Recent reports show that bacterial chromosome exhibits a hierarchical organization, similarly to the eukaryotic chromatin. However, bacterial chromosome undergoes constant topological rearrangements due to the ongoing DNA replication, transcription and translation processes. Organization of this dynamic and highly compacted structure is mainly a result of action of many different DNA-binding proteins; topoisomerases, condensins and small, basic nucleoid-associated proteins (NAPs).

The *Mycobacterium* genus encompasses human (e.g., *Mycobacterium tuberculosis*) pathogens that have enormous impact on global health. A major challenge in the treatment of tuberculosis arises from the distinctive cell biology of mycobacteria. Unlike other rod-shaped bacteria, mycobacteria grow apically and divide asymmetrically.

We currently know little about the organization of the mycobacterial chromosome and its dynamics during growth and under different conditions including adaptation to a hostile environment (e.g., macrophages). We hypothesize that a diverse and specific repertoire of mycobacterial DNA-binding proteins (i.e., NAPs and condensins) that shape chromosome structure is dedicated to helping the cell adjust to different growth phases and conditions.

We plan to answer the following questions:

(1) What is the role of NAPs in shaping chromosome structure during different growth phases and under unfavorable conditions?

(2) How do the condensins cooperate with NAPs in a global effort to maintain the chromosome structure during growth of the asymmetrically dividing mycobacteria?

(3) How are the mycobacterial chromosomes equally divided between uneven daughter cells?

We believe that answering these questions will provide mechanistic insights into processes that ensure the maintenance of proper chromosome structure under different conditions, including unfavorable environments and govern chromosome separation in asymmetrically dividing mycobacterial cells.