



Newsletter

1-2024

About this edition:

In this Newsletter, we highlight two of our new proteomics services and we finish our series on QconCAT design.

The next occasion to meet us is in April at the Analytica in Munich.

New Services:

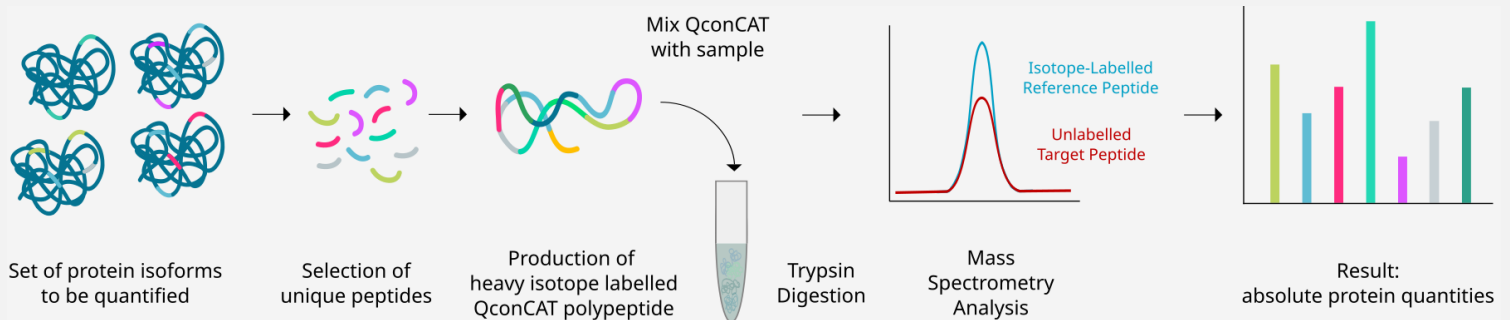
Isoform-specific protein quantification

Obtaining quantitative data for different isoforms of the same protein is often challenging due to the lack of isoform-specific antibodies. These problems can be overcome by using our proprietary QconCAT technology and targeted LC-MS/MS.

In the last months, PolyQuant developed a bioinformatic pipeline that enables us to **identify unique isoform peptides** and to design optimized QconCAT proteins for research on differential isoform expression **independent of antibodies**.

As an example, our new workflow enabled us to design a QconCAT reference standard for distinguishing p53 isoforms.

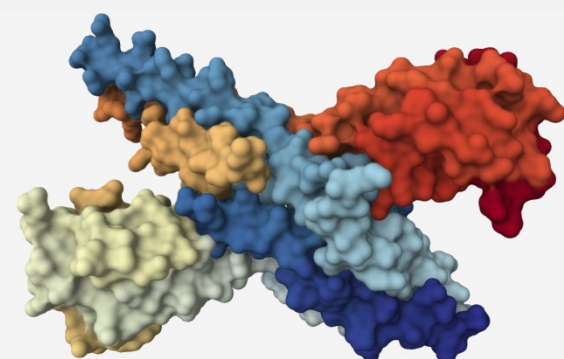
For more information on how to implement our workflow to your protein isoforms of interest, please visit our [website](#).



Protein Complex Stoichiometry

Function, activity and location of protein complexes can be regulated via post-translational modification of key subunits but also through composition of its subunits.

For **qualitative and quantitative** analysis of protein complexes using mass spectrometry, we have developed **antibody-free** proteomics workflows that enable further insight into the regulation of protein complexes, metabolic pathways and signaling cascades in their native environment. More information can be found on our [website](#).



How to design the most appropriate QconCAT for your research project

Part 3: Scale and Purity

In our previous newsletters, we discussed strategies for peptide selection (2-2023) and labeling options (3-2023).

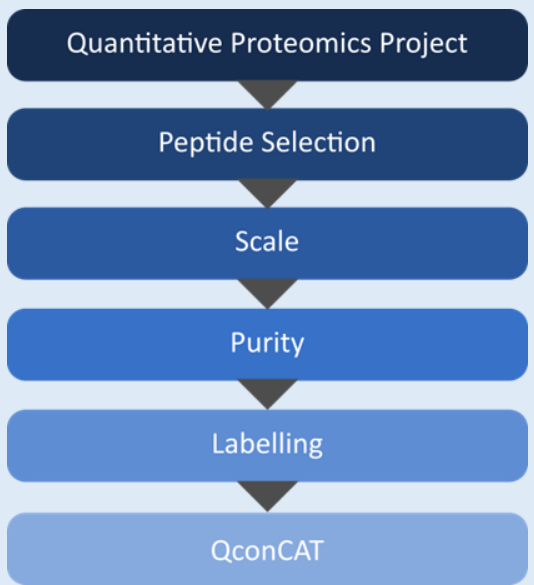
Depending on the intended application, there are different requirements for scale and purity of the produced QconCAT.

