Crystal Structure of Hyperthermostable Thioredoxin Peroxidase from *Aeropyrum Pernix* K1

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Thioredoxin peroxidase from an aerobic hyperthermophilic archaeon, *Aeropyrum pernix* K1, (ApTPx) participates in the thioredoxin system, which is an antioxidant system to reduce hydrogen peroxide. ApTPx belongs to the peroxiredoxin family. We determined the crystal structure of ApTPx at 2.0 Å resolution. The overall structure is a decameric ring consisting of five homodimers with outer and inner diameters of approximately 130 and 50 Å, respectively. The monomer structure can be divided into two domains, a main domain and an arm domain. The arm domain is characteristic to ApTPx among peroxiredoxins. The redox active resolving cysteine is located on the arm domain and occupies the characteristic position when compared with mesophilic peroxiredoxins. A dimer interface is created by interaction between main domains. The dimerization results in formation of an intersubunit β-sheet. The arm domains stick out of the main body of the dimer. Assembly of homodimers to form a decameric ring is contributed by two types of interactions, one is by main domains and the other is by main and arm domains, latter of which is solely observed in ApTPx. Higher proportion of the monomer surface is buried in the decameric ring of ApTPx compared with mesophilic peroxiredoxins, suggesting that the high affinity in the protein complex contributes to the hyperthermostability of ApTPx.

Keywords: peroxiredoxin, *aeropyrum pernix*, thioredoxin system