MASS SPECTROMETRY

# Product Overview

Life Science Mass Spectrometry

Innovation with Integrity

# Driving Innovation in Proteomics, Metabolomics, Pharma/Biopharma and other fast-growing Fields of Life Sciences

Bruker is enabling scientists to make breakthrough post-genomic discoveries and develop new applications that improve the quality of human life. Bruker's high performance scientific instruments and high value analytical and diagnostic solutions enable scientists to explore life and materials at molecular, cellular, and microscopic levels. In close cooperation with our customers, Bruker is enabling innovation, improved productivity, and customer success in post-genomic life science molecular and cell biology research, in applied and pharma applications, in microscopy and nano-analysis, as well as in industrial applications. Bruker offers differentiated, high-value life science and diagnostics systems and solutions in preclinical imaging, clinical phenomics research, proteomics and multiomics, spatial and single-cell biology, functional structural and condensate biology, as well as in clinical microbiology and molecular diagnostics.

## Premier Provider of High-Performance Scientific Instruments and Life Science Research and Diagnostic Solutions

- Since 1960 track record of technological pioneering
- Culture of disciplined entrepreneurship
- Extensive collaborations with renowned science labs
- Deep chemistry, biology and physics applications expertise

## Market Leader in High-Performance Scientific Instruments

**+9700**
Employees

**+100**
Countries worldwide

**+1750**
Employees dedicated to R&D

**+4000**
Patents pending or granted

Bruker holds **#1** or **#2** market positions in 70% of our portfolio.

# Trapped Ion Mobility Mass Spectrometry

## timsTOF - The next generation ion mobility separation

*Bruker's timsTOF instruments revolutionized mass spectrometry by unlocking an additional dimension of separation with high sensitivity and speed. Trapped ion mobility increases peak capacity and confidence in compound characterization. Whether you need a reliable workhorse, a high-throughput powerhouse, a single-cell specialist, an ultra-sensitive flagship instrument, or a MALDI-guided SpatialOMx® expert there is the right timsTOF for your research needs. PASEF® (Parallel Accumulation Serial Fragmentation) is a powerful new technique that enables faster and more accurate identification, characterization, and quantification of proteins, peptides, lipids and other molecules providing significant benefits in their analysis. PASEF is an innovative feature incorporated into our timsTOF mass spectrometers that revolutionizes MS/MS sequencing.*

## timsTOF series

The timsTOF family offers unparalleled performance and versatility for a wide range of applications. The timsTOF Pro 2 delivers robust and comprehensive results for any challenge, while the timsTOF HT boosts the dynamic range and ion capacity to achieve maximum identification rates in proteomics experiments. The timsTOF SCP sets the global benchmark for single-cell proteomics, enabling robust and reproducible analysis of individual cells. The timsTOF Ultra 2, featuring the exclusive CaptiveSpray Ultra 2, further expands on this and sets new standards for single-cell and other very low input workflows, such as immunopeptidomics, reaching the highest sensitivity on the market.

| | timsTOF Pro 2 | timsTOF HT | timsTOF SCP | timsTOF Ultra 2 |
|---|---|---|---|---|
| resolution: | 60,000 | | | |
| acquisition rate: | up to 120 Hz in dda-PASEF | up to 300 Hz in dda-PASEF | up to 300 Hz in dda-PASEF | up to 300 Hz in dda-PASEF |
| PASEF methods: | dda-PASEF, dia-PASEF, diagonal-PASEF (midia, synchro), prm-PASEF | | | |
| source / laser: | ESI, CaptiveSpray 2, VIP-HESI, GC-APCI | | | ESI, Captive Spray Ultra 2, VIP-HESI, GC-APCI |
| size [mm]: | 980 x 1400 x 2570 | 980 x 1400 x 2570 | 1230 x 750 x 1990 | 1230 x 750 x 1990 |

# timsTOF fleX Solutions:

**MALDI-2 Technology — Bringing enhanced depth and sensitivity**

The MALDI-2 post-ionization boosts sensitivity by up to 2-3 orders of magnitude compared to traditional MALDI, depending on sample, matrix and analyte. This technique enables access to a wider range of chemical classes by reducing ion suppression effects. MALDI-2 is fully integrated in Bruker's software solutions and switching between ESI, MALDI and MALDI-2 is only one click away.

**microGRID — A powerful MALDI stage technology for accurate and robust high resolution imaging**

Bruker's microGRID technology combines MALDI stage and smartbeam 3D laser beam positioning to facilitate high quality imaging down to 5 µm spatial resolution during SpatialOMx® imaging. microGRID eliminates data striping, fading or oversampling effects in high resolution imaging data. The technology seamlessly integrates in Bruker's fully automated SCiLS autopilot workflow, making it attractive not only for experts but also for novelists as well as routine applications.

