

Instructor: Dr. Stefan Tholen, Proteomics Platform – Core Facility (ProtCF)

Timeline:

Initial Meeting / Theoretical Introduction

Date: November 4, 2022

Time: 09:00-13:00 h

Venue: Seminar room (2nd floor), Institute of Surgical Pathology, Breisacher Strasse 115a

Second Meeting

Date: ~ 2 weeks after initial meeting

Time: will be coordinated within working groups

Venue: Schilling lab (2nd floor), Institute of Surgical Pathology, Breisacher Strasse 115a

Number of participants: limited to 5-6 doctoral students

Content:

Proteins perform essential functions in the body and become deregulated in disease. The entirety of proteins present in a cell, tissue or other biological system is known as its proteome. The analysis of the proteome can help to get a better mechanistic understanding of research questions in health and disease.

Often, proteome analyses aim at one of the following questions:

- Which proteins are present in a biological system? (Protein Identification)
- How does protein abundance change during a biological process? (Quantitative Proteomics)
- Which post-translational modifications are present (phosphorylation, glycosylation, proteolytic truncation, etc.)?
- What are the interaction partners of a protein?

In this short course (for up to six students) you will get an overview about all stages of a proteomic experiment including experimental design, sample preparation, mass spectrometric measurement, and data analysis.

In the initial meeting, you will get a general introduction about proteomics and especially about sample preparation. In addition, we will discuss whether your own samples/experiments can be analyzed during this course. If not, we will provide samples. In the end of the first meeting everyone will get a "Sample Prep Kit" for sample preparation using the S-Trap sample processing technology. In the following two weeks every participant can perform the sample preparation in her/his home lab.

In a second meeting we will meet in small groups of 2-3 participants and start the mass spectrometric measurement. Furthermore, you will get an introduction about data analysis using MaxQuant.

