Newsletter

2-2026

About this edition:

This issue features a recent research publication employing our QconCAT technology. We also take a closer look at the workflow behind these results, providing insight into how QconCAT reference standards contribute to targeted proteomics and absolute protein quantification projects.

You will also find information about an upcoming conference where we look forward to connecting with members of the scientific community, as well as news from our laboratory, as we welcomed our new FPLC, supporting our protein production unit.

Upcoming conferences – where to meet us next

We are looking forward to attending the Viruses of Microbes (VoM) conference, taking place in Prague from July 6th-10th, 2026.

The conference will feature research topics like virus-host interactions, therapeutic applications and bioinformatics for a scientific, clinical and industry audience and provides a great platform for networking and collaboration.

Research Highlight

Sex-based antibody subclass maturation drives direct enzymatic inhibition in fabry disease patients receiving enzyme replacement therapy

Baldwin T, Kurdi H, Doykov I, Robertson F, Rosmini S, Nordin S, Augusto J, Kozor R, Baruteau J, Davison J, Moreno-Martinez D, Ramaswami U, Vijapurapu R, Geberhiwot T, Steeds R, Moon J, Hughes D, Mills K, Heywood WE.
Front Mol Biosci. 2026 Apr 9;13:1702751.

Currently, Fabry disease patients are treated with enzyme replacement therapy (ERT) with recombinantly produced AGAL (alpha galactosidase A) forms. However, the patient's immune system can recognize these proteins as foreign and the resulting immune response reduces treatment efficiency.
To determine which antibody subclasses patients produce against ERT, Baldwin and colleagues developed a very sensitive assay employing LC-MS/MS. Supported by a custom-made QconCAT reference standard from PolyQuant they could measure exactly which antibody subclasses patients produce against enzyme replacement therapy.
This enabled them to determine absolute amounts for distinct antibody subclasses indicating different responses for IgG4 in male and female patients.

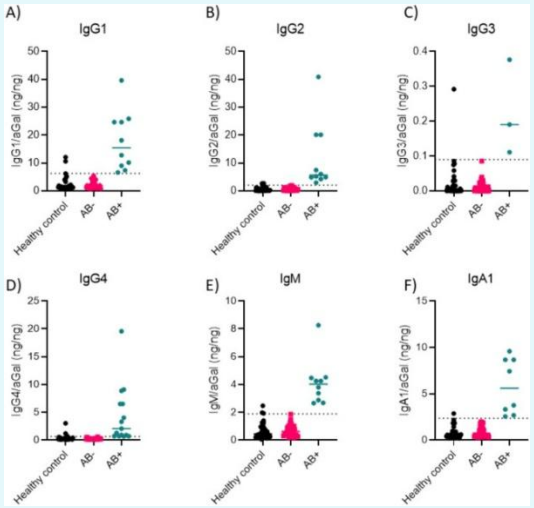


Figure 1: Proposed quantitative reference ranges for antibody subclass and isotype in FD adults using targeted LC-MS/MS.

