Crystal structure of MCoA-ACPT from *Thermus Thermophilus* HB8.

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As a part of Protein 3000 project in Japan, Joint research group of PCprot has solved the crystal structure of malonyl CoA-acyl carrier protein transacylase (MCoA-ACPT) from *Thermus thermophilus* HB8 by the collaboration with RIKEN. The structure has been solved by the molecular replace method (Molrep) using molecular structure of MCoA-ACPT from Escherichia coli. There is 42 % homology in the amino acid sequences in each other. This is the first structure determination of MCoA-ACPT from thermophilic organisms. Crystals were obtained with using full-automatic protein crystallization and observation robotics system named TERA in RIKEN Harima Institute. Data set was collected by the CCD detector at the Pharma-ceutical Industry Beamline (BL32B2) in SPring-8. Data set was processed by the software HKL2000 and 2.2Å data set was obtained.

In the crystal structure MCoA-ACPT from TTHB8 makes dimer that is relatively tight, though MCoA-ACPT from TTHB8 is thought to work as monomer in the solution. By the way, MCoA-ACPT exists in the bacterial body but not in the human body. Therefore it is very possible that this structure would give the light to the structure based drug design for antibiotics.

Keywords: protein 3000 project in Japan, malonyl CoA-acyl carrier protein transacylase, *thermus thermophilus* HB8