Crystal Structure of Methylthioribose-1-phosphate Isomerase from *BacillusSubtilis*

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Methionine salvage pathway plays an important role to recycle organic sulphur from a sulphahydryl derivative of the nucleoside. Recently, five enzymes in the pathway have been characterized from *Bacillus subtilis* [1]. One of them was characterized as a methylthioribose-1-phosphate isomerase (MtnA), which catalyzes the isomerization of methylthioribose-1-phosphate to methylthioribulose-1-phosphate.

In this work, we report the three-dimensional structure of MtnA from *B. subtilis* at 2.4 Å resolution, which is the first structure of the well-characterized MtnA. The crystal structure reveals the homodimeric architecture, which corresponds to the result observed in the analysis of dynamic light scattering. A search of protein coordinates in the Protein Data Bank with the program DALI [2] shows that probable MtnA from Thermotoga maritima, regulatory subunit of aIF2B from Pyrococcus horikoshii and yeast Ypr118w are structurally the most similar to that of MtnA from B. subtilis. Although insertion/deletion occur frequently in the sequence alignment, B. subtilis MtnA has a high degree of similarity with the secondary structures and the active site structures of these proteins. These observations probably suggest that these functionally unknown or putative proteins have the same function as that of Bacillus MtnA. For the purpose of investigation into the detailed catalytic mechanism of MtnA, the crystallization of MtnA complexed with its substrate is currently in progress.

[1] Ashida H., Saito Y., Kojima C., Kobayashi K., Ogasawara N., Yokota A., *Science*, 2003, **302**, 286. [2] Holm L., Sander C., *J. Mol. Biol.*, 1993, **233**, 123. Keywords: crystal structure determination, metabolism enzyme, isomerase