



Newsletter

1-2023

About this edition:

In our first newsletter for 2023 we are happy to announce the start of our collaboration with the Fraunhofer Institute for Toxicology and Experimental Medicine (ITEM) in Regensburg.

We also introduce new products and services and discuss applications for QconCATs in food analytics.

Research project: Predictive potential of tumor biomarkers

PolyQuant and the Fraunhofer Institute for Toxicology and Experimental Medicine (ITEM) in Regensburg are collaborating on a project aiming at the prediction of appropriate second-line anti-cancer therapy with the help of biomarkers (funded by the Bavarian Government – [BayVFP](#)).



Our project contribution includes characterization of tumor persister cells and resistant tumor cell lines using mass spectrometry, as well as selection of predictive biomarkers. The produced reference standards will be used for highly sensitive measurements of biomarkers in low cell numbers.

New products and services:

Recombinant SIL proteins for quantitative mass spectrometry

QconCATs are valuable tools for absolute quantification of large numbers of proteins. However, for some applications full length proteins may be the better choice. Stable isotope labelled (SIL) proteins are the gold standard for targeted proteomics as these proteins have the same biochemical properties as the target protein. As for QconCATs, the SIL proteins can be added at early time points during sample preparation, providing highly accurate quantification results.

We offer production of full-length proteins, labelled with a stable isotope of choice. Select a protein from our continuously expanding list of available proteins or contact us to plan an individual protein expression project.

Our offer:

Recombinant full length proteins

- From gene to protein
- Production in *E. coli* and in cell free expression systems
- For application as reference standard in targeted mass spectrometry

Isotope labeled or unlabeled

- Select a label of your choice (e. g. ^{13}C Arg/Lys, $^{13}\text{C},^{15}\text{N}$ Arg/Lys, ^{15}N ...)

Different purification levels

- Crude extract
- High purity

Quality controlled

- All recombinant proteins are routinely tested for purity, quantity and labeling efficiency (irrespective of the purification grade).



Cov-MS2

The SARS-CoV-2 pandemic led to a high demand for molecular diagnostics. Currently, the demand for COVID testing declines as SARS-CoV-2 is losing its threat and is beginning to be treated similarly to the seasonal viral infections of the respiratory system. As the symptoms caused by these viruses are hard to distinguish, molecular diagnostics are required for reliable diagnosis.

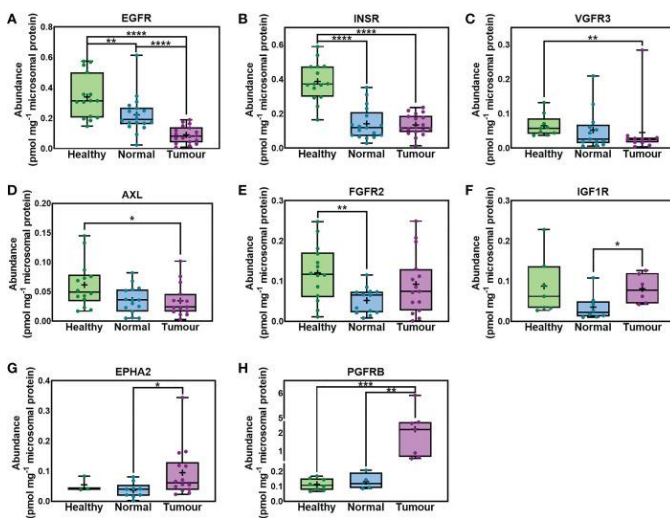
Mass spectrometry has a huge potential for development of molecular diagnostics as it enables accurate and sensitive detection of e.g. virus particles.

Metaproteomics

The relatively new research field of metaproteomics rapidly grew over the last years. Analysing the proteomes of the many organisms present in microbial communities (e.g. in sewage, soil, water...) is a challenging task with high demands on peptide separation, MS instrument performance and data processing.

