# Towards The Structural Analysis of An F-Plasmid Protein, TraW

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The process of bacterial conjugation, often referred to as lateral gene transfer, is an important process in the evolution of bacteria for growth in unique environments and is a main route for the development of multi-drug resistant bacteria in health care settings. Bacterial conjugation is a contact dependent mechanism, one which can be achieved through the type IV secretion system (T4SS). The transfer of mobile DNA elements like virulence factors, genes for antibiotic resistance as well as many others are achieved through this conjugative system. This multiprotein complex spans the inner and outer membrane of gram-negative and gram-positive bacteria and as well as some archaea. The T4SS is able to produce many different pili that are able to extend to neighbouring cell and retract drawing them in closer to form a mating bridge to allow for conjugation to occur.

There are many proteins involved in this process, one being TraW which plays a role in pilus assembly and is specific to the F plasmid from Escherichia coli, an important conjugative plasmid. Mutations in traW have shown to abolish the ability of cells to form extended F pili. It has also been shown that the N-terminal domain of TraW interacts with the C-terminal domain of TrbC and that this interaction is essential for conjugative DNA transfer to occur.

By removing the flexible portion of TraW needed for binding to TrbC, or the disordered region of the protein found at the N-terminal, this resulted in a more stable protein deltaTraW. Here we show a bead model of deltaTraW in solution by fitting the experimental data resulted from small angle x-ray scattering to an AlphaFold model of the mutated form.