

# Intermolecular Interactions in Proteins - Abstract

**Mgr. Jiří Kysilka**

Non-covalent interactions are responsible for the protein folding and the molecular recognition during the protein interaction with other molecules, including various ligands, other proteins and solvent molecules.

In order to understand these processes, exhibited by protein molecules, a proper description of non-covalent interactions is needful. Most methods that are computationally available for the systems of biological interest have difficulties handling with the dispersion term. In this thesis, a density functional theory / coupled clusters (DFT/CC) correction scheme is utilized for a set of small molecules, interacting with a graphitic surface. The results serve as a benchmark for the interaction of the functional groups of proteins with hydrophobic environment.

In the following part of this thesis, the role of non-covalent interactions in proteins was studied for the processes of protein-protein interaction and protein hydration. Interaction interfaces has been localized in a set of 69 protein dimers and their composition has been characterized. Interfaces has been shown to prefer branched-chain hydrophobic amino acids (Ile, Leu, Val), aromatic amino acids (Phe, Tyr) and exclude the charged amino acids except of Arg. It was demonstrated that the relative preferences for choosing interacting partner are similar for amino acids at the interfaces and in the protein interior. However, the interaction of interface pairs is systematically stronger. These results can be directly utilized for the proposed interface localization algorithm.

Protein hydration structure has been studied on a T4 phage lysozyme as a case study protein. Its multiple records in the protein databank were utilized in the superposition and clustering algorithms. 224 distinct water binding sites – water clusters – were localized and their interaction with the protein was examined. Water clusters has been shown to prefer oxygen atoms to nitrogen atoms, while interacting with backbone and side-chain atoms to a similar extent. Moreover, water clusters prefer binding to protein atoms unsaturated with their internal hydrogen bonds. Although there was no clear correlation between the occupancy of a water cluster and its interaction energy, the high occupancy of a water cluster seems to be connected to the high overall number of cluster hydrogen bonds.