Cystathionine γ-synthase from Thermoacidophilic Archaeon, *Sulfolobus tokodaii* strain 7.

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*Sulfolobus tokodaii* strain 7 is an aerobic thermoacidophilic crenarchaeon. The strain was isolated from Beppu hot spring in Kyusyu, Japan in 1983. The complete genomic sequence of this strain has been determined by the whole genome shotgun method. The genome contained 2826 potential protein-coding regions (open reading frames, ORF)\(^1\). There is an ORF of cystathionine γ-synthase (CGS, EC 4.2.99.9) in *Sulfolobus tokodaii* strain 7. CGS catalyses the first step in transsulfuration, a pyridoxal 5’-phosphate (PLP) dependent γ-replacement leading to the formation of L-cystathionine from a homoserine ester and L-cysteine. The enzymes are attractive targets for the development of new antimicrobials and herbicides. The ORF of stCGS contains 1134 bp (377 aa). The homology of stCGS with ecCGS (CGS from *E. coli* \(^2\)) and ntCGS (CGS of *Nicotiana tabacum* \(^3\)) are 34% each. stCGS was expressed without complications to high levels in *E. coli* Rosetta-gami (DE3), using a plasmid vector pET-ST0506 (cloned cgs gene with pET-11a). Recombinant stCGS was purified to homogeneity by heat treatment, DEAE column chromatography and gel filtration. The result of the characterization revealed that its pH stability and optimum pH are at pH 5-9 and pH 7, respectively. The subunit molecular mass of the gene product (stCGS) was estimated by SDS-PAGE to be approximately 42,000. The relative activity to γ-elimination substrates (O-succinylhomoserine, O-acetylhomoserine, methionine sulfone, vinylglycine) and β-elimination substrates (O-phosphoserine, cysteine, β-chroloalanine) are 100, 35.0, 15.9, 954, 31.1, 26.3 and 105%, respectively. stCGS was stable, when it was treated at 80 °C, for 30 min. The high thermostability could contribute to further development of this enzyme as a prodrug. The crystal structure of stCGS has been partially solved by molecular replacement with the known structure of ecCGS (PDB ID:1CS1), and refined at 2.5 Å resolution. The overall structure is very similar to other PLP-dependent enzymes of γ-family\(^4\)\(^5\).