Contribution of the Bicoid domains to the dynamics of *hunchback* expression boundary establishment in Drosophila

In many biological systems, morphogenetic gradients are essential for the establishment of axial polarity: they act as source of positional information which allow each cell to activate in a dose-dependent manner the expression of target genes responsible for the determination of its identity. Bicoid (Bcd) is the main morphogen involved in the formation of antero-posterior (AP) axis of the fruit fly embryo. The team adapted to living embryos the MS2-MCP system which allows fluorescent tagging of nascent RNA accumulation at their locus of synthesis. Building up with the MS2 system, a recent study of the team used a synthetic approach to decipher, at the mechanistic level, the functioning of Bicoid and its two partners Hunchback (Hb) and Zelda (Zld) in the *hb* promoter, the main Bcd target gene. These recent results allow developing a model of transcription activation downstream of Bcd gradient which involves several mechanistic steps.

The Bcd protein, which is highly involved in the transcription activation mechanism, is a protein of 489 amino acids, composed of 7 identified functional domains. Most of the activation domains of Bcd have highly disordered structures and it is unclear if they have a similar function in the transcription process or if they contribute to different mechanistic steps identified previously. My project aims to decipher the contributions of different Bcd domains to the various mechanistic steps of the transcriptional response downstream of Bcd by deleting these domains endogenously. I performed analysis on the function of the Bcd C-terminal domain in *bcd-ΔC* mutant. With the help of MS2-MCP system, preliminary information about functions of the C domain are extracted.