## timsTOF fleX series

The timsTOF fleX combines trapped ion mobility with Bruker's powerful MALDI technology, adding a high resolution spatial dimension and enabling SpatialOMx® as an essential innovation for molecular imaging on one platform. The timsTOF MALDI PharmaPulse® (MPP) adds a label-free high throughput solution (HTS) with extreme speed and robustness to the timsTOF fleX portfolio. The options MALDI-2 and microGRID provide unprecedented sensitivity and high spatial resolution for imaging experiments down to cell size resolution in SpatialOMx® workflows.

| | timsTOF fleX | timsTOF MALDI Pharma Pulse® |
|---|---|---|
| resolution: | 60,000 | |
| acquisition rate: | up to 300 Hz in dda-PASEF | |
| PASEF methods: | dda-PASEF, dia-PASEF, diagonal-PASEF (midia, synchro), prm-PASEF, iprm-PASEF | |
| source / laser: | ESI, CaptiveSpray 2, VIP-HESI, GC-APCI; MALDI (smartbeam 3D), MALDI-2 (MALDI-2 laser) | |
| size [mm]: | 825 x 1920 x 750 | |
| optional: | microGRID, MALDI-2 | |

# MALDI-TOF and TOF/TOF Mass Spectrometry

## Bruker's flagship FLEX series is the global leader for MALDI applications

*For over 30 years, matrix assisted laser desorption ionization (MALDI) TOF MS has proven its analytical capability. Offering unparalleled speed (time to results) and flexibility, MALDI-TOF MS stands out for its low sample volume requirements and ability to handle a broad range of sample content, including salts and buffers.*

### neofleX

Discover the neofleX™ MALDI-TOF/TOF, a high-performance benchtop mass spectrometer designed for speed and flexibility. With smartbeam 3D laser, it supports multiomics, offering robust imaging and analysis.

### rapifleX series

The rapifleX® MALDI-TOF/TOF system features a 10 kHz smartbeam 3D laser, adaptable ion optics, and advanced informatics for high-throughput screening and detailed protein characterization.

### smartfleX

The smartfleX MALDI-TOF system offers seamless polarity switching, smartbeam laser tech, and IR laser-based source cleaning for minimal downtime, providing access to the full MALDI analyte space.


| | neofleX MALDI-TOF/TOF | rapifleX [TOF and TOF/TOF] | smartfleX |
|---|---|---|---|
| resolution: | 30,000 | 43,000 | 2,000 |
| mass range: | up to 500,000 m/z | up to 500,000 | up to 500,000 m/z |
| mass accuracy: | 1.5 (int. calib.) [ppm] | 1 (int. calib.) [ppm] | ≤ 150 (int. calib.) [ppm] |
| laser: | smartbeam™ 3D | smartbeam™ 3D | smartbeam™ |
| laser frequency [Hz]: | 10,000 (MS) / 5,000 (TOF/TOF) | 10,000 (MS) / 10.000 (TOF/TOF) | 200 |
| size [mm]: | 1570 × 710 × 730 mm | 950 x 800 x 2750 | 500 × 710 × 1070 mm |
| optional: | - | autoloader | - |
| Fields of Application: | Imaging, Pharma QC workflows, | Imaging, Pharma QC workflows, UHT screening | Intact protein verification, Profiling, QC |

# MALDI Solutions

**rapifleX MALDI PhamaPulse**

The rapifleX MALDI PharmaPulse (MPP) enhances label-free HTS, combining the mass detection of enzymes, substrates and products with the required speed to comb through compound libraries containing millions of substances. The use of mass spectrometry allows the measurement of unmodified substrates in primary screens, greatly reducing false positive rates, and minimizes compounds sent to confirmation screens. The system is designed for automatic handling of 1536 well sample plates to screen more than a million compounds in a week in support of drug discovery.

## microflex series

The microflex® LRF MALDI-TOF MS offers 15k resolution, PAN pulsed ion extraction, and a gridless reflector for unmatched sensitivity. Ideal for QC, biomarker discovery, and analysis across various applications.

## autoflex maX series

The autoflex® maX MALDI-TOF MS features a 2 kHz smartbeam-II laser, enhanced dynamic range, and intuitive Compass software for rapid, high-quality data across diverse application fields.

