

Thermus thermophilus HB8 タンパク質の機能発見研究：
機能未知タンパク質 Universal Stress Protein の X 線結晶構造解析

Functional identification of protein from *T. thermophilus* HB8:

Crystal structural analysis of universal stress protein

飯野均¹, 海老原章郎¹, 広津健^{1,2}, 倉光成紀^{1,3}

Hitoshi Iino¹, Akio Ebihara², Ken Hirotsu^{1,2}, Seiki Kuramitsu^{1,3}

(¹理研・播磨研, ²大市大・院理, ³阪大・院理)

(¹RIKEN/Harima Inst., ²Osaka City Univ., ³Osaka Univ.)

e-mail: iino-h@spring8.or.jp

The universal stress protein (Usp) superfamily [Pfam PF00582 (Bateman *et al.*, 2000)] is characterized by a conserved domain consisting of 130-160 amino acids. More than 1,000 Usp proteins are found in various organisms of bacteria, archaea, and eukaryotes (Kvint *et al.*, 2003, Siegele, 2005, Weber & Jung, 2006). *Escherichia coli* harbors six proteins containing the Usp domain (Nachin *et al.*, 2005). These were induced under a large number of stress conditions; nutrient starvation, heat shock, oxidants, uncouplers, and DNA-damaging agents. However, the biochemical mechanism of Usp protein remains unknown.

The genome sequence of the extremely thermophilic bacterium *Thermus thermophilus* HB8, published by the Structural-Biological Whole Cell Project (www.thermus.org), revealed that five proteins belong to Usp superfamily. Two are in a single domain, two are in tandem, and one is a component of the probable potassium uptake protein trka. TTHA0895 is a single domain Usp protein from *Thermus thermophilus* HB8 and consists of 137 amino acids residues with a molecular mass of 14759 Da.

In order to analyze the structural properties, TTHA0895 was crystallized in the absence and presence of ATP, respectively. The form I, crystallized in the absence of ATP, belongs to the tetragonal $P4_32_12$ with unit-cell parameters $a = b = 73.1$, $c = 57.9$ Å, and the form II, crystallized in the presence of ATP, belongs to the orthorhombic space group $I222$ with unit-cell parameters $a = 33.1$, $b = 75.1$, $c = 88.7$ Å. The crystals probably contain one monomer in the asymmetric unit. X-ray data have been collected to 1.65 and 1.55 Å resolution for forms I and II, respectively.

Here we report X-ray structures of the biological units in two forms, and the possible ATPase activity of TTHA0895.