Structural studies of the peroxiredoxin AhpE from *Mycobacterium tuberculosis*

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Peroxidases of the peroxiredoxin (Prx) family reduce hydrogen peroxide and alkyl hydroperoxides to water and alcohol. Members of this family have been identified in a variety of organisms from bacteria to plants and mammals.
Peroxiredoxins act in the regulation of reactive oxygen intermediates levels in cells and tissues, protecting them against oxidative stress. They also play an important role in various physiological and pathological processes including metabolism, immunity, inflammation, cell signaling and apoptosis. Peroxiredoxins are divided into three classes: 2-Cys Prxs, atypical 2-Cys Prxs and 1-Cys Prxs. All Prxs share the same basic catalytic mechanism, in which an active-site cysteine (N-terminal) is oxidized to a sulfenic acid by the peroxide substrate. The recycling of the sulfenic acid back to a thiol is what distinguishes the three enzyme classes. The *Mycobacterium tuberculosis* genome show the presence of at least four members of the Prx family, namely bacterioferritin co-migratory proteins Bcp and BcpB and alquil hydroperoxide reductases AhpC and AhpE. Proteins involved in the mycobacterial antioxidant defense system have been proposed as good targets for antituberculosis drug development.
M. tuberculosis AhpE was overexpressed in *E. coli*, purified and submitted to crystallization trials. X-ray diffraction data were collected using synchrotron radiation. AhpE 3D structure was solved by molecular replacement methods and refined at 1.85 Å resolution. Active site analysis showed some conformational differences associated to the redox state of the enzyme. AhpE belongs to the 1-Cys Prx group, the less characterized class of peroxiredoxins. Structural comparisons with other peroxiredoxins can contribute to a better understanding of the mechanism of action of this enzymes' family.

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