

"The impact II, a very high resolution quadrupole time-of-flight instrument for deep shotgun proteomics", *Mann et al.*



<http://bit.ly/1LaasKU>



● **Q-TOF Newsletter**

Bruker Daltonics further improves its knowledge generation platform for omics, biologics and small molecule workflows.

At the 63rd ASMS (Saint Louis, MO), Bruker is introducing new workflow capabilities for the **impact™ II** and **maXis™ II** QTOFs as the most versatile and productive knowledge generation platforms.

impact II and maXis II are the latest evolutions of Bruker QTOF platform. They provide superb qualitative and quantitative competences for omics, intact protein analysis, bio-therapeutics, food testing and forensics.

Their robustness and application oriented software solutions further help driving productivity and maintaining focus on the research goals.

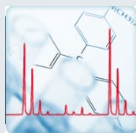
Combined:

- Spectral accuracy
- Acquisition speed
- High resolving power
- Robustness

for more Productivity and Versatility in:

- Omics
- Quantitation
- Intact protein profiling
- Characterization of biologics
- Small molecule screening and quantitation

Augmented by:



ProteinScape™



PathwayScreener™



**HMDB
Metabolite
Library™**



**BioPharma
Compass™**



**TASQ™
Screen & Quant**

Biology's diversity demands versatility and maXis II delivers

Unparalleled versatility

Equipped with the latest innovations in TOF technology, Bruker's maXis II delivers market-leading resolution of 80,000 FSR. This heralds a new era in QTOF technology with unprecedented performance across wide-ranging applications to resolve the most demanding analytical challenges. maXis II offers the best of what only TOF can do: combined resolution, sensitivity, spectral accuracy and dynamic range; across the entire instrument mass range.

