Revealing the DNA loading mechanism during the initiation of the transcription of RMA polymerase II

Jeremy Lapierre[1], Pr. Jochen Hub[1]
[1]*Computational Biophysics Group, Theoretical Physics, Saarland University, Saarbrücken, Germany*

The RNA polymerase II is a cornerstone of the central molecular biology dogma, as it is the enzyme allowing the transcription of DNA to RNA, from which protein translation (by mRNAs) and molecular regulation (by non coding RNAs) are possible.

Therefore, understanding the underlying mechanism of this macromolecular complex is of paramount importance for sharpening our comprehension of life.

This study aims to reveal the transition between the open and close conformation of the DNA within the RNA polymerase II, during the initiation of the transcription.

To do so, we will use molecular dynamics (GROMACS engine) and enhanced sampling methods to be able to capture such an important conformational change. Furthermore, with respect to the use of sampling algorithms, a new reaction coordinate will also be studied. This new reaction coordinate will be implemented thanks to the PLUMED software. Therefore, we intent to be able to derive the pathway of this conformational transition and its free energy landscape.

Finally, particular attention will be given to the TFIIE transcription factor, to understand how it drives DNA opening and its influence on Pol II cleft obstruction in the closed complex.