POLYQUANT

QconCAT – a valuable tool for quantitative proteomics

- Absolute quantification of up to 50 proteins with a single QconCAT

- Quantify whole proteomes in a single experiment using several QconCATs

- Scalable production for high throughput analyses

- High purity of stable isotope labelling

- Minimize sample preparation bias by early addition of the internal standard

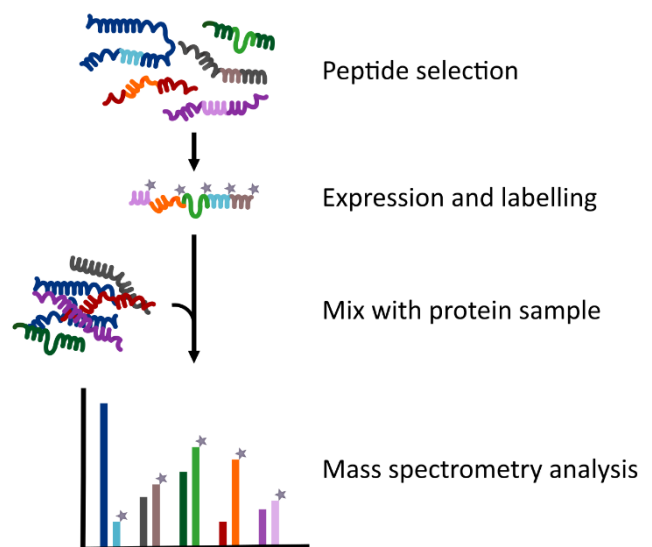## Explore and extend the advantages of mass spectrometry

QconCATs (**Q**uantification **conCAT**amer) are custom-made synthetic proteins, usually comprising of up to 50 heavy isotope-labelled proteotypic peptides, functioning as true internal standards for absolute protein quantification.

Advantages

➡ Synthesize difficult peptides without limitation in peptide length and include flanking amino acids.

➡ Prevent peptide loss through absorption to vessel walls.

➡ Target peptides are released from QconCAT proteins in a 1:1 ratio.

➡ Skip preparation of time-consuming peptide mixes and spike your analyte sample with up to 50 reference peptides in a single pipetting step.

Knowledge and support

Our experienced team supports you by selecting proteotypic peptides based on available data from previous mass spectrometry analyses or by *in silico* analysis.

Peptide selection

Expression and labelling

Mix with protein sample

Mass spectrometry analysis

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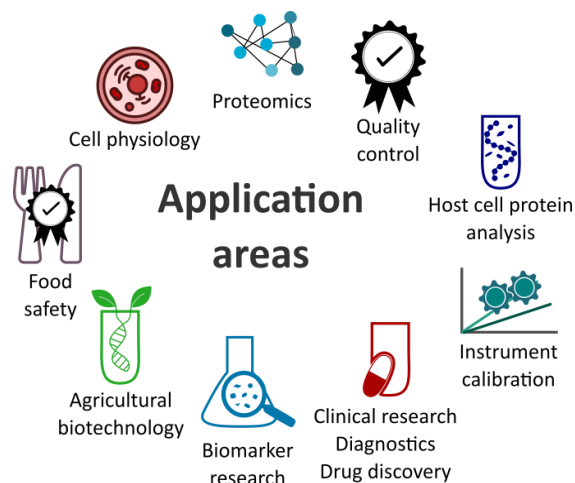info@polyquant.com
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Established technology

