Structural and Dynamic Analysis of a Thioredoxin-motif containing protein from the Conjugative F plasmid of *Escherichia coli*

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The transfer of genetic material within a bacterial population through the process of conjugation is an evolutionarily conserved tactic by which novel genetic elements are distributed for survival in unique environments. The *Escherichia coli* F-plasmid houses all genes necessary for the assembly of its conjugative machinery to facilitate successful DNA transfer. These genes encode proteins that facilitate or make up parts of the F-conjugation complex including; pilus formation, mating pair formation (Mpf), DNA transfer complex and exclusion factors. The transfer proteins TraF and TrbB are hallmark proteins of F-like, and both contain thioredoxin motifs. Indeed recent bioinformatics and biochemical evidence indicates that TrbB is a disulfide bond isomerase closely related to DsbC. However TraF, essential for the assembly of the conjugative F pilus, does not contain the active site cysteines of thioredoxins; it retains an as yet undefined function independent of redox activity. While it is apparent that TrbB plays a role in the redox chemistry of the F T4SS, how TraF functions remains unclear. In order to characterize the structural differences between these two thioredoxin-motif containing T4SS proteins, TraF has been analyzed crystallographically (space group C2; a = 119.87 Å, b = 34.36 Å, c = 46.21 Å and β = 90.40°, and crystals diffracted to 2.3 Å resolution, and through time-resolved hydrogen deuterium exchange mass spectrometry.