Proteins are essential molecules which, upon synthesis in the cell, are in the form of a linear assembly of amino acids. In order to become biologically active, these linear assemblies must fold into a unique three-dimensional structure. This process is promoted by a special class of proteins, called the molecular chaperones. One of the most important molecular chaperones is the GroEL-GroES complex of the *Escherichia coli* bacterium. When this bacterium is infected by viruses, the viral proteins which constitute specific parts of the virus such as the head (capsid) and the tail are folded by the GroEL-GroES chaperone complex. Conversely, bacteriophage T4 uses a chaperone complex consisting of the host’s GroEL and gp31, from the bacteriophage itself. This hybrid complex is essential for the folding of the phage capsid.

During her doctoral studies, Stéphane Calmat studied the dynamics and mechanism of the chaperone-assisted folding of the capsid protein using fluorescence spectroscopy. She determined the time that the capsid protein needs to bind to the chaperonin complex, acquire its three-dimensional structure inside of the folding cavity and release from the complex afterwards. Her research shows that the capsid protein of bacteriophage T4 is the fastest-folding of all the proteins studied so far with the GroEL chaperone.