Cloning and Expression of Hyperthermophilic *Aeropyrum pernix* K1 Archaea Chaperonin A in *E. coli*

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Chaperones, such as the GroE complex of the bacteria *E.coli*, assist the folding of proteins under non-permissive folding conditions by providing a cavity in which the newly translated or translocated protein can be encapsulated. Recently, the genome sequence of hyperthermophilic archaeon *Aeropyrum pernix* K1 was identified and revealed an existence of a gene which had high sequence similarity (63%) to the gene encoding the thermosome A (*ths A*) gene in *Pyrodictium occultum.* The archaea chaperonin gene from *Aeropyrum pernix* K1 comprises an open reading frame of 1,871 bp, encoding a polypeptide of 557 amino acid residues. The archea chaperonin gene (cpn*A*, 1,871 bp ORF) from *A. pernix* K1 genome was amplified by PCR and subcloned into the pET3d vector. When the plasmid pET-3d-cpnA (6.1 kb) expressed by using *E. coli* Rosetta (DE3), the transformant cell was grown on LB plate containing 50 mg/ml ampicillin. The molecular weight of the recombinant protein was estimated to be 60.7 kDa by SDS-PAGE. In order to analyze proteome in *E. coli,* the recombinant *E.coli* protein was treated by heatshock at 70 ~ 90℃ for 20min, resulting in higher than 80% of purification yield of cpnA. The biochemical characterisitics of including ATPase activity of cpnA will be reported.