

### Understanding chromatin dynamics in antigenic variation

Using the protozoan parasite *Trypanosoma brucei*, the causative agent of African sleeping sickness, our research aims to elucidate some of the very fundamental and evolutionarily conserved mechanisms of chromatin formation. At the same time we try to understand how changes in chromatin structure can help the parasite to evade the host immune response via antigenic variation. To this end we have established numerous system-wide approaches in *T. brucei*, including ribosome-profiling, high-resolution ChIP-seq and Hi-C technology as well as a mass spectrometry-based approach to quantify levels of histone acetylation. Using these techniques, we are able to investigate how different chromatin structures are established at specific loci along the genome, how they are formed across the nucleus in 3 dimensions and how they affect gene expression.

Key questions of our research are:

- How are histone variants and histone modifications targeted to specific genomic loci?
- How are chromatin, 3D genome architecture and gene expression linked?
- What role does regulatory ncRNA play in the regulation of gene expression?