



Newsletter

3-2025

About this edition:

We are happy to announce the official launch of EcoCAT, our new QconCAT Kit for HCP analysis of proteins produced in *E. coli*.

Get useful information about best practices in HCP analysis using LC-MS/MS and how our peptide reference standards support instrument calibration with our two new whitepapers.



The QconCAT technology is being used for 20 years and we highlight the latest publication employing a QconCAT from PolyQuant.

And if you like to meet us in person: we will attend this year's BioEurope in Vienna.

New Product:

EcoCAT

A QconCAT Kit for targeted measurement and quantification of *E. coli*-derived host cell proteins

Biopharmaceutical drugs involving recombinant proteins produced in *E. coli*, require identification and risk analysis of all residual host cell derived contaminations (host cell proteins/HCP).

PolyQuant's [EcoCAT Kit](#) provides **100 heavy isotope (15N) labelled reference peptides** for absolute protein quantification of **48 common and critical** *E. coli*-specific host cell proteins (HCP) using LC-MS/MS in nanoFlow.

Our [Kit](#) is compatible with various sample preparation protocols (e. g. in-solution, FASP, SP3) and different machine methods (e.g. DIA/SWATH, PRM/MRM, SureQuant) and enables easy setup of multiprotein methods.



[Contact us](#) for more information or support for using the EcoCAT Kit or build on **established routine protocols** for targeted LC-MS/MS measurement of the Kit's peptides using our [HCP-analysis service](#).

PolyQuant on the road

After visiting Oxford for attending the 15th International Bacteriophage Conference and the Prague Bio Conference, we are excitedly looking forward to attending the [BioEurope 2025](#) in beautiful Vienna taking place from November 3-5, 2025. You can visit us at the German Pavilion in Hall B, Booth B68-11.




Whitepapers

Quantitative LC-MS/MS for Host Cell Protein Analysis in Biopharmaceutical Development and Production

The inclusion of LC-MS/MS in the US Pharmacopeia acknowledges the valuable contributions mass spectrometry can add host cell protein analysis and marks a significant milestone for the biopharmaceutical industry.


In this whitepaper we summarize current best practices in HCP analysis (methods, qualified standards etc).



Quantitative LC-MS/MS Analysis for Host Cell Protein Analysis in Biopharmaceutical Development and Production


Introduction

Production of biopharmaceutical drugs depends on cultivation or fermentation of appropriate host organisms. The use of genetically modified host organisms inherently leads to the presence of process-related impurities like DNA, lipids or proteins. Host Cell Proteins (HCPs) can negatively affect function and stability of the product or have adverse effects on the patient. Therefore, to ensure safety and efficacy of the final drug product, it is highly important to remove these impurities.



LC-MS/MS system calibration using peptide reference standards

Generation of reliable data, especially for measuring host cell protein abundance, depends on the optimal performance of mass spectrometry instrumentations. Our peptide calibration standards QCAL and RePLiCal were specifically designed for assessment of instrument performance, chromatographic retention time and to control for sample preparation artifacts. Here we present the key features for each of our calibration standards.



LC-MS/MS system calibration using peptide reference standards

Introduction

Protein analytics using mass spectrometry has become increasingly important in the past decades, especially the application in biopharmaceutical research, development and production. This development was recently acknowledged with the addition of a new chapter in the US Pharmacopeia (USP<1132.1> “Residual Host Cell Protein Measurement in Biopharmaceuticals by Liquid Chromatography-Mass Spectrometry) providing detailed information on the use of reference standards.

- Discovery proteomics: enabling the identification of thousands of proteins present in a sample but with limited and unprecise quantitative information
- Targeted proteomics: allowing more in-depth and quantitative analysis of a limited number of proteins, usually facilitated by addition of heavy isotope-labelled reference standards

Most importantly for analysis of

Research Highlight

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. Topor, as well as hibernation are states of reduced metabolism, lower body temperature and reduced heart rate. Both hibernation states involve mitochondrial adaptations, shifting from carbohydrate metabolism to fatty acid oxidation. 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.

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