Crystal Structures of Ribosomal Protein L10 in Complex with L7/12 N-Terminal Domains

Mihaela Diaconu, Markus C. Wahl, *Max Planck Institute for Biophysical Chemistry, Göttingen, Germany.* E-mail: mdiacon@gwdg.de

The L7/12 stalk of the large ribosomal subunit comprises protein L10 and multiple copies of L7/12. It is involved in binding of translation factors and stimulation of factor-dependent GTP hydrolysis. The stalk is disordered in available crystal structures of ribosomes or 50S subunits. We have determined crystal structures of *Thermotoga maritima* L10 in complex with three L7/12 N-terminal domain (NTD) dimers. The structures are in agreement with a multitude of biochemical data. A globular NTD of L10 encompasses the binding region for 23S rRNA. A long C-terminal helix (α8) of L10 shows a modular design with consecutive binding sites for L7/12 dimers. L10 helix α8 assumes different positions with respect to the NTD in different crystal forms and thus constitutes a mobile platform for the attached L7/12 molecules. The number of L7/12 dimers varies with the length of L10 helix α8 in different species. The structure of the L7/12 NTD dimers agrees with one mode of dimerization observed in isolated L7/12. The hinge region of L7/12 can bind in α-helical form to the NTD in isolation but is displaced by L10 upon complex formation and becomes disordered. The organization of the complex supports its function in factor recruitment and GTPase activation.

Keywords: L10-L7/12 complex, L7/12 stalk, ribosome structure