For **exploratory analyses**, especially when there are only a few proteins of interest involved, an **un-purified QconCAT** (crude extract) allows fast determination of absolute protein quantities.

For more **advanced projects** and projects involving large numbers of peptides (> 30 peptides of interest) a **purified QconCAT** is advantageous due to higher storage stability, enabling highly reproducible results for continuing studies/analyses.

Production of large amounts of QconCAT with **highest purity** is central for e.g. **routine or high throughput analyses** for clinical studies, quality control assays etc.

Our experienced team will be happy to consult you in order to obtain the optimal QconCAT for your proteomics project.



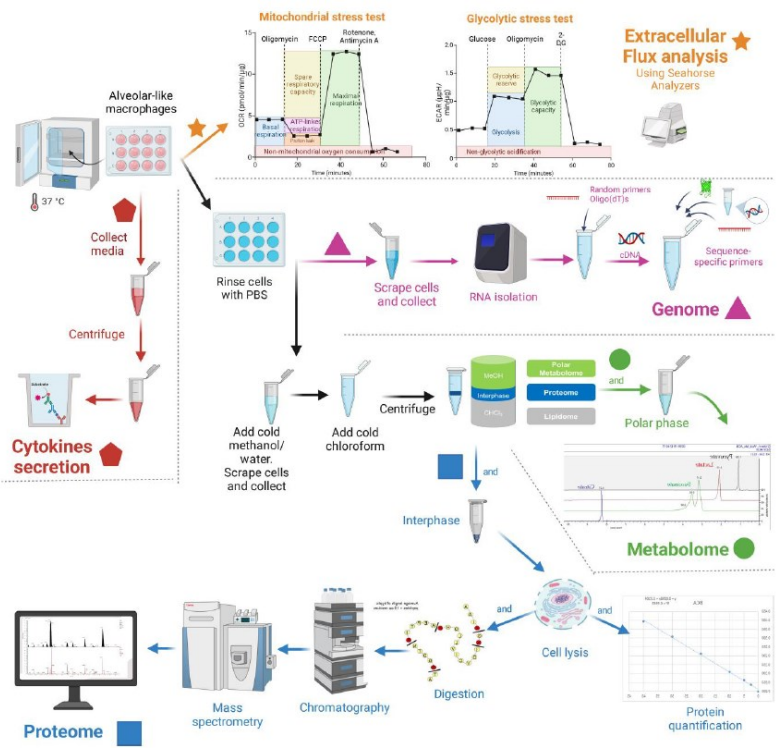
Publication Alert:

Effects of lysine deacetylase inhibitor treatment on LPS responses of alveolar-like macrophages

Russo S, Kwiatkowski M, Wolters JC, Gerding A, Hermans J, Govorukhina N, Bischoff R, Melgert BN
[J Leukoc Biol . 2024 Feb 23;115\(3\):435-449.](https://doi.org/10.1186/s12924-024-00449-4)



In their recently published study, Russo et al. examined if the anti-inflammatory effects of lysine deacetylase inhibitors were associated with metabolic changes in macrophages using a multiomic approach, monitoring gene expression, metabolome and proteome as well as measuring cytokine secretion and the extracellular flux. For examining the proteome, they performed untargeted proteomics analysis to identify the metabolic enzymes of macrophages and a targeted proteomics approach to quantitatively assess the abundance of 59 selected proteins of the primary metabolism. For measuring high abundant proteins, they spiked 2 ng of predigested ¹³C Arg/Lys-labelled QconCATs to 1 µg total protein starting material. For low abundant proteins, they used 0.1 ng QconCAT reference standards from PolyQuant. The peptides were separated on a nano-ultra high-performance liquid chromatography (UHPLC) system with a linear gradient (3 - 60% v/v acetonitrile plus 0.1% v/v formic acid) in 110 min at a flow rate of 200 nL/min. The target peptides were analyzed by a triple quadrupole mass spectrometer (MS) equipped with a nano-electrospray ion source.



Meet us:

Analytica

This year's [Analytica](#) that will take place from April 9th – 12th 2024 in Munich. We are excited to be part of this huge gathering of industry and research.

