RNA molecules are no longer seen as a passive element transferring the genetic information from DNA into protein but are involved in almost all aspects of the cell physiology. This attracted the researchers' attention especially to structure-function relationship of the RNA molecules. Crystallography is a powerful technique for characterisation of the structure of biomolecules, which is a key to understanding their function. Crystallographic structures are real atomic models of investigated molecules. They can be used to understand mechanisms of reaction, characterize interactions with small ligands (potential drugs) or track assembly of large complexes. Crystallography is routinely used for structure determination of proteins. Unfortunately in case of RNA (especially RNA hairpins) crystallographic analysis is difficult. Although hairpins are the most common motif found in all RNA molecules they are not easily available for crystallography due to thermodynamic instability.

This project focuses on development of innovative methods for stabilisation of RNA hairpins by applying complementary approaches taken from organic chemistry and biochemistry of nucleic acids. The proposed methods are simple and efficient. They do not require special equipment and can be performed in almost every laboratory. By applying our techniques it will be possible for the first time to study any RNA hairpin by crystallography. The results will add a meaningful contribution to the basic knowledge of nucleic acid structures. Additionally, they will help in understanding the structural aspects of the RNA hairpins in pathogenesis of human disorders. The crystallographic models will be useful to researchers for interpretation of available functional data and in the future for structure-based drug design which will accelerate development of effective therapies.