## ultrafleXtreme

Elevate your research with ultrafleXtreme, the industry standard for MALDI-TOF/TOF. Achieve high-resolution, dynamic range, and flexibility in applications from proteomics to polymer analysis.

| | microflex LRF | autoflex maX [LIN, LRF and TOF/TOF] | ultrafleXtreme TOF/TOF |
|---|---|---|---|
| resolution: | 15,000 | 26,000 | 40,000 |
| mass range: | up to 300,000 | up to 500,000 | up to 500,000 |
| mass accuracy: | 15 (int. calib.) [ppm] | 2 (int. calib.) [ppm] | 1.5 (int. calib.) [ppm] |
| laser: | Nitrogen | smartbeam II | smartbeam II |
| laser frequency [Hz]: | 60 (MS) | 2,000 (MS) / 200 (TOF/TOF) | 2,000 (MS) / 1,000 (TOF/TOF) |
| size [mm]: | 530 x 680 x 1350 | 825 x 1920 x 750 | 784 x 1332 x 2300 |
| optional: | - | - | - |
| Fields of Application: | Peptide & Protein QC Applications | Imaging, intact biomolecules | Protein and antibody characterization, QC Applications, Imaging |

# Magnetic Resonance Mass Spectrometry

## Unravel nature's secrets

*The analytical fields of MALDI Imaging, intact biomolecules and metabolomics share the requirement for absolute certainty in compound identification. There can be no margin of error in the detection and correct assignment of extremely dangerous byproducts or deadly drug metabolites. With Bruker's MRMS technology, resolution and mass accuracy over a wide mass range reach unrivaled incredible new heights.*

## scimaX MRMS

Bruker's revolutionary superconducting magnet technology is the basis of the smaller footprint scimaXR MRMS system. This key innovation uses conduction-cooled 7T technology, which removes the requirement of liquid cryogen fills or quench ducts. The instrument comes standard with 2xR and Absorption Mode Processing (AMP) technology which means you have performance rivaling high field MRMS at your fingertips.

## solariX MRMS

This workhorse platform for high-field MRMS work (12T and 15T) is useful for ultra-complex mixture analysis requiring larger field strengths, such as analysis of intact biomolecules. These instruments feature long liquid cryogen (LHe) hold time with 1 year fill intervals as regular maintenance.

*scimaX MRMS*

*solariX MRMS*

**MRMS**

| | scimaX | solarix 7T | solarix 12T and 15T |
|---|---|---|---|
| maximum resolution: | > 20,000,000 | > 10,000,000 | > 10,000,000 |
| mass accuracy (internal): | 600 ppb | 600 ppb | 300 ppb (12T), 250 ppb (15T) |
| liquid cryogen annual maintenance: | No | Yes | Yes |
| quench duct requirement: | No | Yes | Yes |
| Source | ESI, MALDI; optional (APPI, APCI, GC-APCI, DIP) | ESI; optional (MALDI, APPI, APCI, GC-APCI, DIP) | ESI; optional (MALDI, APPI, APCI, GC-APCI, DIP) |
| Fields of Application | Imaging, Metabolomics, intact biomolecules | Imaging, Metabolomics, | intact biomolecules |

# Surface Plasmon Resonance

## High performance, high-throughput SPR Analytical Biosensor for the real-time, label-free characterization of molecular interactions

*Surface plasmon resonance is an optical-based, label-free detection technology for real-time monitoring of binding interactions between two or more molecules. A wide range of molecules can be studied, from fragments to small molecules to proteins and viruses. This innovative technology is capable of providing biophysical data such as affinity, kinetics and thermodynamics, in addition to answering basic questions of binding specificity and concentration.*

## Surface Plasmon Resonance

From initial screening to detailed kinetic characterization and thermodynamics measurements, our products enable high-throughput surface plasmon resonance (SPR) analysis of molecular interactions.




**SPR**

| | 24 Pro | 32 Pro | Triceratops SPR #64 |
|---|---|---|---|
| Samples per day: | 4400+ | 4400+ | 4400+ |
| Sensor spots per channel: | 3 | 4 | 8 |
| Sample processing: | Simultaneous processing of up to 8 samples over 24 sensor spots | Simultaneous processing of up to 8 samples over 32 sensor spots | Simultaneous processing of up to 8 samples over 64 sensor spots |
| Software compatibility: | Genedata compatibility | | |
| Automation: | optional plate robot integration for 24/7 operation | | |
| Fields of Application: | Determination of affinities and kinetics of interactions between e.g. protein vs. protein; protein vs. small molecules, protein vs. RNA or DNA; screening of therapeutics and low molecular weight compounds; epitope characterization; concentration analysis; mode of action studies; multiplexing studies | | |

# SPR Solution

**SPR App**

Cactus Tools is the first SPR application for your mobile smartphone. It is a helpful tool, when working with SPR instruments as it contains as a basic knowledge section, a data simulation tool as well as a lab calculator.
Available at the AppStore and Playstore, Download now.

