Crystal structure of Phe-tRNA-synthetase from *T. thermophilus* in complex with phenylalanyl-adenylate.

Dmitry G. Vassylyev (user card # 0003391)

International Institute for Advanced Research, 3-4 Hikaridai, Seika, Soraku, Kyoto, 619-02

The full 3D data set at 2.7Å resolution has been collected from the single crystal of Phe-tRNA synthetase complexed with Phe-adenylate. The data have processed with the programs DENZO and SCALEPACK. The final R-merge is 6.5% and completeness of data is 95%. The structure was refined with the program X-PLOR using the coordinates of uncomplexed Phe-tRNA synthetase as an initial model. After first round of refinement using slowcooling protocol in X-PLOR R-factor dropped to 26.5% (R-free = 31.0%) and the electron density for Phe-adenylate was clearly seen in the (2Fo-Fc) map. The model has been built for Phe-adenylate and refinement was continued. At the final stage of refinement the bulk solvent correction was incorporated and about 200 water molecules have been isolated from the (Fo-Fc) map using 3σ threshold. The final R-factor is 20.5% (R-free = 25%) for 66,600 reflection in the resolution range 30 – 2.7Å and about 9,000 non-hydrogen atoms. Phe-adenylate is represented with clear electron density in the active site of the catalytic subunit of Phe-tRNA synthetase. The conformation of Phe-adenylate resembles that of His- and Ser-adenylates in complexes with their cognate tRNA synthetases. Adenine moiety of Phe-adenylate is sundwiched between side chains of Phe-216 and Arg-321, while the phosphate group is tightly bound to guanidinium group of Arg-204 by two strong hydrogen bonds. All these protein residues are conserved among class II tRNA synthetases. In contrast, Phe side chain of Phe-adenylate forms the unique network of hydrophobic van der Waals interactions with adjacent protein residues in the hydrophobic on the enzyme surface.