Novel players in chromatin

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Abstract:
Post-translational modifications of histones and DNA define distinct chromatin or “epigenetic” states. The set of characterised histone modifications is far from complete and many modifications are awaiting identification and functional characterisation. Additionally, for many modifications it is still unclear how they act and how distinct “epigenetic” (or transcriptional) states are inherited through cellular divisions.

We are aiming i) to identify novel players in chromatin (in particular histone and RNA modifications) and to crack how they (mechanistically) regulate chromatin function, ii) to unravel how chromatin states can mediate “epigenetic” (or transcriptional) memory through cell divisions as well as iii) to understand how cellular metabolism impacts on chromatin architecture and hence transcription. For this we are applying a combination of chromatin biochemistry, different “omics” techniques, and single cell approaches as well as mathematical modelling in mouse models, mESCs and also yeast cells.

CV:
After obtaining a PhD at LMU Munich on the organisation of DNA in E. coli Robert Schneider joined the lab of Tony Kouzarides, Gurdon Institute, Cambridge, UK as PostDoc to study eukaryotic chromatin. There he got fascinated by histone methylation and how this modification regulates transcription. From Cambridge he moved to the Max Planck Institute for Immunobiology and Epigenetics, Freiburg to start his own group, broadening his interest towards novel sites and types of histone modifications and their role in chromatin dynamics and epigenetic reprogramming. In 2012 he was recruited as “Directeur de Recherche” to the IGBMC, Strasbourg where his team studied how core and linker histone H1 modifications mechanistically regulate chromatin function in healthy and diseased cells. Since 2016 he is head of the Institute of Functional Epigenetics at the Helmholtz Center Munich (HMGU) and Professor at the Faculty of Biology of the LMU Munich. The current focus of his team is on the mechanistic function of histone modifications and their links with cellular metabolism, epigenetic memory in single cells as well as RNA modifications.