Crystal structure of the L1-mRNA complex.

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The RNA binding ability of ribosomal protein L1 is of profound interest since the protein has a dual function as a ribosomal protein binding rRNA and as a translational repressor binding its mRNA. In the ribosome L1 protein binds to 23S rRNA and forms the unique structural and functional ribonucleoprotein domain called "L1-protuberance". We determined the crystal structure of L1-rRNA complex at 2.65 Å resolution in 2002 [1] using data obtained at the EMBL beamline BW7A.

Last year we determined the crystal structure of the protein L1 from Thermus thermophilus in complex with a specific fragment of mRNA from Methanococcus vannielii at 2.1 Å resolution using data collected at the EMBL beamline BW7B [2]. The crystals belong to space group P6522 with cell dimensions a=b= 67.9 Å, c=340.5 Å. An oscillation angle of 0.25° was used due to large cell unit parameters of the crystal. Data were processed and merged with XDS. The final model, refined to an R factor of 21.2% (Rfree=24.7%) at 2.1 Å resolution, includes 228 amino acids, 36 nucleotides, 166 water molecules, one butanediol molecule, Mg²⁺ and a K⁺ ion.

The L1-mRNA high resolution structure was compared with the structure of L1 complexed with a specific fragment of 23S rRNA [1]. In both complexes a strongly conserved RNA structural motif is involved in L1 binding through a conserved network of RNA-protein H-bonds inaccessible to the solvent. These interactions should be responsible for specific recognition between the protein and RNA. A large number of additional non-conserved RNA-protein H-bonds stabilize both complexes. The added contribution of these non-conserved H-bonds makes the ribosomal complex much more stable than the regulatory one.

Figure 1: a) The crystal structure of the L1-23S rRNA complex. b) The crystal structure of the L1-mRNA complex.

The L1 proteins in both complexes have similar overall three-dimensional structures. On the contrary, crystal structures of two RNA molecules differ significantly. The rRNA molecule has more complicated three-dimensional structure, because of two loops interacting each other. In mRNA, one of these loops is absent, the other is six residues shorter. Anyway, in both RNAs the junction of the two helices contains nucleotides strictly conserved in all L1-binding sites in large rRNAs as well as in sites specific for L1 in mRNAs from those bacteria and archaea, for which feedback regulation has been experimentally proved. The nucleotides are connected by a network of conserved hydrogen bonds, most of which are inaccessible to the solvent. This network strongly stabilizes the unique three-dimensional structure of the junction region.
In the ribosomal complex protein L1 interacts with RNA through both domains whereas in regulatory one only domain I is used. Therefore, it is possible to suggest that domain II is an evolutionary acquisition of L1 to provide a means of L11 operon translation regulation.

References