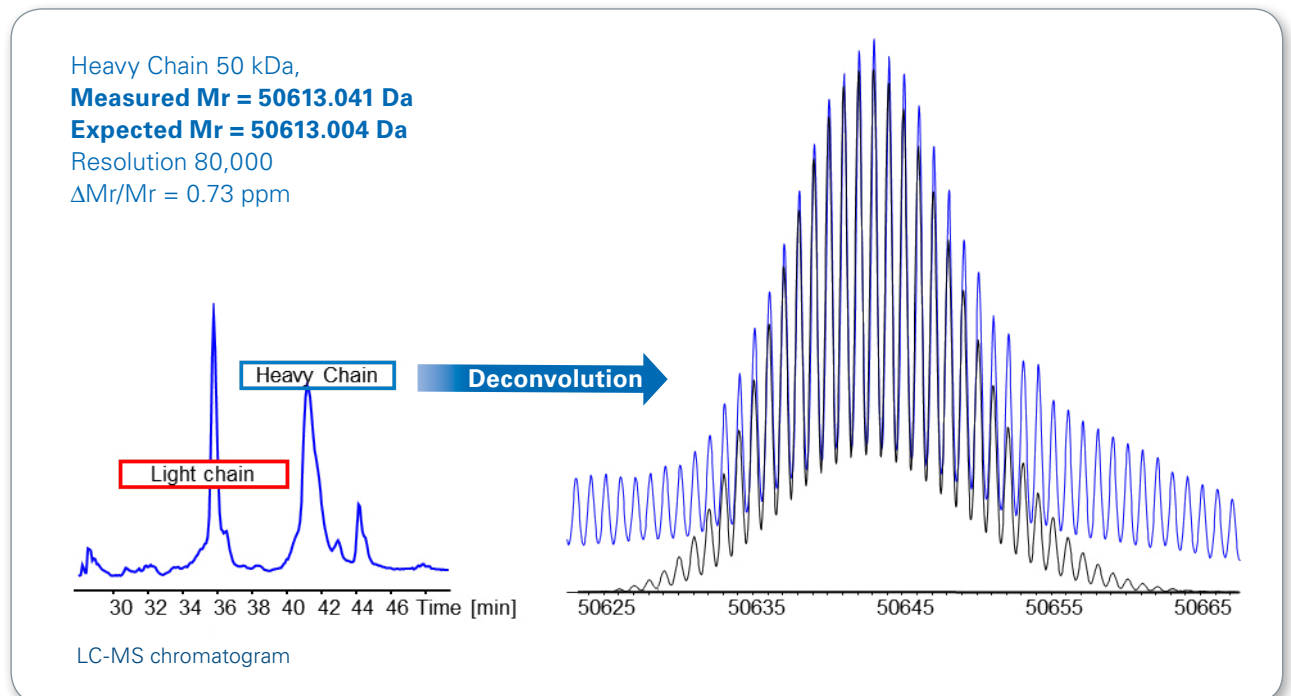
Certainty in molecular analysis

The superb quality data from the maXis II, i.e. accurate mass and true isotopic patterns (TIP), in combination with Bruker's unique ab initio formula discovery tools, SmartFormula™ and SmartFormula 3D™, provide accurate molecular formulae with a maximum level of certainty.

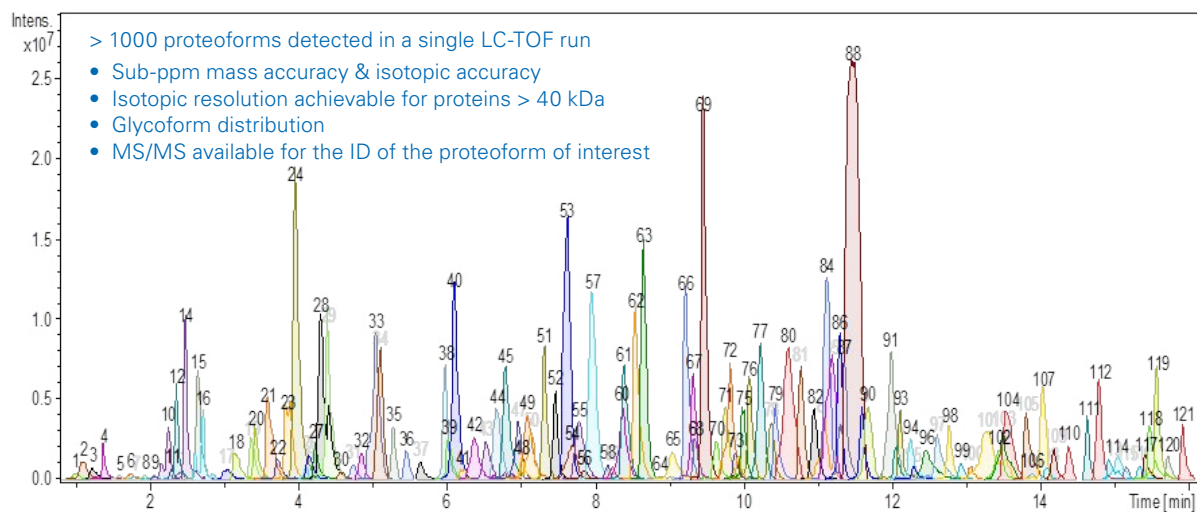
The benefit of enhanced resolution, TIP and mass precision

Enhanced resolution and mass accuracy allows the complete characterization of closely related heterogeneities of a monoclonal antibody subunit. The maXis class leading performance empowers the user to determine the monoisotopic mass of mAb subunits which enables the detection of low MW modifications like deamidation.

Read more on ASMS poster ThP 531.



Intact Yeast Lysate LC-TOF analysis in 20 min



Linking experimental data to biology

impact II is the latest evolution of the impact QTOF platform, it provides superb qualitative and quantitative omics capabilities. The combination with ProteinScape and ProfileAnalysis™ makes the impact II a very versatile and productive platform for omics and biological knowledge generation. ProfileAnalysis enables untargeted label free Proteomics and Metabolomics workflows.

ProteinScape is Bruker's central bioinformatics software combining storage, organization, and processing of proteomic data sets. Utilizing well-established protein and peptide analysis functionalities, it provides a sophisticated tool for further evaluation of glycomics data.