QconCATs are highly versatile tools for various research projects in academia and industry and have been successfully applied in exploratory studies as well as in high throughput analyses.
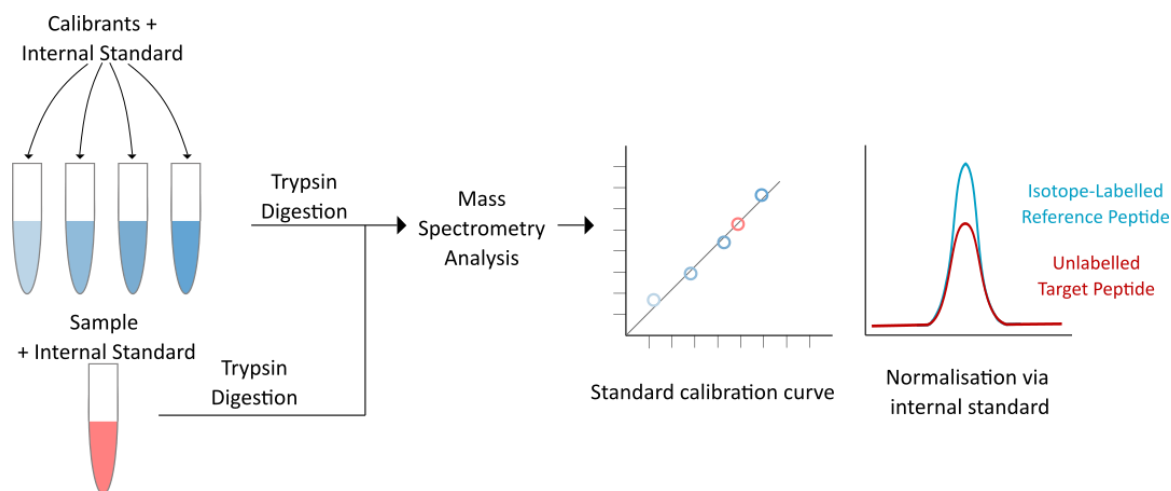
Products based on the QconCAT-technology as well as a list of recent publications and selected examples for QconCAT applications can be found on our website:
www.polyquant.com/products/
www.polyquant.com/qconcat/

Application areas

Cell physiology · Proteomics · Quality control · Host cell protein analysis · Food safety · Agricultural biotechnology · Biomarker research · Clinical research Diagnostics Drug discovery · Instrument calibration

Apply PolyQuant's QconCAT technology to your protein quantification project

Absolute protein quantification using QconCAT reference standards can be established on all commonly used mass spectrometry platforms. Our technology is compatible with other methods and can be integrated into established quantitative protein analysis workflows. In contrast to synthetic peptide reference standards, QconCATs can be added very early during sample preparation and function as internal control for sample processing.

Calibrants + Internal Standard

Sample + Internal Standard

Trypsin Digestion

Mass Spectrometry Analysis

Standard calibration curve

Isotope-Labelled Reference Peptide

Unlabelled Target Peptide

Normalisation via internal standard

Quantification is performed by adding the QconCAT in known quantity to the sample (e. g. a cell extract). Subsequent proteolysis, for example with trypsin, releases the proteotypic peptides both from the target proteins and the QconCAT. These peptides are then analyzed in a mass spectrometer. The intensity of the reference peptide peaks allows calculation of the exact absolute amount of each target protein.

References

- Beynon R. J. et al., **Multiplexed absolute quantification in proteomics using artificial QCAT proteins of concatenated signature peptides.** Nature Methods Vol. 2 (8), August 2005, 587-589.
- Pratt J. M. et al., **Multiplexed absolute quantification for proteomics using concatenated signature peptides encoded by QconCAT genes.** Nature Protocols Vol. 1 (2), 2006, 1029-1043.

POLYQUANT

Absolute protein quantification made easy

- Based on a detailed analysis of your requirements, we will provide you with an isotope-labeled QconCAT concatamer, custom-made for your research project

- High purity isotope labelling with multiple labelling options (e.g. ^{15}N, SILAC ^{13}C)

- All QconCATs (crude or purified) are absolutely quantified and solubility tested

- We will support you in setting up your targeted method in Skyline (receive peptide libraries and iRT values)

- Bioinformatic support for data analysis available upon request

- Full in-house protein quantification service available (includes QconCAT production, sample preparation, method setup, LC-MS/MS measurement, data analysis)

Order your custom-made QconCAT

Contact us or submit your peptide list or a list of target proteins (with sequences or uniprot accession number)	→	PolyQuant performs

Peptide selection

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Gene synthesis — 4 weeks

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QconCAT production — 2 weeks

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Quality control — 2 weeks

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Standard service: Receive the finished QconCAT for your quantification project

Full service: We analyze and quantify your targets and provide you with the quantification results