



# MassSpectator

December 2016, Issue 75

## Upcoming Events

**December 10-14** – 6<sup>th</sup> BrMass-1<sup>st</sup> IbMS, Rio de Janeiro

**December 14** – Symposium Microbiologie, Paris

**December 15** – Webinar “Label-free ultra-high-throughput screening by MALDI Mass Spectrometry”, online

**December 20** – Webinar “Enabling Isotopic Fine Structure Mass Spectrometry”, online

**January 9-10** – ISMS 2017, Rehovot

**January 17** – MALDI-TOF Mass Spec uHTS Workshop, La Jolla

**January 24-25** – Isranalytica, Tel-Aviv

**January 24-26** – CASSS - WCBP 2017, Washington, DC

**February 4-8** – SLAS 2017, Washington, DC

**March 5-9** – PITTCO 2017, Chicago

**March 5-8** – DGHM 2017 / VAAM 2017, Würzburg

## In this issue

Welcome to another inspiring issue of Bruker's **MassSpectator**! This month we are highlighting our High Throughput Screening (HTS) Tutorial at the SLAS 2017 International Conference, the webinar on “Label-free ultra-high-throughput screening by MALDI Mass Spectrometry” on December 15, and the Annual Mass Spectrometry User Meeting for DACH-region.

As noted, we continually strive to improve our engagement with you, so please [✉ contact us](#), and follow us on [twitter](#), [LinkedIn](#), [YouTube](#) and [facebook](#).

Kind regards,

Your Bruker Daltonics Sales & Marketing Team

## Register today for the Bruker High Throughput Screening (HTS) Tutorial at the SLAS 2017 International Conference



Join us in Washington D.C. for the SLAS 2017! Stop by the Bruker booth, #346, and learn how the rapifleX MALDI PharmaPulse system accelerates label-free screening and assay development.

Register now for our **informative tutorial on High Throughput Screening on Tuesday, February 7, from 9:30 – 10:15 am** in Room 151 A of the Walter E. Washington Convention Center in Washington D.C.

[Click here for more information and to register.](#)

## Annual Mass Spectrometry User Meeting for DACH-region – Call for Papers

We would like to invite you to our annual **Mass Spectrometry User Meeting** in Kassel, Germany. As a program, a combination of user talks and selected Bruker presentations on the topics “Characterization of proteins, lipids & carbohydrates”, “Omics & Biomarkers”, “Small Molecules: Identification & Characterization” and “Routine applications” awaits you. Furthermore, you can still submit talks for the named topics. The **Call for Papers** is still open until December 15.

[Click here for more information and to register.](#)

*(Please note, that this meeting addresses users from Germany, Austria and Switzerland only)*

## MALDI-TOF Mass Spec uHTS Workshop in La Jolla

You can now register for our “**MALDI-TOF Mass Spec uHTS Workshop - Accelerating Drug Screening and Discovery with the New rapifleX MALDI PharmaPulse System**” on **January 17, from 9:00 am – 2:30 pm.**

This informative workshop features presentations on the practical aspects and advantages of incorporating mass spectrometry into drug discovery workflows. We've designed this workshop specifically for automation and screening managers at pharmaceutical, biopharmaceutical and CRO companies involved in high-throughput screening and laboratory automation.

[Click here to register.](#)



Save-the-date: See us at WCBP 2017 in Washington, D.C.



Bruker will present a **workshop at the WCBP Symposium** on January 24 at the Mayflower Hotel in Washington D.C. Workshop agenda and registration will be announced soon.

[Click here to learn more.](#)

### Webinar on “Label-free ultra-high-throughput screening by MALDI Mass Spectrometry” on December 15



A new MALDI Time-of-flight (TOF) Mass Spectrometer, designed for ultra-fast label-free screening of biochemical assays will be presented: The rapifleX MALDI PharmaPulse monitors substrates and all products and results in reliable determination of IC50 values, avoiding false positives. Measurement times of about 12 minutes per 1536 MALDI sample plate allow for the first time the use of Mass Spectrometry for primary screens.

[Click here to register.](#)

### Webinar on “Enabling Isotopic Fine Structure Mass Spectrometry” on December 20



A new form of elemental identification named Isotopic Fine Structure Mass Spectrometry (IFS-MS) is presented here that uses high mass resolving power (>500,000) combined with high magnitude fidelity to directly detect the direct heteroatom signature by identifying discrete isotopologues. This type of measurement is vastly superior to previous methods for determining chemical formulae since the type of heteroatoms and quantity can be directly determined from measured spectra, in essence allowing chemical formulae to be “read” directly off of mass spectra. We present the mechanics and requirements behind this approach along with several applications oriented examples.

