In the last half century, computers have revolutionized science by allowing us to test models in silico, offering a point of view of nature that is complementary to the experimental approach. In the field of biophysics, computer simulations allow us to understand the mechanism of function of biomolecules, and to interpret experimental observations and generate new predictions.

One example of the complementarity of experiments and simulations is offered by the copper protein azurin, which serves as a model to understand the dependence of the copper redox potential on the local environment. Although a wide range of redox potentials is observed in azurin’s variants, these appear structurally almost identical by x-ray crystallography. Using molecular dynamics simulations, we show that the distance of the copper from its carbonyl axial ligand can explain the differences in reduction potential of these variants. We find that the copper-carbonyl distance increases in variants that show bulkier mutations in the hydrophobic core due to steric clashes with other residues.

Another focus of our research involves the protein dystrophin, a large protein whose primary role is to protect the muscle cell membrane against the mechanical forces deriving from muscle contraction. It is hypothesized that the protein’s protective role is achieved through the unfolding of its spectrin repeat domains when subject to mechanical stress. In this work, we have characterized the interplay between the changing protein structure as it unfolds, and the structure and dynamics of the surrounding solvent. Our results show that changes in the protein’s surface curvature and hydrophobicity lead to a more ordered water layer that displays faster dynamics.