

s8a.m6.o5 Crystal structure of the S15-rRNA complex at 2.8 Å resolution. A. Nikulin^{1,2}, A. Serganov^{1,2}, E. Ennifar², S. Tishchenko¹, N. Nevskaya¹, W. Shepard³, C. Portier⁴, M. Garber¹, B. Ehresmann², C. Ehresmann², S. Nikonov¹ and P. Dumas² ¹*Institute of Protein Research, Pushchino, Moscow Region 142292, Russia.* ²*UPR 9002 du CNRS, IBMC, 15 rue R. Descartes, 67084 Strasbourg cedex, France.* ³*LURE, Centre Universitaire Paris-Sud, 91898 Orsay cedex.* ⁴*IBPC, rue P. et M. Curie, 75005 Paris, France*

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Notes

In bacterial ribosomes, the small (30S) ribosomal subunit is composed of 16S rRNA and 21 distinct proteins. Ribosomal protein S15 is of particular interest because it binds primary to 16S rRNA and is required for assembly of the small subunit and for intersubunit association, thus representing a key element in the assembly of a whole ribosome. In addition, S15 regulates its own translation by interacting with its own messenger.

Here we report the 2.8 Å-resolution crystal structure of the highly conserved S15-rRNA complex. Protein S15 interacts in the minor groove with a G-U/G-C motif and a three-way junction made of helices 20, 21 and 22 of 16S rRNA. Remarkably, S15 is seen here totally unchanged in comparison of its unbounded state in another crystal structure [Clemons *et al.*, *Structure* **6** (1998) 429-38]. The three-way junction is constrained by a conserved base triple and stacking interactions, and locked into place by magnesium ions and protein side chains, mainly through interactions with the unique three-dimensional geometry of the backbone. Overall, our structure is in very good agreement with the interpretation of one of the two low resolution 30S crystal structures [Clemons *et al.*, *Nature* **400** (1999) 833-40]

The structure has revealed an unexpected feature concerning the geometry of the RNA three-way junction. One C residue, C754, previously supposed to be in interaction with G587 within helix 20, makes a sharp turn and ensures the locking of the three-way junction by interacting with G654 of helix 22. Remarkably, the structure suggests that this crucial C residue, by flipping between G587 and G654, could be responsible of a previously known magnesium-dependent conformational change of the 3-way junction. One may speculate that such movement could be a relevant one during ribosome functioning.

Finally, the present structure is also very suggestive of the interaction between S15 and its mRNA as the G-U/G-C motif also exists in the latter.