

W0370

**Crystal Structure of Putative Phosphomannomutase from *Thermus Thermophilus* HB8.** Shintaro Misaki<sup>1</sup>, Kenji Suzuki<sup>1</sup>, Naoki Kunishima<sup>2</sup>, Mitsuaki Sugawara<sup>2</sup>, Chizu Kuroishi<sup>2</sup>, Masanori Kobayashi<sup>1</sup>, Shoko Fujimoto<sup>1</sup>, Masahiro Sakurai<sup>1</sup>, Kazumi Nishijima<sup>1</sup>, <sup>1</sup>Joint Research Group, Pharmaceutical Consortium for Protein Structure Analysis (PcProt), SPring-8 1-1-1 Kouto, Mikazuki-cho Sayo, Hyougo 679-5198 Japan, <sup>2</sup>Highthroughput Factory (HTPF), RIKEN Harima Institute at SPring-8 1-1-1 Kouto, Mikazuki-cho Sayo, Hyougo 679-5198 Japan

The Crystal structure of putative phosphomannomutase from *Thermus Thermophilus* HB8 (PTHB8) has been solved by the MAD method with Se-Met, as a part of protein 3000 project in Japan. Crystals of PTHB8 were obtained with using the automatic crystallization robot named TERA in HTPF, MAD data of three wave lengths, peak, edge and one remote, were collected by the Rigaku CCD detector (Jupiter210cs) with the crystal under liquid nitrogen exposure (Cryo equipment) at the BL32B 2 (Pharmaceutical industry Beamline) in the SPring-8. As a result of diffraction experiments, MAD data sets (up to 2.2 Å resolution) were collected. The crystal data is as followed, C<sub>2</sub>, Z=8, a=106.0, b=54.8, c=82.9 Å, β=109.1°. The structure was solved by the program package Solve and Resolve. The result of Solve, three sites of Se were clearly obtained. This protein has 6 Se-Met sites in the sequence. But three of them exist very near the N-terminal and are supposed to be disordered. The result of Resolve, initial model excluded approximately 20 residues each of N-terminal and C-terminal was built. Figure 1 shows the overall molecular structure modeled by the initial map. This structure might be the first structure because it was not be able to find any homologous protein in the Protein Data Bank. In the presentation, details of the structure will be presented. And also it would be mentioned about PcProt, which is composed of 22 pharmaceutical companies in Japan. Author thanks Chikahiro Nagata, a member of Joint Research Group of PcProt, for the contribution, and technical staffs of HTPF for protein production and crystallization. The expression plasmid of PTHB8 (TT 0515/HTPF00194) was supplied from the RIKEN Structurome group.

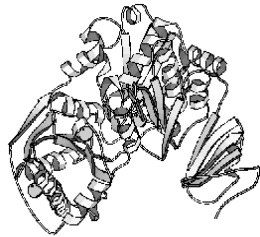


Fig.1. Overall molecular structure.