

Abstract No. skri376

**Shape-complimentary Evolution of Ribosomal RNA-protein Interactions: Crystal Structure of 53-mer Domain I RNA Bound to L24 Protein**

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Beamline(s): X8C

The ribosomal protein L24 initiates the ribosomal assembly process via interaction with three separated regions within the domain I of 23S rRNA [1]. One of these regions, an isolated 53-mer junctional domain I fragment is able to form a stable complex with the free L24 protein [2].

We have determined the crystal structure of 53-mer domain I RNA bound to L24 protein. from *T. thermophilus* at 3 Å resolution. The crystals belong to the C2221 space group with unit cell dimensions  $a=77.72$  Å,  $b=85.27$  Å,  $c=101.99$  Å. The structure was solved by MAD technique on Os ions and refined with Refmac program. The final model contains one L24-RNA complex with R-factor = 24.9% (R-free=27.7%) using all data with  $F>0$ . C-terminal residues 90-120 and the loop region residues 48-56 are disordered in the crystal.

The archea sequence of RNA fragment contains an extra U308 nucleotide extensively involved in interaction with L24 protein. In the case of prokariotic L24 RNA complex missing interacting contacts are compensated by additional interaction of protein with adjacent sugar-phosphate backbones of RNA.

- (1) Klein, D.J. et al (2001) EMBO J. 20: 4214.
- (2) Stelzl, U. et al (2000) PNAS USA 97: 4597.

**Acknowledgements:**

This work was supported by a NIH grant CA49982 to D.J.P.  
We thank Dr. Leonid Flaks for assistance with data collection and processing.

