



Newsletter

1-2025

About this edition:

This year we celebrate the **20th anniversary** of our QconCAT technology.

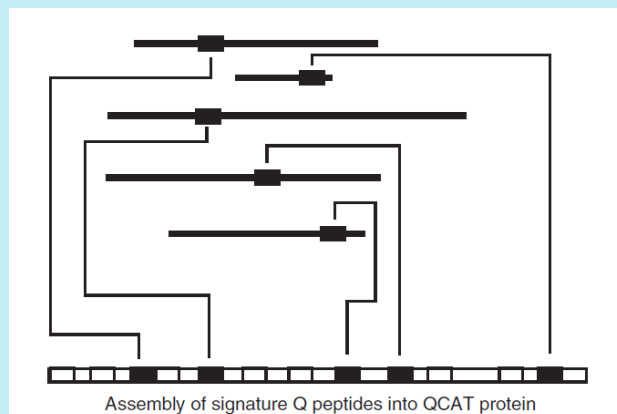
In this edition of our quarterly Newsletter, we therefore dive into the history of QconCATs, present current research and our own internal applications of the QconCAT technology.



We want to thank our customers for their loyalty and trust in our QconCATs and Proteomics Services with various special offers, starting with **-20%** on Calibration Standards and QconCAT Kits.

How it all started

20 years ago, in August 2005, [Rob Beynon et al.](#) published the QconCAT technology. This innovative technique made large-scale targeted proteomics with hundreds of protein targets feasible. QconCATs provide beneficial features like high stability, equimolar peptide stoichiometry, as well as internal workflow and digestion control. By recombinant expression as a protein, QconCATs circumvent difficulties in peptide synthesis and solubility. Over the years, the QconCAT technology was applied in numerous research projects and throughout this year we will highlight selected publications on our social media channels ([LinkedIn](#), [BlueSky](#)).



Assembly of signature Q peptides into QCAT protein
Illustration of QconCAT (QCAT) design (Fig. 1a - Beynon et al., Nature Methods, 2005)

Spring

SPECIAL OFFER

-20%

on **Calibration Standards**
and **QconCAT Kits**

Spring Promotion

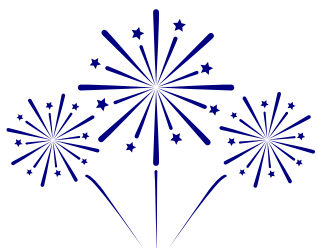
Benefit from our **time-limited special offer** and receive high quality products at low prices.

Until June 30th 2025, save -20% on [Calibration Standards](#) for HPLC and Mass Spectrometry Instrumentations and our [CVDQuant](#) QconCAT Kit.

Research Highlights

We are very happy that 2025 started with two research publications conducted with QconCATs from PolyQuant.

Looking forward to more QconCAT research in this very special year!



Transporter Expressions as Part of Required Scaling Factor to Support In vitro In vivo

Extrapolation for Blood-Brain Barrier Drug Permeability

Al-Majdoub ZM, Cheong J, Mizuno K, Hogan J, De Bruyn T, Kanta A, Guo J, Hop CECA, Zientek M, Galetin A, Ogungbenro K, Rostami-Hodjegan A, Barber J

[Eur J Pharm Sci. 2025 Jan 16:107022.](#)

Al-Majboub et al., used the QconCAT technology to measure expression levels of the transporters P-gp and BCRP in rat brain microvessels and commonly used transporter expressing cell lines (MDCK1, MDCK II and LLC-PK1). Their work enabled them to obtain data important for generation of scaling factors to enable in vitro in vivo extrapolation of transporter-mediated processes and to support the development of a PBPK model of the brain in rats.



Drug Metabolism and Disposition



Absolute membrane protein abundance of P-glycoprotein, breast cancer resistance protein, and multidrug resistance proteins in term human placenta tissue and commonly used cell systems: Application in physiologically based pharmacokinetic modeling of placental drug disposition

Al-Majdoub ZM, Freriksen JJM, Colbers A, van den Heuvel J, Koenderink J, Abduljalil K, Achour B, Barber J, Greupink R, Rostami-Hodjegan A.

[Drug Metab Dispos. 2025 Jan;53\(1\):100007](#)

In this study, Al-Majdoub et al., used QconCAT-based targeted proteomics to quantify the abundance of 6 transporters [P-gp, BCRP, multidrug resistance protein (MRP) 2, MRP3, MRP4, MRP6] and 1 plasma protein marker ATP1A1 (Na⁺/K⁺ ATPase) in 5 placenta samples and associated cell lines. The abundance data were then used in a PBPK model for IVIVE-based prediction of fetal drug exposure.

News

Speed up your quantitative HCP Analysis for recombinant proteins produced in *E. coli*

Recombinant protein production is often performed in *E. coli*, achieving high protein yields in a short period of time.

Based on our internal quality control procedures for *E. coli*-derived recombinant proteins, we designed a QconCAT reference standard comprising of the most common *E. coli* proteins co-purifying with recombinant proteins.

Our HCP Analysis workflow enables us to perform a **global analysis** of *E. coli*-derived contaminations and parallel **quantification** of the most common HCPs in a **single mass spectrometry experiment**.

[Contact us](#) for more information.

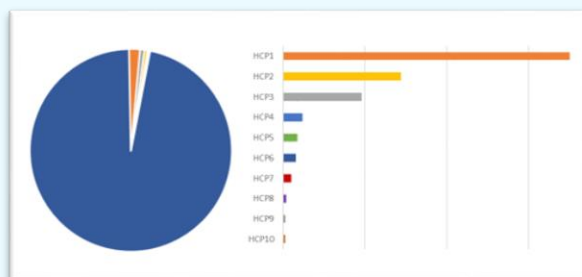


Fig 1. Illustration of HCP analysis results. Left: HCP levels relative to main protein. Right: absolute quantities of Top 10 HCP (µg/µL).

Quantify your GFP-tagged proteins with one standardized protocol

Some proteins are difficult to quantify using mass spectrometry (few tryptic peptides, low signal intensity, etc.). Also, stable isotope labelled reference standards are often not quickly at hand. Therefore, we thought of an alternative approach: instead of targeting the protein, you can target the tag.

If you are working with GFP-labelled proteins, our [¹⁵N-labeled GFP](#) can be used as reference standard to determine absolute quantities of any of your GFP-tagged proteins.

[Contact us](#) to order our MS-GFP standard or to take advantage of our established workflows for absolute quantification of GFP-tagged proteins.

