Our research aims to examine the role of proteins called NAPs (nucleoid associated proteins) in the regulation of bacterial gene expression. NAPs bind DNA to organize bacterial chromosomes and increase their compaction. Binding of these proteins to DNA is believed to modify the accessibility of DNA to transcription factors and RNA polymerase - the proteins that control gene transcription. Additionally, binding of NAPs to DNA is alleged to be influenced by physiological state and stress conditions, which in this way affect the expression of bacterial genes. The proposed project will examine the influence of NAPs on gene expression in soil bacteria – *Streptomyces*.

Streptomyces are appreciated as producers of a variety of bioactive compounds, including antibiotics. Markedly, these valuable bioactive compounds are rarely effectively produced at optimal growth conditions. That is because their production is strictly regulated by complex mechanisms that bacteria use to adjust to growth conditions. Some NAPs were already shown to be involved in such regulation. Here, we will dissect the interplay between the NAPs and other transcriptional regulators in the control of gene expression with particular focus on the genes encoding biosynthetic pathways for bioactive compounds.

To answer our research questions, we will employ techniques based on next generation sequencing that allow to assess the global transcriptional activity of the cell, to determine the binding of transcription factors to DNA or to analyse the whole chromosome organisation. Additionally, we will also use microscopy-based analyses including high-resolution microscopy to examine chromosome structure and protein binding to DNA. We will study the chromosome structure and gene expression using the above-mentioned techniques in the wide set of carefully designed modified *Streptomyces* strains under optimal and stress conditions. We will also verify if elimination of NAPs from Streptomyces strains may increase the production of bioactive compounds, such as antibiotics.

Our studies will deliver an unprecedented systematic and comprehensive insight into bacterial chromosome organisation and its impact on gene expression. They are also expected to elucidate the complex regulatory network that control the production of highly valued bioactive compounds.