[Click here to register.](#)

### 1<sup>st</sup> eMetabolomics conference – on-demand stream

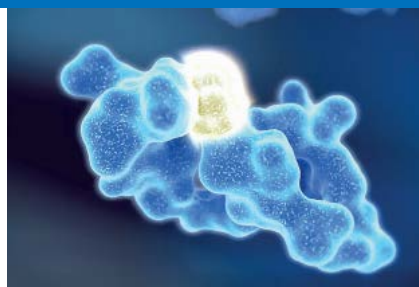


**High performance proteomics and metabolomics with the impact II Q-TOF powers improved understanding of how to achieve increases in bio-production efficiency using rational strain design.**

You can now stream this informative keynote lecture “Increasing arginine production in *Corynebacterium glutamicum* by rational strain design in combination with metabolomics and proteomics” on demand. The talk was presented during the 1<sup>st</sup> eMetabolomics conference in Session B “Applications of Metabolomics in Agriculture and Industry” by Dr. Aiko Barsch.

[Click here to stream the recording.](#)

### New Poster Note: mAb Characterization - automated detection of disulfide bonds by the rapifleX



**FAST and simplified approach to analyze trisulfide formation in biopharmaceuticals.**

New rapifleX TOF/TOF was used to automatically detect disulfide bonds in four monoclonal antibodies followed by straight-forward analysis of trisulfide formation.

[Click here to download the Poster Note.](#)

## New blog article: No longer unknown – novel cytochrome c oxidase subunit revealed



A few years ago, researchers solved the structure of the cbb3-1 cytochrome c oxidase from *Pseudomonas stutzeri*. They were surprised to detect the presence of a fourth protein subunit, consisting of a single transmembrane helix, for which no proteomic or genomic information was available. In a recently published article, they have now described the identification and characterization of that previously unknown subunit...

[Click here to read the full article.](#)

## Webinars



- September 6<sup>th</sup>: Hydrogen Exchange Mass Spectrometry automation for the maXis Ultrahigh Resolution QTOF
- July 26<sup>th</sup>: Applications of GC-MS-MS and LC-Ion Trap MS-MS in Postmortem Forensic Toxicology
- June 28<sup>th</sup>: Streamlining Drug Development: Native LC-MS for Rapid Screening and Drug Product QC Release Testing of Antibody Drug Conjugates
- June 28<sup>th</sup>: Structure Elucidation with Trapped Ion Mobility Spectrometry
- June 16<sup>th</sup>: Uncovering Metabolic Pathways in Disease to Support Drug Discovery Using High Resolution MALDI Imaging Mass spectrometry

## Latest Literature

- Brochure: MetaboScape® 2.0
- Brochure: solariX XR
- Brochure: Poster Hall Metabolomics Ed. III
- Brochure: timsTOF™
- Brochure: rapifleX™
- Brochure: Training Courses 1.0
- Brochure: MALDI Biotyper Poster Hall 2016
- Flyer: HDX Solution
- Poster Note: PN-41 Localization and Identification of Peptides from Tissue using high-speed MALDI TOF/TOF mass spectrometry
- Poster Note: PN-36 Towards the fast and increasingly simplified analysis of trisulfide formation in biopharmaceutical antibodies
- Poster Note: PN-35 A trial of TLC-MALDI for analysis of industrial materials
- Poster Note: PN-34 2 $\omega$ -FT-ICR Mass Spectrometry with Quadrupolar Detection
- App-Note: LCMS-118 Unraveling the Human Blood Plasma O-Glycoproteome
- App-Note: LCMS-116 What are we eating? MetaboScape® Software; Enabling the De-replication and Identification of Unknowns in Food Metabolomics
- App-Note: LCMS-115 Automated Quality Control of Active Pharmaceutical Ingredients (API) by LC-UV-ion trap MS using Compass Open Access
- App-Note: LCMS 114 Rapid Analysis of Low Level Testosterone in Serum with the Bruker EVOQ Elite LC-TQ
- App-Note: LCMS-113 Rapid Analysis of Low Level Estrogens in Serum with the Bruker EVOQ Elite LC-TQ

Find more scientific contributions [here](#).

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