Crystal Structure of a Conserved Hypothetical Protein TT1657 from *Thermus thermophilus* HB8

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Thermus thermophilus HB8 is a good model to study the structure-function relationships. Because its proteins show high thermostablility, it is easier to solve their tertiary structures and the collection of structures will give sufficient information to study the structure-function relationship comparatively.

Here, we studied one of the *Thermus thermophilus* hypothetical proteins, TT1657, by the X-ray crystallography. The crystal structure was solved by the Se-MAD method. This protein forms dimer in the crystal and it is consistent with the result of the gel filtration experiment. Although BLAST search indicated that this protein has higher homology with some hypothetical proteins and weaker homology with phosphoesterases and phosphatases, DALI search shows high structural homology with some of phosphatases.

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