J., Capel M., Moore P.B. and Steitz T.A. "Placement of protein and RNA structures into a 5 Å resolution map of the 50S ribosomal subunit". Nature, (1999), 400: 841 - 847.

s8a.m3.o2 **New crystal Structures of Ribosomal Proteins Associated with Peptide Bond Formation and GTPase Activation.** M.C. Wahl, *Max-Planck-Institut für Biochemie, Abteilung Strukturforschung, D-82152 Martinsried, Germany.*
Keywords: protein biosynthesis, ribosomal proteins L4 and L12 (L7), X-ray crystallography.

Various studies implicate ribosomal protein L4 both structurally and functionally in the peptidyl transferase activity of the bacterial ribosome. Furthermore, L4 molecules from the γ-branch of proteobacteria serve as autogenous feedback regulator of transcription and translation of their own S10 operons. The high resolution crystal structure of L4 from *Thermotoga maritima* (1) shows an alternating α/β fold and a large disordered loop region (Fig. 1A). Mutational and crosslinking results as well as the conservation pattern and electrostatic potential distribution suggest separate binding sites for rRNA and S10 mRNA. Another area of L4 could serve for protein•protein interactions or may be surface-exposed in the translational and transcriptional machineries.

Protein L12, present in four copies on the ribosome, is presumably involved in the binding of translation factors and stimulates factor-dependent GTP hydrolysis. In two crystal structures of L12 from *Thermotoga maritima* (2) the asymmetric units comprise two full-length molecules and two N-terminal fragments which are associated in a specific, hetero-tetrameric complex (Fig. 1B). Solution studies corroborate the existence of L12 tetramers, indicating that similar complexes may occur *in vivo* and *in situ*. The two observed dimerization modes are not found in previously proposed L12 models. The structures also display different monomer conformations in the hinge regions, in agreement with the suggested dynamic role of the protein in the ribosomal translocation process.

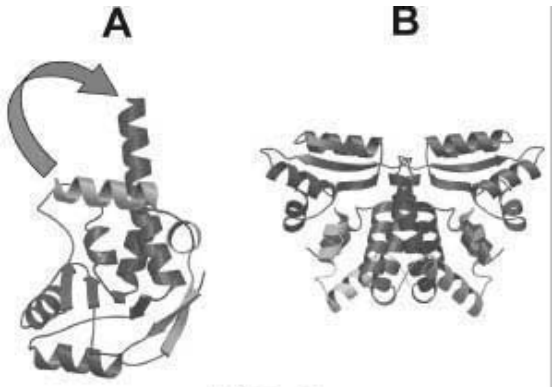

Fig. 1

[1] Worbs, M., Huber, R. & Wahl, M.C. Crystal Structure of Ribosomal Protein L4 Shows RNA Binding Sites for Ribosome Incorporation and Feedback Control of the S10-Operon. *EMBO J.*, **19**, 807-818 (2000).

[2] Wahl, M.C., Bourenkov, G.P., Bartunik, H.D. & Huber, R. Flexibility, Conformational Diversity, and Two Dimerization Modes in Complexes of Ribosomal Protein L12 from *Thermotoga maritima*. *EMBO J.* **19**, 174-186 (2000).