Summary

In my dissertation I present two studies in computational chemistry. The first examines the partial unfolding of an enzyme in urea. The enzyme cytochrome c reacts with peroxides, but normally this “peroxidase” property is weak. However, the solvation in urea leads to a 1000-fold increase of the peroxidase activity. Urea loosens the structure of the protein and thus makes the active site inside the protein more accessible for the peroxides, leading to a higher reaction rate. My simulations of cytochrome c in urea showed the partial opening of the reactive site. At the same time the overall structure of the protein remained intact, allowing it to return to its original, less active state when the concentration of urea is lowered. This may enable the recycling, stable storage and multiple activation of cytochrome c peroxidase for industrial application.

The second study investigates the structural changes of a viral protein under acidic conditions. Many viruses are enveloped hollow particles covered with proteins. At acidic pH these proteins transform and enable the virus to merge with the host cell and infect the host. Histidine is a small component of proteins that is sensitive to the acidic pH at which the infection takes place. My simulations of a viral envelope protein showed that the local changes of the histidines at acidic pH are capable of triggering irreversible and global rearrangements in the protein. These may be important for the merger of the virus with the host cell and therefore for infection.