Structural Analysis of the L7/12 Ribosomal Stalk

Markus C. Wahl[a], Mihaela Diaconu[a], Ute Kothe[b], Frank Schlünzen[c], Niels Fischer[a], Jörg Harms[c], Alexander G. Tonevitski[d], Holger Stark[a], Marina V. Rodnina[b], [a]*Max Planck Institute for Biophysical Chemistry, Göttingen, Germany.* [b]*University of Witten-Herdecke, Germany.* [c]*DESY, Hamburg, Germany.* [d]*Moscow State University, Russia.* E-mail: mwahl@gwdg.de

The L7/12 stalk of the large ribosomal subunit encompasses protein L10 and multiple copies of L7/12 and is involved in translation factor related functions. We have determined crystal structures of *Thermotoga maritima* L10 in complex with L7/12 N-terminal domains and of an archaeal L10 N-terminal domain *in situ* on the 50S subunit. A mobile C-terminal α-helix of L10 harbors three consecutive binding sites for L7/12 dimers in *T. maritima* and two in *E. coli*, where the helix is shorter. The N-terminal domain of L10 recognizes the overall fold of the thiostrepton loop of 23S rRNA and interacts with L11. Together with structures of isolated L7/12, we devised a complete atomic model of the stalk and reinterpreted the morphology and dynamics of the stalk region as seen in electron microscopic reconstructions of ribosomes. Flexible hinges in both L10 and L7/12 lead to a high freedom of motion for the L7/12 C-terminal domains. Our structural data and analysis of L7/12 mutants by fast kinetics reveal that the L7/12 C-terminal domains can reach far out into solution to bind translation factors. They thereby promote factor recruitment to the ribosome. The L7/12 C-termini can then reach back towards ribosome-bound factors to stimulate GTP hydrolysis by stabilization of the factors' active GTPase conformation.

Keywords: ribosome structure, translation factor recruitment, GTPase activation