



The IMB ([www.imb.de](http://www.imb.de)) is a research centre on the campus of **Mainz University, Germany**. It is generously funded by the Boehringer Ingelheim Foundation and the state of Rhineland-Palatinate. Our research focuses on the *biology of the cell nucleus* and ranges from the molecular level to systems and computational approaches. Researchers at IMB are supported by strong core facilities that offer state-of-the-art services in bioinformatics, cytometry, genomics, microscopy, proteomics, and protein production.

The group of **Falk Butter** is looking for a MSc. Student in Proteomics (start date negotiable).

Genetic information of genes are utilized by transcribing them into RNA and in most cases translated into proteins. Proteins are polymers that function in the majority of biological processes and thus, the knowledge of their expression is critical to understand cellular activity. Traditionally transcriptomics is used as a proxy to infer protein abundance in cells. However, mass spectrometry has become a powerful tool in studying the proteome at a quantitative level directly. This allows to gain information not just on induced transcriptomic changes, but also investigate translational effects of the absence of individual proteins, i.e. changing translation efficiency, protein stability or protein turnover.

#### **MSc. project: A proteomic screen in yeast**

You will conduct a quantitative proteomics screen on hundreds of yeast knockout strains. To this end, you will culture yeast knock-out strains in 96-well format and prepare protein lysate. The protein lysate will be digested and the tryptic peptides labeled with tandem mass-tags (TMT) to allow multiplex measurement of the proteome of several knockout strains in a single mass spectrometry run. You will measure the samples in a high-resolution mass spectrometer and do a preliminary analysis of the data, checking quality control and investigate proteome alterations.

We are looking for a highly reliable and meticulous student with very good organizational skills to keep track of hundreds of samples. Prior laboratory experience is expected, as we require highly reproducible and accurate pipetting skills with multichannel pipettes. You will work with other members of the group, thus good interpersonal skills are also necessary. In exchange, we provide the opportunity to gain experience in the planning and execution of a large-scale proteomics project including hands-on experience in mass spectrometry and bioinformatics data analysis.

**Please send your application (CV, Motivation Letter, University Degrees and Grade Transcripts) to [f.butter@imb.de](mailto:f.butter@imb.de).**

#### **References**

Matsuda et al. (2017) Targeted proteome analysis of single-gene deletion strains of *Saccharomyces cerevisiae* lacking enzymes in the central carbon metabolism. PLOS One, doi: 10.1371/journal.pone.0172742

Isasa et al. (2015) Multiplexed, Proteome-Wide Protein Expression Profiling: Yeast Deubiquitylating Enzyme Knockout Strains. J Proteome Res, doi: 10.1021/acs.jproteome.5b00802