Download on the App Store

GET IT ON Google Play

# Ultra-High Resolution QTOF Mass Spectrometry

## Outstanding accurate mass capabilities

*Obtaining the most complete and true picture of a sample set is a consistent goal. Complex sample matrices demand ever higher levels of sensitivity and speed to truly advance scientific knowledge. However, there are everyday practical realities that are required to be routinely overcome. The outstanding dynamic range, high mass accuracy, and MS/MS performance enable Bruker's UHR QTOF MS systems to deliver confident, reliable results for both targeted analytical testing and broader discovery research applications.*

## ESI QTOF

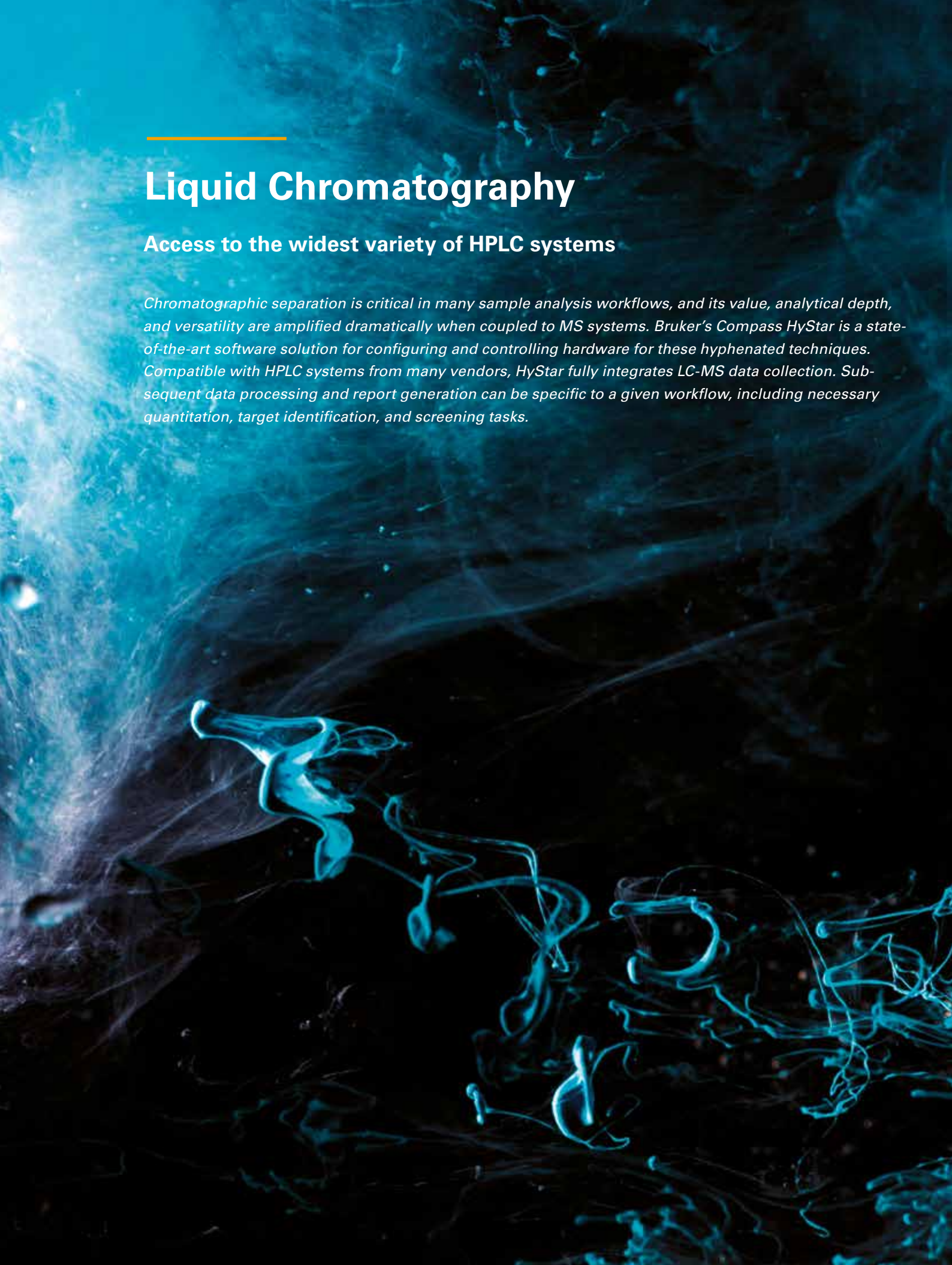
Our ESI QTOF mass spectrometers are the showcase instrument platform for life science research, drug discovery and development, and screening applications involving the analysis of both targeted and unknown compounds in complex matrices. The systems provide cutting edge performance in one-shot analysis for identification and quantitation from small molecules up to high MW antibodies, and the dynamic source configuration offers significant analytical versatility.


| compact | | impact II | | maXis II | |
|---|---|---|---|---|---|
| resolution: | 30,000 | resolution: | 60,000 | resolution: | 80,000 |
| scan speed: | 1-50 Hz (MS & MS/MS) | scan speed: | 1-60 Hz (MS & MS/MS) | scan speed: | 1-50 Hz (MS & MS/MS) |
| fragmentation: | CID | fragmentation: | CID | fragmentation: | CID, ETD |
| source: | All systems can have: ESI, APCI II, APPI II, ionBooster, GC APCI, DirectProbe DIP, CaptiveSpray, VIP-HESI | | | | |
| size [mm]: | 624 x 510 x 1240 | size [mm]: | 1200 x 800 x 1980 | size [mm]: | 1320 x 800 x 2845 |

