

Optimization of a high-throughput LC-MS/MS based method to quantify immunoglobulins in complex matrices

Immunoglobulins are amongst the most abundant plasma proteins that play an essential role in humoral immunity. They are structurally diverse, consisting of 5 isotypes which can further be subdivided in classes. Monitoring concentrations of global and antigen-specific immunoglobulin isotypes and subclasses can aid in diagnosis, monitoring of disease activity, and provide mechanistic insights into B-cell development. Immunoglobulin concentrations are usually quantified using immune-based methods, such as ELISA or Nephelometry. However, these methods lack molecular specificity and their quantification accuracy can be influenced by sequence polymorphisms and other proteoforms. Additionally, the multiplexing possibilities are severely limited. To this end, we have designed a multiplexed targeted LC-MS/MS method to quantify all immunoglobulins in the blood.

In this project we aim to optimize the sample preparation and LC-MS/MS method to facilitate high-throughput analysis of immunoglobulin concentrations in blood for (pre-)clinical research. The method will be validated in a cohort of clinical samples. During your internship you will work and get experience with state-of-the-art nanoflow liquid chromatography and high resolution mass spectrometry equipment, as well as the complex analysis and interpretation of your results. Therefore, an affinity for LC-MS/MS and protein analysis is preferred.

University students looking for a dynamic and interesting internship for at least 6 months are encouraged to contact:

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