

E0013

Dimeric Structural Significance for Ligand Binding in Putative Peptidyl-tRNA Hydrolase from *Pyrococcus horikoshii* OT3. K. Shimizu, Y. Fujimoto, M. Sugahara, N. Kunishima, RIKEN Harima Inst., RIKEN Spring-8 Center, Sayo-cho, Sayo-gun, Hyogo, 679-5148, Japan.

In the biosynthesis process of the protein translation, peptidyl-tRNA molecules may happen to dissociate from the ribosome before mRNAs readout do not reach the stop codon. Peptidyl-tRNA hydrolases (Pths) catalyze removal of peptidyl moiety from peptidyl-tRNA molecule and the resultant free tRNA and peptide will reuse for the protein translation. So far, we have determined two crystal forms of putative Pths from *Pyrococcus horikoshii* OT3 (*Ph*Pths): (1) form 1 at 1.2 Å resolution, $P4_12_12$ and (2) form 2 at 1.9Å resolution, $P4_322$. *Ph*Pths protomer are composed of an α/β fold with a four-stranded antiparallel β -sheet in its core surrounded by two α -helices on each side. Both forms show a biologically dimer and the asymmetric unit of forms 1 and 2 includes 1 and 2 molecules, respectively. We will present the structural difference between two forms and furthermore discuss the dimeric structural significance for the recognition of the substrate, tRNA in *Ph*Pths dimer.

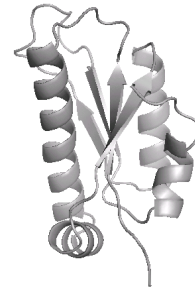


Fig. 1 Ribbon diagram of the crystal structure, *Ph*Pths protomer.

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