# Liquid Chromatography

## Access to the widest variety of HPLC systems

*Chromatographic separation is critical in many sample analysis workflows, and its value, analytical depth, and versatility are amplified dramatically when coupled to MS systems. Bruker's Compass HyStar is a state-of-the-art software solution for configuring and controlling hardware for these hyphenated techniques. Compatible with HPLC systems from many vendors, HyStar fully integrates LC-MS data collection. Subsequent data processing and report generation can be specific to a given workflow, including necessary quantitation, target identification, and screening tasks.*



## nanoElute 2 – Ready for the Next Generation of 4D-Proteomics™

The nanoElute 2® is a high-performance nanoflow liquid chromatography system with an intuitive and flexible user interface, covering a broad range of applications from single cell to high-throughput routine proteomics. This next generation instrument has been refined for unrivalled robustness, ultimate performance, and ease-of-use to provide you with the highest chromatographic resolution, resulting in exceptional peptide identification and quantification.


| | nanoElute 2 |
|---|---|
| flow range: | 50 - 2,000 nL |
| pressure limit: | 1,000 bar |
| connections: | UHPLC finger-tight connections; reusable torque limiting bottom sealing capillaries for all sample lines |
| size [mm]: | 790 × 490 × 900 |
| additional information: | Trouble-free operation, ease-of-use along with top performance |
| gradient delay volume | < 0.4 uL |
| Fields of Application | single cell to high throughput routine proteomics |

## Elute PLUS LC Series – Simply more for your MS analysis

Elute PLUS LC systems are built with intelligent novel flow control algorithms to deliver robust and precise gradients regardless of solvent compressibility, pressure, and flow rates. Elute LC systems incorporate self-priming and self-purging capabilities through the built-in pump, offering a simple and fast exchange of mobile phases and avoiding any leaks associated with manual operations.

The unique feature of automatic solvent compressibility measurement compensates for flow pulsation and flow rate reduction caused by solvent compression. This principle makes it easy to maintain and transfer LC methods. Additionally, the column switch (up to six) option provides great flexibility for routine labs, allowing higher productivity e.g., for the analysis of different sample types for overnight LC-MS runs.
The Elute PLUS series has been improved to give you the best retention time stability and peak shape, as well as full robustness when switching methods and solvents, successfully enhancing high-throughput analysis.


| | Elute PLUS LC | | |
|---|---|---|---|
| | UHPLC | OLE | HT |
| flow range: | 1 - 5,000 µL 1 | 1 - 5,000 µL 1 | 1 - 5,000 µL 1 |
| pressure limit: | 1,300 bar | 1,300 bar | 1,300 bar |
| carryover: | 0,001% | 0,001% | 0,003% |
| size [mm]: | 690 × 500 × 610 | 690 × 500 × 610 | 550 × 1,180 × 500 |
| additional information: | Faster and high resolution separations | Combine the advantages of UHPLC and online liquid exraction | UHPLC combined with PAL3 autosampler for high sample throughput |
| Fields of Application | All fields of application | Applied markets, online extraction | Applied markets and Pharma, high throughput |