Application Spotlight: How QconCATs are used in a typical workflow

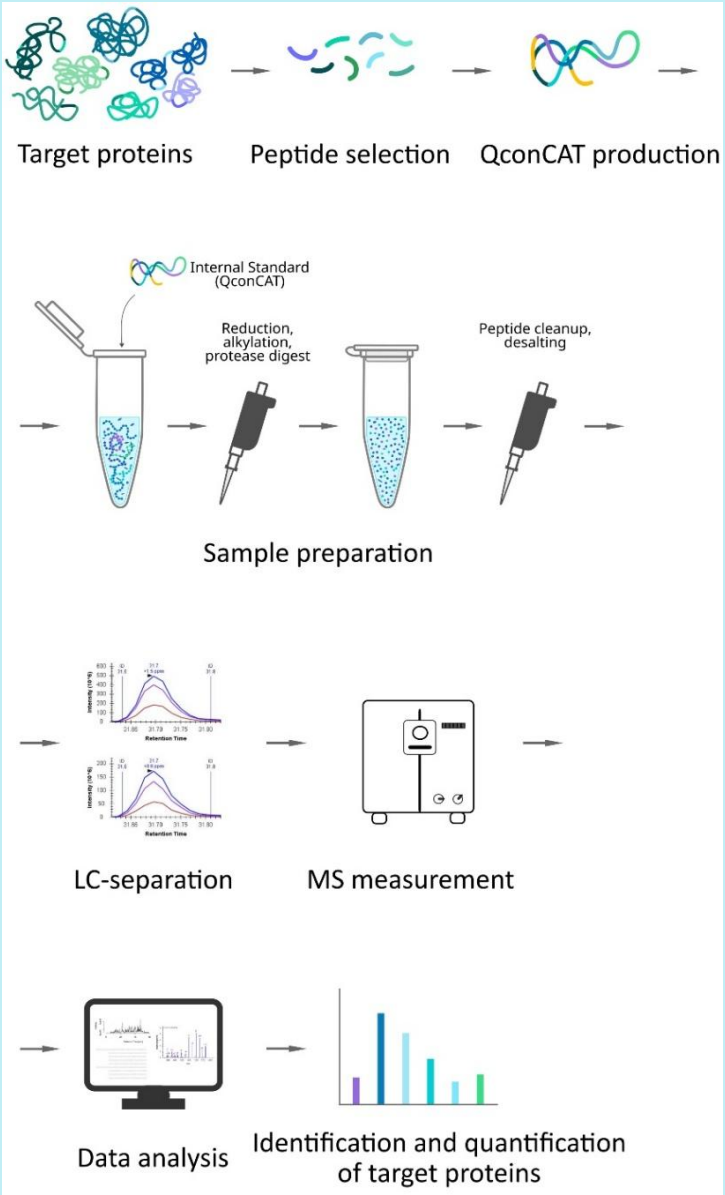
Seeing our technology contribute to new scientific findings is always exciting. This edition's research highlight is an excellent example of how isotope-labelled reference standards can provide valuable insights into highly specific research questions. We would like to take this opportunity to outline a typical workflow for absolute protein quantification supported by QconCATs and LC-MS/MS.

1) **Peptide selection and QconCAT production**
   Based on experimental data or *in silico* analysis of the target proteins, proteotypic peptides are selected and produced as a single protein, the QconCAT (Quantification conCATamer).

2) **Sample preparation**
   Spike your analyte sample with a defined amount of QconCAT reference standard and process the sample for LC-MS/MS analysis.
   Early addition of the internal reference standard enables you to control your sample preparation workflow, minimizing sample preparation bias.

3) **LC-MS/MS analysis**
   Separate the peptides by liquid chromatography and analyse them by mass spectrometry. Because the analyte peptides and the stable isotope-labelled reference peptides are chemically equivalent, they typically co-elute and can be distinguished in the mass spectrometer by a defined mass shift introduced by the isotopic label.

4) **Data analysis**
   High quality signals from QconCAT peptides facilitate identification of the target peptides and removal of noise. Quantify your target peptides by comparing the signal intensities of the reference peptides to the native counterpart, enabling you to calculate the absolute amount of each target protein in your sample.



Although often operating behind the scenes, stable isotope labelled reference standards help ensuring data accuracy and reliability of quantitative MS measurements. By being concatenated into a single protein, QconCATs enable researchers to add dozens of reference peptides in a single pipetting step to be released in a 1:1 ratio with kinetics comparable to the analyte peptides.
If you would like to learn more about our QconCAT reference standards and possible applications, we would be happy to discuss your specific requirements.

News from our Lab

Our protein production team received a new device: a brand new ÄKTA Go!
We would like to thank Cytiva for their support setting up the system to be used in our protein production and purification workflows but also in analytical projects.