The Scope of the thesis

The thesis provides in-depth presentation of my characterization of the structural and dynamical studies of the *Escherichia coli* transcription elongation factor, NusA, and the translesion DNA polymerase IV, DinB, as well as structural basis of NusAs role in transcription-coupled DNA repair (TCR) using advanced high-resolution solution-state nuclear magnetic resonance (NMR) spectroscopy and other complementary biophysical and biochemical methods. The thesis is divided into five chapters, as follows:

- **Chapter I: Introduction.** A brief review of the thesis literature background.
- **Chapter II: Methodology.** Description of the methodology basis of the research approach used in the thesis.
- **Chapter III: Results, Discussion.** Highlights of the major findings in the individual projects and their significance in advancing previous knowledge.
- **Chapter IV: Future perspectives.** Outlook for possible future studies to clarify questions raised by my results.

In addition to the above sections, the thesis also includes the following four papers.

- **Paper I (Manuscript)** elucidate the structural dynamics underlying the *Escherichia coli* transcription elongation factor, NusA, it's autoinhibition, and reveal how autoinhibited isolated free NusA is functionally activated.
- **Paper II (Submitted)** Reveals intrinsic dynamics of translesion DNA polymerase IV (DinB) Thumb domain studied under high-resolution solution-state NMR. Also, the underlying binding kinetics that govern DinB-interactions with DNA as well as RNA polymerase core are presented.
- **Paper III (Manuscript)** provides a detailed structural study of the interaction complex of NusA and the translesion DNA polymerase IV (DinB) including binding kinetics, which is a crucial event in the initial stages of the translesion synthesis DNA repair process.
- **Paper IV (Manuscript)** investigates the interaction between NusA and the UvrD helicase during transcription-coupled DNA repair, with structural characterization of the interaction interface together with the apparent binding kinetics.