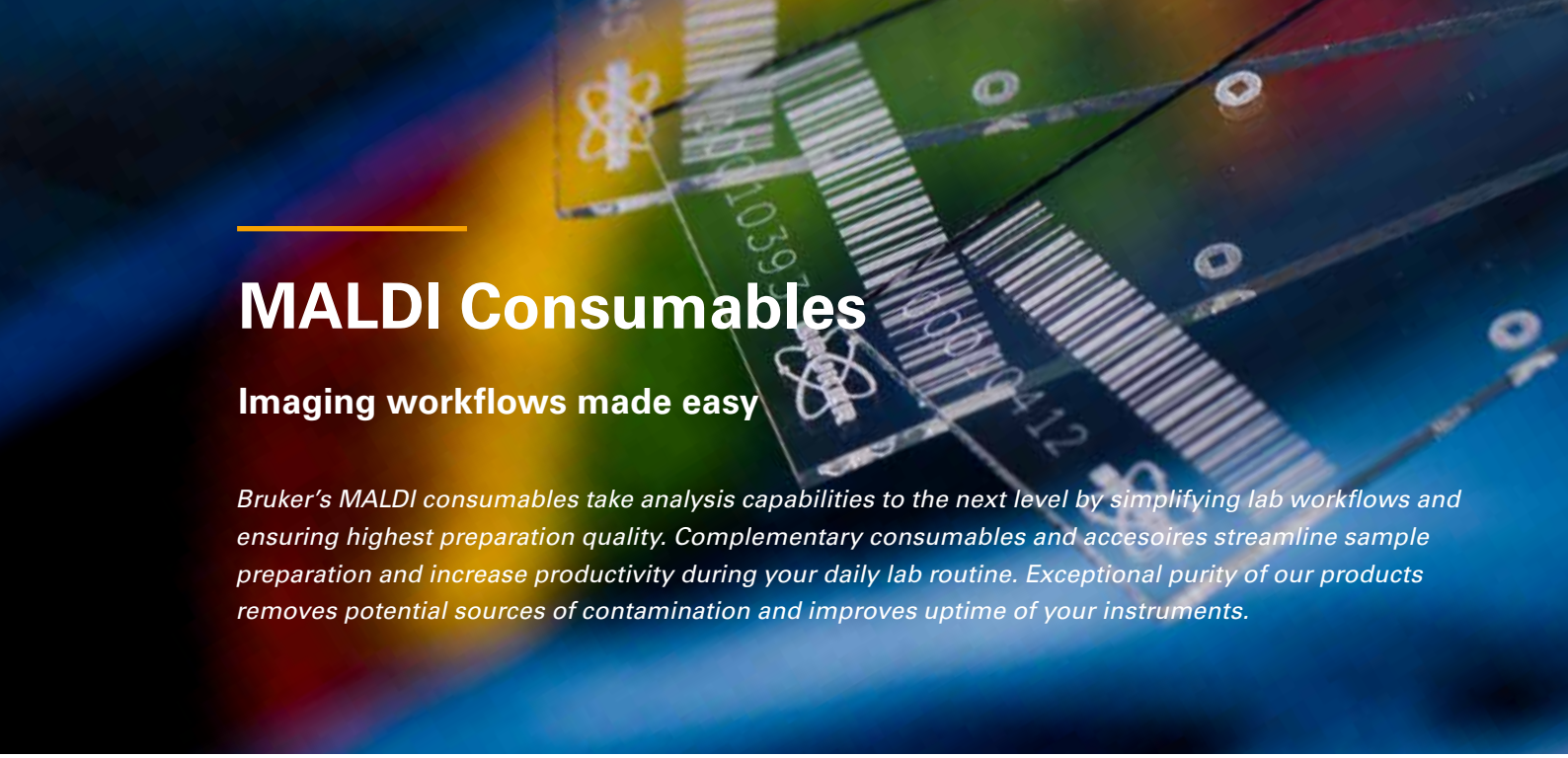
# PepSep Columns and PepSep Emitters

## Make proteomics faster, easier and more affordable

*More samples. Less time. Better reproducibility.*

*Achieve precise separation with our cutting edge reversed-phase HPLC columns. Experience deeper coverage, higher throughput, and robustness, meeting the demands of even the most challenging samples. Tested at lightning fast PASEF speeds, PepSep® columns are the ultimate choice for all your proteomics applications. Get ready to elevate your analysis to new heights!*

| | Columns | | | | | Emitters |
|---|---|---|---|---|---|---|
| | **PepSep ULTRA XL** | **PepSep ULTRA** | **PepSep XTREME** | **PepSep MAX** | **PepSep MAX HT** | **CaptiveSpray 2 Emitter** |
| | Ultra power for spectral library generation. | Ultra-high sensitivity and reproducibility at PASEF speeds. | Exceed sample throughput limits at PASEF speeds with high 4D-sensitivity | Maximize performance to accurately analyze 1000s of samples. | Maximize speed, resolution and dynamic range. | Ready to use fixed tip emitter. Simple plug and play design. |
| Size | 50 cm x 75 µm x 1.5 µm | 25 cm x 75 µm x 1.5 µm | 25 cm x 150 µm x 1.5 µm | 10 cm x 150 µm x 1.5 µm | 5 cm x 150 µm x 1.5 µm | 10 µm or 20 µm |
| Features | Designed for longer gradients which are essential for spectral library generation. | Unmatched sensitivity with greater protein ID in immunopeptidomics and single cell proteomics. | Speed and sensitivity in a single column solution provides improved coverage, throughput, sensitivity, and reproducibility. | Accurate quantitative analysis of 1000+ plasma samples at turbo speeds. | Ideal for applications where speed is essential, such as the analysis of clinical samples or the screening of drug libraries. | Save time with pre-assembled static tips and ZDV union, ready to use out of the box. Compatible with all CaptiveSpray sources. Sold as a pack of two. |



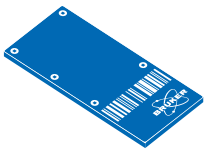
# MALDI Consumables

## Imaging workflows made easy

*Bruker's MALDI consumables take analysis capabilities to the next level by simplifying lab workflows and ensuring highest preparation quality. Complementary consumables and accesoires streamline sample preparation and increase productivity during your daily lab routine. Exceptional purity of our products removes potential sources of contamination and improves uptime of your instruments.*

## IntelliSlides® – Maximize information content per pixel with intelligence

Bruker's IntelliSlides® are the perfect tool for SpatialOMx®. They simplify your MALDI Imaging workflows by enabling automated setup of each measurement. IntelliSlides incorporate permanent inscriptions on the conductive slide surface that indicates optimal placement of samples and pre-inscribed fiducials (teach marks) for Imaging. Additional unique serial numbers and barcodes fully automate sample registration and software tracking. Automated image acquisition is available on Bruker's timsTOF fleX and rapifleX instruments with the SCiLS autopilot included in flexImaging 6.0 and above.



