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Crystal structure of putative phosphomannomutase from *Thermus Thermophilus* HB8

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The Pharmaceutical Consortium for Protein structure Analysis (PcProt) and Highthroughput Factory (HTPF) of RIKEN Harima Institute is now carrying a collaborate in Structural Genomics. One of the results the collaboration is the structure analysis of putative Phosphomannomutase (PMM) from *Thermus thermophilus* HB8 which is analyzed at the1.7Å resolution.

PMM is the enzyme which converts mannose-6-phosphate into mannose-1-phosphate, and this enzyme are widely distributed from bacteria to human. For example, PMM is participating in an alginic acid biosynthetic pathway in *Pseudomonas aeruginosa*, and alginic acid has contributed to bacterial biofilm formation in *P. aeruginosa*.

The selenomethionie derivative of *T. thermophilus* PMM was prepared by the Highthroughput Factory of RIKEN Harima institute, and crystallized by TERA which is a full automatic crystallization and crystal observation robot.

MAD data collection was performed in the BL32B2 (Pharmaceutical Industry beamline), with anomalous scattering of selenium. From those data, the initial phase and model were determined using SOLVE/RESOLVE software. After the refinement, the 280 waters were identified and the R-factor is 0.22 (free R is 0.25).

The determined structure of *T. thermophilus* PMM has four domains, arranged in an overall heart shape. (Fig 1.) That is very similar to *Pseudomonas aeruginosa* PMM (PDB ID: 1P5D) and rabbit Phosphoglucomutase (PGM, PDB ID: 1JDY). Sequence homology between *T. thermophilus* PMM and *P. aeruginosa* PMM, and between *T. thermophilus* PMM and rabbit PGM is 27.8% and 29.6% respectively. Almost of active site residues of *P. aeruginosa* PMM (R20, K118, S108, H109, R247, H308 and H329) are conserved in the *T. thermophilus* PMM (R20, K119, S109, H110 and R254) and rabbit PGM (R22, K129, S116, H117 and R292).

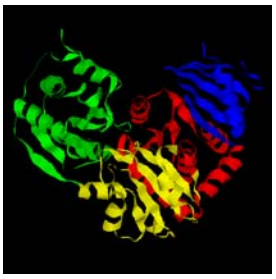

Fig.1 Structure of *T. thermophilus* PMM

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