Themen der AG Rehli für Masterarbeiten (MolMed/Biochemistry)

Interplay between chromatin remodeling machines and transcription factors.
This project addresses the fundamental question of how transcription factors establish access to their binding sites in chromatin. In previous work, we could show that the hematopoietic master regulator PU.1 requires its interaction with SWI/SNF to access binding sites in chromatin de novo. The current project aims at continuing this work to further characterize the remodeler interaction and to determine its functional relevance in hematopoiesis as well as compared to other ETS family factors.

Epigenetic variation between individuals: mechanisms of cis- and trans-regulation
It is generally accepted that epigenetic mechanisms contribute to phenotypic variability. However, the exact processes leading to inter-individual epigenetic differences are largely obscure. Besides being established by environmental influences, epigenetic differences between individuals may also be inherited, however, the relationship between epigenetic traits and inter-individual genetic differences is often unclear. By comparing two inbred mouse strains, we could show that strain-specific DNA methylation events partially controlled in trans, indicating the presence of strain-specifically acting epigenetic modifier genes. The project aims at identifying and characterizing a gene on chromosome 12 that confers strain-specific DNA-methylation during embryo development.

Genetic engineering of hematopoietic stem cells
The CRISPR/Cas9 technology offers unprecedented opportunities to manipulate signaling pathways or developmental programs via genetic engineering. In this project we aim at establishing protocols to genetically manipulate genes (e.g. by adding epitope-tags, replacing domains, etc.) in cord blood-derived hematopoietic progenitor cells, to study their effect on gene transcription, chromatin landscapes and lineage differentiation.

Contact: michael.rehli@ukr.de