## fleXmatrix® – The key to success in MALDI MS analyses

fleXmatrix® kits enable easy and convenient preparation of matrix solutions for MALDI Imaging. Pre-portioned and packaged in convenient tubes, fleXmatrix® is stable and easy to handle to simplify sample preparation, particularly for standard spraying or sublimation methods. Different fleXmatrix® kits are dedicated to the imaging of proteins, peptides, and lipids, and a specialized matrix for MALDI-2 post-ionization analysis. fleXmatrix® is perfectly suited for the use with Bruker's IntelliSlides® and can be measured on all Bruker MALDI mass spectrometry imaging platforms.

## MALDI PharmaPulse® HTS accessories – A complete HTS solution

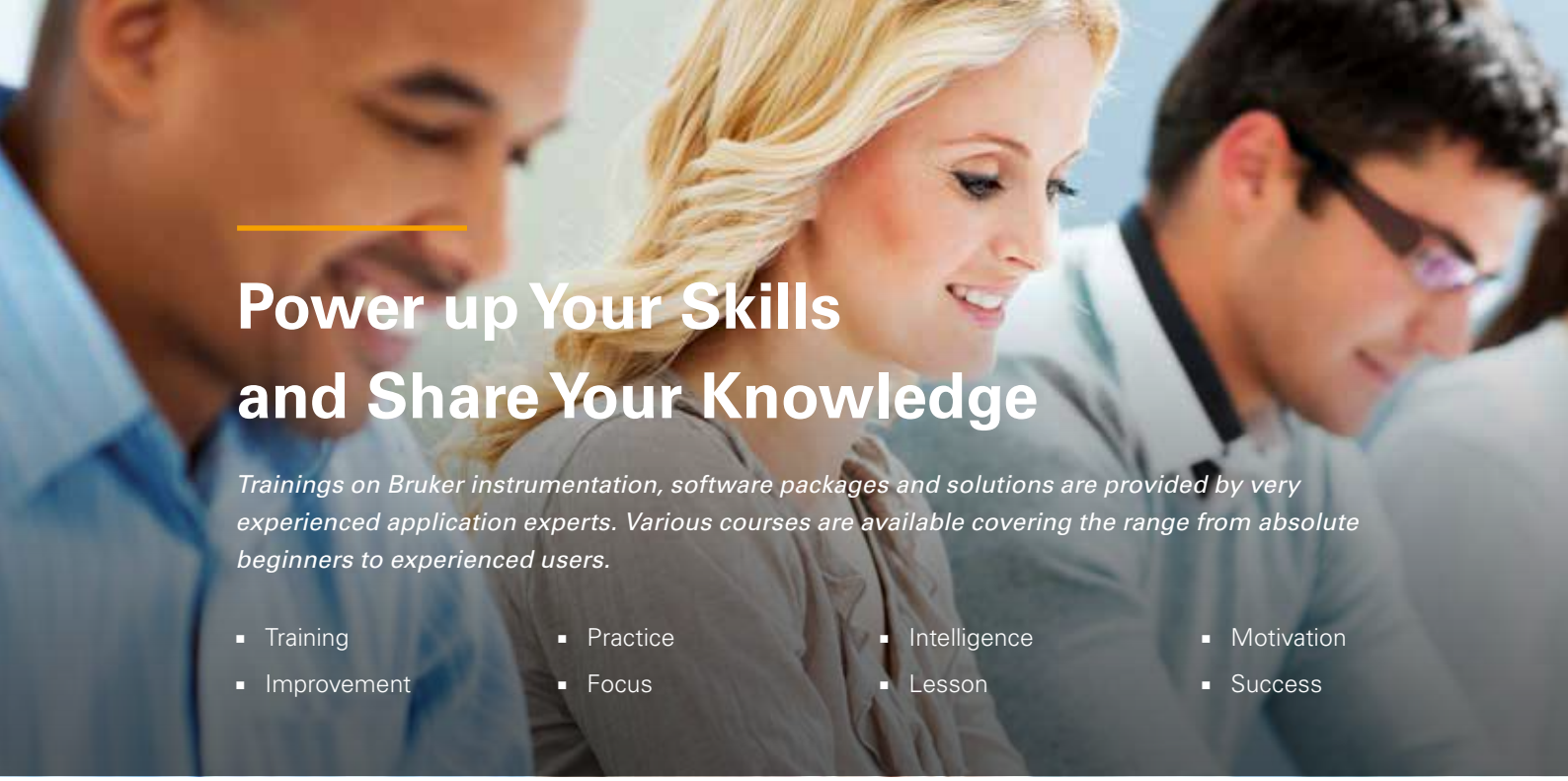
Brukers MALDI PharmaPulse® HTS accessories are an integrated solution specifically developed to improve the effiency of your HTS and uHTS daily lab workflows. The disposible Plain HTS MALDI Plates 1.0 mm are designed for automated MALDI preparations by high-performance liquid handlers in any format ranging from 96 to 1536 and beyond. These plates fit perfectly in Brukers lightweight HTS MALDI Plate Adapter 1.0 mm which is specifically designed for safe and efficient sample handling by lab robotics.

