Effecting the antioxidant defenses of *Mycobacterium tuberculosis*

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**Abstract:** Tuberculosis (TB) is one of the leading contagious diseases that cause mortality. In *Mycobacterium tuberculosis* (*Mtb*) strains that are resistant to isoniazid, the primary antibiotic for TB treatment, it was found that there was an increased expression in alkylhydroperoxidase subunit C (*MtAhpC*). *MtAhpC* has several distinctive features, allowing it to serve as a good drug target. One such characteristic is present on the catalytic helix α3, which in contrast to other prokaryotic AhpCs, undergoes a significant upward rigid-body movement. In the current study, mutations on the *MtAhpC* helix α3 were carried out, to determine its crucial residues. Here, the importance of residue F68 of helix α3 in the movement of helix α3 is demonstrated, enabling the formation of a disulfide bond of the catalytic cysteine residues. These results in the current study provide valuable insights into the helix α3 of *MtAhpC*, thus allowing the establishment of a foothold on drug design. This then allows the application of molecular docking to identify a ligand that can target *MtAhpC* specifically, prior to chemical synthesis of the ligand.

**Keywords:** Tuberculosis; *Mycobacterium tuberculosis*; *MtAhpC*; Isoniazid-resistant tuberculosis