Crystal Structure of a Protein Disulfide Oxidoreductase from *Aquifex Aeolicus*

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Protein disulfide oxidoreductases (PDOs) are ubiquitous redox enzymes that catalyse dithiol-disulfide exchange reactions. These enzymes include the families of thioredoxin (TRX), glutaredoxin (GRX), protein disulfide isomerase (PDI), disulfide bond forming (Dsb) and their homologues. In 1995 a hyperthermostable PDO has been purified from the archaeon *Pyrococcus furiosus* (*Pf*PDO). This protein has an unusual molecular mass of 26 kDa, compared to the small sizes of most GRXs and TRXs, and its amino acid sequence shows no overall similarity to previously studied PDOs. Interestingly, it presents two active sites with the conserved CXXC sequence motif. The resolution of its three-dimensional structure revealed important conformational details suggesting that *Pf*PDO may be related to the PDI, known only in eukaryotes.

Comparison of the genomes from archaea and bacteria showed the existence of a group of redox proteins similar to *Pf*PDO. The unusual features of these enzymes suggest that they could constitute a new family of PDOs. We have recently focused our attention on a protein isolated from the thermophilic bacterium *Aquifex aeolicus (AaPDO)* and belonging to this putative new enzyme family. In order to provide insights into the function, structural diversity and evolution of PDOs, a structural and functional study on this protein has been carried out. **Keywords: crystal structure, PDO, thermostable enzymes**