We have developed tools and protocols, covering all steps from protein extraction to data analysis. This allows us to determine the organisms present in a sample as well as their proportions and to provide you with a comprehensive analysis of protein expression for each organism.

Research update



In collaboration with the University of Ghent, we have developed a detection kit for respiratory infections, enabling detection of SARS-CoV-2, Influenza A/B and RSV with high precision, employing mass spectrometry.

Visit our [website](#) for more information.

- Determine the biodiversity of microbial or viral communities and multi-organism systems
- Large-scale identification and quantification of proteins from microbial communities
- Quantification of per-species biomass
- Identification of main species



Proteomic quantification of receptor tyrosine kinases involved in the development and progression of colorectal cancer liver metastasis

Vasilogianni AM, Al-Majdoub ZM, Achour B, Peters SA, Rostami-Hodjegan A, Barber J. *Front Oncol.* 2023 Feb 20;13:1010563.

Vasilogianni et al used a QconCAT standard (KinCAT) to measure absolute protein abundance of 21 human receptor tyrosine kinases (RTKs) in healthy and cancerous liver tissue using LC-MS/MS. They observed both up- as well as downregulation of several RTKs in cancerous tissue indicating potential of these proteins as biomarkers for monitoring cancer progression and response to therapeutic intervention.

Research focus: Food Analytics

Correct labelling of food products is important to consumers as they want to be informed about all ingredients with respect to allergies and food intolerance. Additionally, several food fraud scandals highlighted the importance of food products being tightly controlled.

International safety standards are in place, certifying the quality of the food product and thus demand for appropriate testing strategies. Here, we highlight two research articles using mass spectrometry to determine the species of the animals used for production of sausages and to detect allergens in cookies and chocolates.



Quantification of species-specific meat proteins in cooked and smoked sausages using infusion mass spectrometry

Magdalena Montowska and Anita Spych
[J Food Sci Technol](#) (December 2018) 55(12):4984–4993

The identity of raw meat can be determined through PCR but in case of processed meat, identification of the animal species or additives is difficult. Montowska and Spych used mass spectrometry, identifying 11 species-specific meat proteins and 14 unique heat-stable peptide markers in cooked and smoked sausages. Their assay employed label-free mass spectrometry, allowing only relative quantification. A well designed QconCAT would refine this assay, allowing the absolute determination of the amounts of each ingredient as well as the share of undeclared meat or additives.

PolyQuant GmbH, founded in 2007, provides DIN ISO 9001:2015 certified products, services and bioinformatics support focusing on mass spectrometry-based absolute protein quantification using our proprietary QconCAT technology. QconCATs by PolyQuant have been successfully applied to numerous projects in academia and industry worldwide and have been used for projects such as biomarker identification and validation, quality control and life science research.



PolyQuant GmbH

Industriestr. 1
93077 Bad Abbach
Germany
Tel. +49 (0) 9405 96999 10
Fax. +49 (0) 9405 96999 28
www.polyquant.com

Commercial register of the local courts: Amtsgericht Regensburg, HRB 10564
Managing director: Dr. Florian Christoph Sigloch, Dr. Werner Deininger

PolyQuant GmbH – your service provider in targeted proteomics



Development and Validation of a Quantitative Method for Multiple Allergen Detection in Food Using Concatemer-Based Isotope Dilution Mass Spectrometry

Gavage M, Van Vlierberghe K, Dieu M, Renard P, Arnould T, De Loose M, Gevaert K, Gillard N, Van Poucke C.
[JAOAC Int.](#) 2022 Oct 26;105(6):1585-1595.

Gavage et al. developed and validated a LC-MS/MS method for detection of allergens in a highly processed (cookies) and a complex matrix (chocolate) using a stable isotope labelled peptide concatenation as internal standard. The final reference standard comprised of 19 allergen-specific peptides, enabling the precise and repeatable detection and quantification of allergens from hazelnuts, peanuts, milk and egg. The method was validated in two different laboratories.

