During my PhD at EMBL Hamburg I concentrated on the development and the application of tools for the structural characterization of flexible systems i.e. natively unfolded proteins and proteins with large loops with no well-defined secondary structure using small angle scattering (SAS). More specifically, I participated in the development of the Ensemble Optimization Method and subsequently applied it on the structural analysis of the natively unfolded protein tau, responsible for the Neurofibrillary Tangles in the brains of patients with Alzheimer's disease. Even though the protein effectively lacks secondary structure, it was shown that it has distinct structural features that are important to its physiological function as well as its aggregation. Another notable project was the solution of the structure of the full length tumor-suppressor protein p53, employing a combination of data from X-ray crystallography, Nuclear Magnetic Resonance, Electron Microscopy and SAS.

My focus while working at Spring-8 Japan was the structural characterization of non-viral gene delivery systems, more specifically cationic micelles. The calix[4]arene-based systems that we investigated exhibited shape persistence, i.e. the micelles consist of a well-defined (and small) number of molecules. We analyzed the data with a combination of rigid body modeling and molecular dynamics simulations and found that the micelles are hexamers and even though the molecules are highly positively charged they are arranged in unusually rigid cubic structures.