Glycosylation sites profiling helps with understanding the relationship of structure, location and function of glycoproteins.

Our users benefit from the hardware and software capabilities that give Bruker platforms a unique efficiency for this task.

ProteinScape powered by GlycoQuest

- Detect glycopeptides in complex LC-MS/MS data sets
- Identify glycan and peptide moieties
- Glycan composition and peptide sequence analyzed in one spectrum

Learn more:



Poster-Note 03



ProteinScope

- Protein ID, Quant, Characterization, PTM discovery
- Includes GlycoQuest

GlycoQuest

- Glycans ID
- Glycopeptides screening and characterization

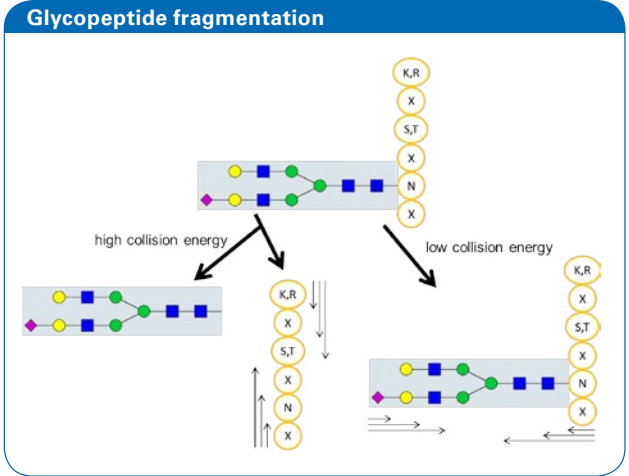
Omics Knowledge Generation

3rd Party Software

- MaxQuant: Protein ID and quantitation
- Skyline: Targeted quantitation

Metabolomics

- PathwayScreener: Pathway-driven targeted metabolomics
- HMDB Metabolite Library



Bruker HMDB Metabolite Library

Evaluate Bruker HMDB Metabolite Library hits ...

... and link to biological information

The screenshot shows a list of metabolite hits with columns for Name, SMILES, and Molecular Weight. A red box highlights the 'Link to Biological Information' button. A blue arrow points from the mass spectrum plot to this button.

Improve metabolite identifications

The Bruker HMDB (Human Metabolome Data Base) Metabolite Library is exclusively provided by Bruker and was generated in collaboration with Prof. Liang Li and Prof. David Wishart and their teams at the University of Alberta, Canada.

The Bruker HMDB Metabolite Library is a manually curated mass spectral library that facilitates the identification of metabolites in (human) metabolomics research. The library is stored on your PC providing private search capabilities and contains MS and MS/MS spectra and additional information on >750 reference standards. Compounds include metabolites found in urine, blood, other biofluids, and cell extracts.

Learn more:



