

Crystallographic Study of Fructokinase from *Sulfolobus tokodaii* strain7

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Fructokinase (FK) (ATP:D-fructose-6-phosphotransferase, EC 2.7.1.4) catalyses the phosphorylation of fructose-6-phosphate with ATP. This enzyme is essential for removing fructose to prevent the reverse reaction, in glycolytic pathway. The crystal structures of FK were reported only for prokaryote, *Bacillus subtilis* and *Salmonella enterica*. To reveal the tertiary structure of FK from an Archaea *Sulfolobus tokodaii* strain7, we have performed X-ray analyses of the protein. *Sulfolobus* FK produced in *E. coli* was purified by column chromatography, and crystallized. X-Ray diffraction data taken at 100K show that there are two forms with $P2_12_12_1$ and $P6_122$. Their initial crystal structures were derived by molecular replacement with 2-keto-3-deoxygluconate kinase from *Thermus thermophilus*, and refined to 2.8Å and 1.85Å resolutions, respectively. The two tertiary structures are similar to each other, but quite different from that of *Bacillus* FK with a little bit high sequence identity (29%). The present structures are rather similar to *Salmonella* FK though the sequence identity is low at 27%. An interesting feature is that although the function is different from *Thermus* 2-keto-3-deoxygluconate kinase, but the two tertiary structures are similar at higher sequence identity (35%).

Keywords: fructokinase, *sulfolobus tokodaii* strain7, x-ray crystal structure analysis