Newsletter

4-2025

About this edition:

As we finish celebrating the **20th anniversary** of the QconCAT technology, we walked down memory lane to recapitulate the various research that was made possible with this technology.

And as always, our December Newsletter also features current publications using QconCAT reference standards from PolyQuant.

QconCATs: simplifying proteomics projects since 2005

Initially designed for reducing the workload for large-scale quantitative mass spectrometry projects, QconCATs have become a valuable and highly versatile tool for a multitude of proteomics projects.

The creative minds of our customers and those of our own scientists have come up with innovative ways of applying the QconCAT technology to advance their research. Here we highlight our favourite projects and publications of the past 20 years.

Biomarker Research

2008-2012 **DECANBIO Project**
Novel MS-based strategies to Discover and Evaluate Cancer Biomarkers in urine
13 QconCATs, 400 reference peptides

2008-2014 **CoPY Project**
Global quantification of the yeast proteome
120 QconCATs, 6000 reference peptides

2013-2018 **TransCard Project**
Translating disease into cardiovascular health
19 QconCATs, 1000 reference peptides

Quantitative Proteomics

2013 Absolute quantification of selected proteins in the human osteoarthritic secretome

2016 Direct and Absolute Quantification of over 1800 Yeast Proteins via Selected Reaction Monitoring

2018 The COMMD Family Regulates Plasma LDL Levels and Attenuates Atherosclerosis Through Stabilizing the CCC Complex in Endosomal LDLR Trafficking

2020 PIKES Analysis Reveals Response to Degraders and Key Regulatory Mechanisms of the CRL4 Network

Diagnostics

2021 Cov-MS: A Community-Based Template Assay for Mass-Spectrometry-Based Protein Detection in SARS-CoV-2 Patients

2024 Novel Multiplexed Plasma Biomarker Panel Has Diagnostic and Prognostic Potential in Children With Hypertrophic Cardiomyopathy

2024 Multiplex Assay to Determine Acute Phase Proteins in Modified Live PRRSV Vaccinated Pigs

Medical Research

2016 Translational Targeted Proteomics Profiling of Mitochondrial Energy Metabolic Pathways in Mouse and Human Samples

2022 A family of QconCATs (Quantification conCATemers) for the quantification of human pharmacological target proteins

2023 Personalised modelling of clinical heterogeneity between medium-chain acyl-CoA dehydrogenase patients

2023 Quantification of drug metabolising enzymes and transporter proteins in the paediatric duodenum via LC-MS/MS proteomics using a QconCAT technique

… and this year's research highlights are:

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 ASPET

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

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 (Naþ/Kþ 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.

Docosahexaenoic acid prevents peroxisomal and mitochondrial protein loss in a murine hepatic organoid model of severe malnutrition

Horcas-Nieto JM, Rios-Ocampo WA, Langelaar-Makkinje M, de Boer R, Gerding A, Chornyi S, Martini IA, Wolters JC, Wanders RJA, Waterham HR, Van der Klei IJ, Bandsma RHJ, Jonker JW, Bakker BM.
Biochim Biophys Acta Mol Basis Dis. 2025 Apr 29;1871(6):167849.

Horcas-Nieto et al. studied the effects of malnutrition on hepatic peroxisomal and mitochondrial protein levels in a murine hepatic organoid model. They employed QconCAT reference standards to target 57 murine peroxisomal proteins as well as their human orthologues. Up to 28 peroxisomal proteins were sufficiently abundant to be detected and quantified in the hepatic organoids, showing a time-dependent reduction in response to amino-acid deprivation.

Clinical Pharmacology & Therapeutics

Changes in Protein Expression of Renal Drug Transporters and Drug-Metabolizing Enzymes in Autosomal Dominant Polycystic Kidney Disease Patients

Tillmann AC, Peters DJM, Rostami-Hodjegan A, Wilson P, Norman J, Barber J, Al-Majdoub ZM.
Clin Pharmacol Ther. 2025 May 15.

Tillmann et al. examined changes of DMET in the kidneys of ADPKD patients using QconCATs from PolyQuant. They observed only few changes in early-stage patients and a significant reduction of the abundance of most measured proteins in end-stage patients. Their work will support prediction of increased sensitivity to drug-drug interactions using physiologically based pharmacokinetic (PBPK) models.

Mitochondrial proteomic adaptations to daily topor in the Djungarian hamster (Phodopus sungorus)

Kovacs A, Henning RH, Permentier H, Wolters JC, Herwig A, Bouma HR
J Comp Physiol B. 2025 Jul 15.

Kovacs A et al. used targeted and quantitative proteomics to measure the levels of 40 proteins of the mitochondrial metabolism during daily topor. To examine differences in the mitochondrial proteome between daily topor and hibernation, the authors quantified key proteins using QconCATs from PolyQuant as reference standards at different states in the livers of Djungarian hamster. They could show that mitochondrial proteomic adaptations in the Djungarian hamster show both conserved and divergent patterns compared to deep hibernators.

Cardiovascular Research

Loss of GPR146 decreases plasma levels of HDL cholesterol via post-translational upregulation of SR-B1 protein levels

Zhang B, Loaiza N, Rimbert A, Oldoni F, Blauw L, Rensen P, Martinez L, Robert J, von Eckardstein A, Wolters JC, Huijkman N, Kloosterhuis N, Smit M, van de Sluis B, Kuivenhoven JA, Tharehalli U
Cardiovasc Res. 2025 Nov 21

Zhang B. et al. investigate the function of GPR146 in regulating lipoprotein metabolism using *Gpr146* knockout and knockdown models. Using various experimental approaches, they examined lipoprotein abundance, mRNA levels and expression of key regulatory proteins using Western blotting and targeted proteomics supported by a #QconCAT reference standard.
Their work demonstrates that loss of GPR146 increases expression of the major hepatic HDL receptor scavenger receptor class B1 (SR-B1) at the cell surface of hepatocytes and enhances HDL uptake through a post-translational mechanism.