**Structure determining methods for describing the structures and interactions of intrinsically disordered proteins**

Our aim is to combine complex biophysical and functional studies of proteins with the determination of secondary structure by CD spectroscopy. The generally used CD spectrum analysing programs often overestimate the beta-structure content of the samples, making the study of disordered proteins problematic. The new CD spectrum analysis algorithm is suitable to differentiate between beta structures and true structural disorder, giving a more reliable estimate of the two structural components. Through the analysis of the binding motifs of IDPs, we were able to improve the algorithm to give even more accurate results in the secondary structure determination.

During our collaboration we studied the p53-mdm2 binding and the secondary structural changes that occur in the TAD region of p53 upon binding. We concluded that although both the wild-type and mutant TAD region are disordered in the free form, the wild type TAD has a higher alpha-helical propensity than the mutant TAD, influencing the capability of mdm2 binding.