s8a.m3.o3 **Functional implications of tRNA Mimicry. Crystal Structure of Ribosome Recycling Factor.** M. Selmer[1], S. Al-Karadaghi[1], G. Hirokawa[2], A. Kaji[2] and A. Liljas[1]. [1]*Molecular Biophysics, Center for Chemistry and Chemical Engineering, Lund University, Sweden* [2]*Department of Microbiology, School of Medicine, University of Pennsylvania, Philadelphia, USA.*
Keywords: protein biosynthesis.

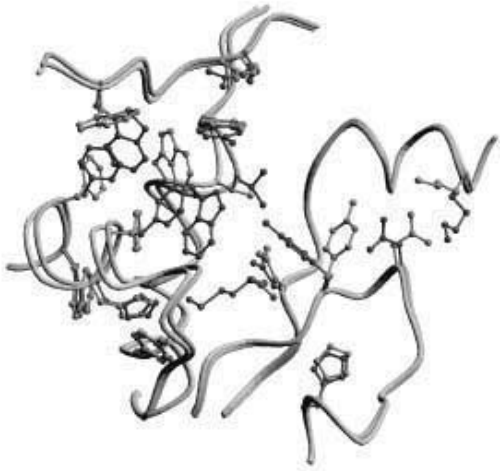
Ribosome recycling factor (RRF) together with elongation factor G (EF-G) catalyses the fourth step of protein synthesis; ribosome recycling. In this step the post-translocational complex is separated into its components.

The crystal structure of *Thermotoga maritima* ribosome recycling factor (RRF) has been determined to 2.55 Å resolution.[1] RRF overlaps almost perfectly with a tRNA molecule except that the amino acid binding CCA end is missing. The mimicry suggests that RRF binds to the tRNA binding ribosomal A-site and is translocated to the P-site by EF-G. This mechanism is supported by studies of antibiotic action on the RRF reaction.

[1] Selmer et al. (1999) Science 286, 2349-2352

s8a.m3.o4 **Proofreading mechanism hypothesis based on the structure of the Methionyl-tRNA synthetase liganded to L-methionine.** L. Serre, G. Verdon, T. Choinowski, N. Hervouet, J.L. Risler, C. Zelwer *Centre de Biophysique Moléculaire, C.N.R.S., rue Charles Sadron, 45071 Orléans Cedex 2, France, zelwer@cnrs-orleans.fr*.
Keywords: protein biosynthesis.

Aminoacid selection by aminoacyl-tRNA synthetases requires efficient discrimination mechanisms to avoid the cognate tRNA to be incorrectly charged. A proofreading mechanism enables *E. coli* methionyl-tRNA synthetase (EcMetRS) to discriminate *in vivo* L-methionine against L-homocysteine at the activation step[1]. The crystal structure of the complex between EcMetRS and L-methionine solved at 1.8 Å resolution exhibits some intriguing differences with the free enzyme structure[2]. Thus, the methionine δ-sulphur replaces a water molecule H-bonded to Leu13N and Tyr260O? in the free enzyme and rearrangements of aromatic residues enable the protein to form an hydrophobic pocket around the ligand side-chain[3]. The subsequent formation of an extended water molecules network contributes to relative displacements, up to 3 Å, of several domains of the protein. The structure of this complex is discussed in relation with a likely mechanism for the discrimination between methionine and homocysteine and with cross-talks between different domains of the enzyme.



[1] Jakubowski H. Proofreading in vivo: editing of homocysteine by methionyl-tRNA synthetase in Escherichia coli. *Proc. Natl. Acad. Sci. U S A*, (1990), **87** : 4504-4508.
[2] Mechulam, Y. Crystal structure of *E. coli* methionyl-tRNA synthetase highlights species-specific features. *J. Mol. Biol.,* (1999), **294 :** 1287-1297**.**
[3] Figure legend: Superimposition of native and liganded MetRS backbones at the active site. Green side chains: native, red: complex. L-methionine: magenta.