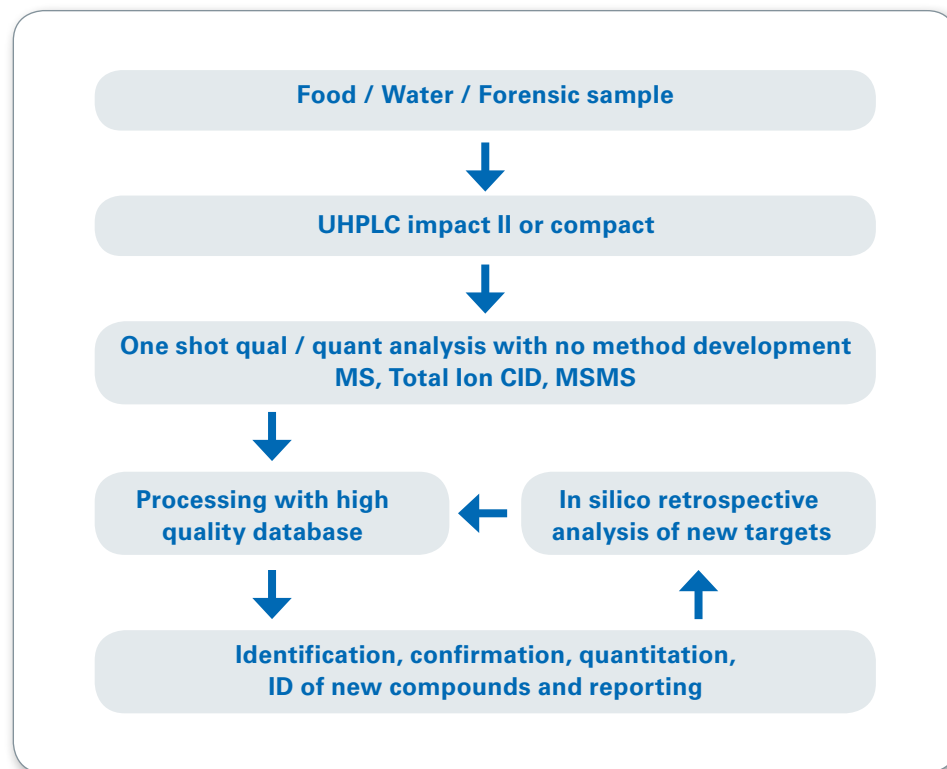
One-Shot Full Picture of the Sample

Powerful, screening and quantitation solutions for pesticides in food / feed and water as well as forensic toxicological drug analysis in human body fluids

Bruker offers complete solutions with comprehensive accurate mass compound databases for forensic toxicology and food safety testing. This includes the industry leading impact II or compact bench top QTOF system with application specific screen & quant workflows powered by our new TASQ™ software.

Innovative technologies that deliver the highest sensitivity and confidence in results

Full Sensitivity Resolution and high dynamic range are prerequisites to reach extreme low level of detection. High-resolution Extracted ion Chromatograms and bbCID acquisition with full scan MS delivers compound identification with unprecedented confidence.



Learn more:



brochure
Pesticide-
Screener



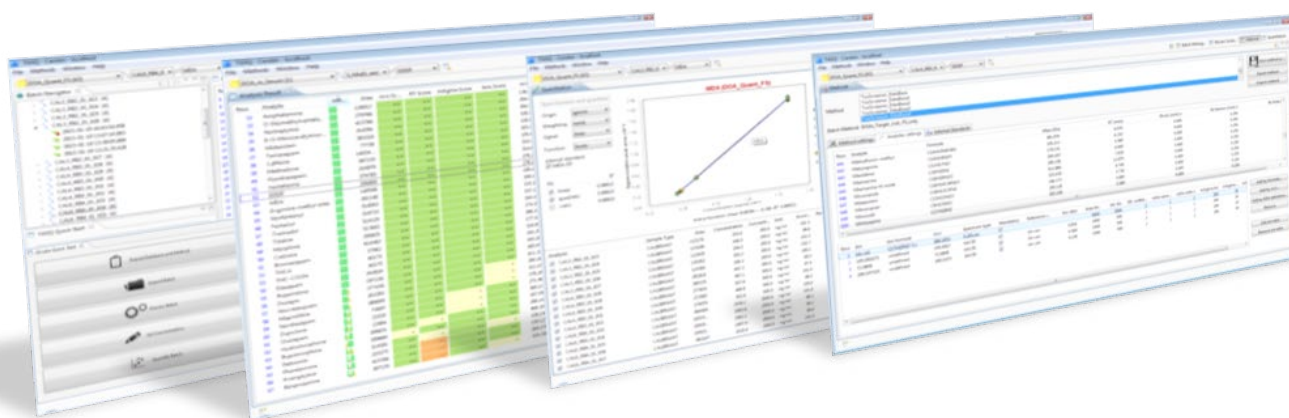
brochure
ToxScreener



brochure
TASQ

Powerful TASQ software streamlines the entire workflow

Provision of comprehensive bbCID accurate mass databases with TASQ software allows users to perform screening and quantitative workflows with minimal effort in a single experiment.



Batch Management

Review Screening

Quant Management

Analyte Management

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