We combine x-ray crystallography and biophysics with molecular simulation to study the structure, folding and dynamics of proteins, with a particular focus on the design and engineering of proteins for medical and biotechnological application. Our team is a unique and exciting mix of experimentalists and computational biologists using modeling and simulation to make predictions that can be tested in the lab.

Research Projects

1. Designing potent protease inhibitors as potential anti-cancer agents
2. Using computational and experimental methods to design and evolve novel proteins
3. The evolution of protein dynamics

Selected significant publications: