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| ESRF | **Experiment title:**<br>Structural studies of proteins with potential for antibiotic targets and clinical diagnosis | **Experiment number**:<br>LS 2144 |
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## Report:

**Crystal structure of *Pyrococcus furiosus* phosphoglucose isomerase: Implications for substrate binding and catalysis**

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**Abstract**
Phosphoglucose isomerase (PGI) catalyses the reversible isomerization between D-fructose-6-phosphate and D-glucose-6-phosphate, as part of the glycolytic pathway. PGI from the archaeon Pyrococcus furiosus (Pfu) was crystallized and its structure determined by X-ray diffraction to 2Å resolution. Structural comparison of this archaeal PGI with the previously solved structures of bacterial and eukaryotic PGIs reveals a completely different structure. Each subunit of the homodimeric Pfu PGI consists of a cupin domain whose overall structure is similar to other cupin domain containing proteins and includes a conserved transition metal binding site. Biochemical data on the recombinant enzyme suggests that $Fe^{2+}$ is bound to Pfu PGI. However since catalytic activity is not strongly influenced by either the replacement of Fe(super2+) by a range of transition metals, nor by the presence or absence of the bound metal ion, we suggest that the metal may not be directly involved in catalysis, but rather may be implicated in substrate recognition.