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Hydrophobic Amino Acid Patch is Critical for the Stability of the N-Terminal Domain of the Bacteriophage P22 Tailspike Protein

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The homotrimeric P22 tailspike protein (TSP) is the receptor binding protein for the *Salmonella* bacteriophage P22. It is the terminal protein to be added to the assembling virus to complete its assembly process. The P22 virus TSP is also involved in bacteriophage infection by binding to the initial receptor, host lipopolysaccharide. Although all functions of the TSP are of interest, the N-terminal domain (NTD) of the TSP is required for terminal assembly binding. This trimeric TSP NTD takes on a dome-like shape and this dome shape requires three hydrophobic amino acids. The presentation describes how this fact was determined.

Biography:

Dr. Villafane obtained his bachelor and doctoral degrees from the New York University and his Masters Degree at the University of California at Berkeley. His postdoctoral studies were carried out the Massachusetts Institute of Technology. Dr. Villafane is currently Professor of Microbiology at the Alabama State University in Montgomery, Alabama, USA. His laboratory has studied how bacterial viruses and their proteins fold and how they assemble and interact with the cell surface to infect the cell.