Universität Regensburg

FAKULTÄT
BIOLOGIE UND VORKLINISCHE MEDIZIN
Institut für Biochemie, Genetik und Mikrobiologie

Universität Regensburg · D-93040 Regensburg

Prof. Dr. Joachim Griesenbeck
Telefon +49 941 943-2846
Telefax +49 941 943-2474
Universitätsstraße 31
D-93053 Regensburg

joachim.griesenbeck@ur.de
https://go.ur.de/griesenbeck

DFG-funded PhD position: "Studies on the role of RNA polymerase I -specific protein subunits in transcription in the chromatin context"

The Chair of Biochemistry III in collaboration with the Department of Structural Biochemistry at the University of Regensburg is looking for motivated and committed candidates for a DFG-funded PhD position (65% TV-L E13). The prerequisite is a completed master's degree in biochemistry, biology, or a similar degree program.

Please send applications to joachim.griesenbeck@ur.de. For further information see https://go.ur.de/griesenbeck.

The specific scientific doctoral thesis will focus on the role of Pol I specific protein subunits for transcription in the chromatin context. We use a variety of biochemical, genetic, molecular, cellular, and structural biology techniques to answer our questions.

Further information on the research topic

In the eukaryotic cell nucleus, the genetic information is encoded in the DNA sequence as a large nucleoprotein complex, the chromatin. The main protein components of chromatin are histone proteins, which form an octameric complex with the DNA so-called nucleosomes. The DNA complexed in nucleosomes is compacted and is not accessible for important nuclear processes such as transcription. The activity of genes can therefore be influenced by the chromatin structure. Chromatin undergoes dynamic changes to give the transcription apparatus access to the DNA. Our research aims to contribute to a better understanding of the interplay between chromatin structure and transcription. As a model system we investigate the transcription of ribosomal (r)RNA genes by RNA Pol I in *S. cerevisiae* (hereafter referred to as yeast).

In all eukaryotic cells, the DNA-dependent RNA polymerase I (Pol I), consisting of 14 protein subunits, is responsible for the transcription of an essential precursor of ribosomal (r)RNA. Although Pol I has only one target gene, the enzyme is responsible for over 60% of nuclear RNA synthesis in actively dividing cells. This enormous synthesis capacity is due to the efficient Pol I transcription machinery and multimerization of the rRNA genes. In yeast, about 150 rRNA genes are in tandem repeating units on chromosome XII. Interestingly, not all rRNA genes of Pol I are transcribed even in dividing cells. Thus, about half of the genes assume a nucleosome-depleted, transcribed, so-called "open" chromatin state and the remaining genes a nucleosomal, non-transcribed, "closed" chromatin state. The ratio between the two chromatin states can change dynamically. One focus of our investigations is to describe the function of Pol I subunits in the context of these chromatin remodeling processes.