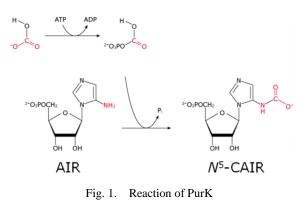
Thermotoga maritima 由来 PurK の結晶構造解析 **Crystal structure of PurK from** *Thermotoga maritima* ○宮澤良太¹, 金川真由美², 馬場清喜^{2,3}, 中川紀子^{2,4}, 海老原章郎², 河合剛太^{2,5}, 三瓶嚴一^{1,2} ○Ryota Miyazawa¹, Mayumi Kanagawa², Seiki Baba^{2,3}, Noriko Nakagawa^{2,4}, Akio Ebihara², Gota Kawai^{2,5}, and Gen-ichi Sampei^{1,2}

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The 6th reaction in the purine nucleotide biosynthetic pathway is the conversion from 5-aminoimidazole ribonucleotide (AIR) to 4-carboxy-5-aminoimidazole ribonucleotide (CAIR). This reaction is catalyzed by different way among species. Higher eukaryotes, such as human, and some archaea use a single enzyme, AIR carboxylase (class II PurE). Other organisms such as plants, yeasts and prokaryotes use two enzymes, N^5 -



aminoimidazole ribonucleotide (N^5 -CAIR) synthetase (PurK) and CAIR mutase (class I PurE). N^5 -CAIR synthetase (PurK) converts AIR, ATP and bicarbonate to N^5 -CAIR, ADP, and Pi (Fig. 1).

Here, we determined the crystal structure of PurK from *Thermotga maritima* (TmPurK) in the ADP bound form. The space group, maximum resolution and R-value (free R-value) for this structure is P_{21} , 2.2 Å and 21.6% (26.5%), respectively.

We compared this structure with structures of PurK from *T. thermophilus, A. aeolicus* and *S. tokodaii*, which we have determined, and from *E. coli* and *A. clavatus*, which has already been determined by the other group [1, 2]. All PurK share similar overall structure, including dimer conformation, and four domains, N, A, B, and C, for each monomer. Interestingly, there are differences among four molecules of TmPurK in asymmetric unit (Fig. 2), suggesting the conformational dynamics in PurK.

References

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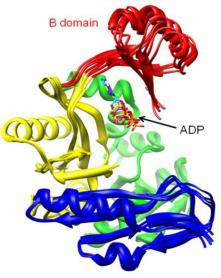


Fig. 2. Four molecules of TmPurK