# Ion Sources

## Dynamic Source Configuration

Bruker's LC-MS systems support a wide range of source options from both Bruker and from third-party vendors.

| Source Type | | Description |
|---|---|---|
|  | **CaptiveSpray Ultra 2** | The CaptiveSpray Ultra 2 combines nano-flow sensitivity with ease of use, thanks to its "on-off" design and zero-adjustment positioning. It ensures the highest signal-to-noise ratio and clearer data for advanced proteomics research. Optimized for the timsTOF Ultra 2. |
|  | **CaptiveSpray 2** | The next generation of the CaptiveSpray ion source builds on the exceptional nano-flow performance of its predecessor while introducing unparalleled ease of use into proteomics workflows. |
|  | **VIP-HESI dual source** | This VIP-HESI source is compatible with Bruker's timsTOF and QTOF systems and generates a higher sensitivity for a broad range of components. The vacuum insulated probe enhances ionization efficiency whilst minimizing thermal degradation of analytes. Matrix is rapidly and efficiently removed from the source via an active exhaust maximizing system robustness. |
|  | **APCI** | Atmospheric Pressure Chemical Ionization is used in metabolomics, as well as for drug or pesticide screening for less polar molecules where ESI fails to deliver reasonable quantities of ions. |
|  | **APPI** | Atmospheric Pressure Photo Ionization is used for less polar or non-polar molecules that cannot be ionized by ESI or APCI. |
|  | **DIP** | The DirectProbe add-on for the Bruker APCI II and APPI II ion sources allows for direct analysis of liquid and solid samples without tedious sample preparation. |
|  | **GC-APCI II** | The GC-APCI II source with a unique flexible heated transfer line and calibrant delivery enables GC coupling to any Bruker TOF, QTOF, trap, or FTMS system originally designed for LC coupling. |



# Power up Your Skills and Share Your Knowledge

*Trainings on Bruker instrumentation, software packages and solutions are provided by very experienced application experts. Various courses are available covering the range from absolute beginners to experienced users.*

- Training
- Improvement
- Practice
- Focus
- Intelligence
- Lesson
- Motivation
- Success

## General Remarks and Information for Training Courses

### Registration
For registration, please access the online registration at www.bruker.com or contact training@bruker.com.

### Registration
After submission of your registration, you will get a summary of the submitted information automatically. This is not a confirmation. The registrations will be taken into consideration on a first come, first served basis.

### Confirmation
After receiving your registration, we will confirm your participation. If the selected training course is already fully booked, we will inform you immediately.

### Training costs
Training costs include the course fees as well as lunch and beverages during the training. Travel and accommodation are excluded. Please contact your local Bruker Training Center to get a list of recommended hotels located nearby.

### Course language
All courses will be held in English unless otherwise agreed with the customer.

### Cancellation
Bruker Daltonics GmbH & Co. KG reserves the right to cancel the training if the minimum number of participants is not achieved one month prior to the training date. Customers may cancel in writing not later than one month prior to the training date at a full refund of the training price. If customer cancels later than two weeks before the training, the full training fee will be charged. Customers may substitute a participant without extra charge or payment in this case. Bruker needs to be informed to register the new participant beforehand.

### Training material
Training material will be provided by the trainer. Any recordings of training or parts of training are prohibited. Bruker general terms and conditions of supply and service apply.

### Learn More and visit:
https://www.bruker.com/de/services/training/mass-spectrometry.html

# Software Solutions

## Compass and Bioinformatics

***Bruker Daltonics software solutions provide maximum information via streamlined, easy to use processes***

### BioPharma Compass®

Field of Application: BioPharma

BioPharma Compass provides integrated workflows for biopharmaceutical industry supporting 21 CFR Part 11 requirements. Workflows comprise all aspects from data acquisition to report generation, characterization and comparative quantitative assessments in multiple attribute monitoring (MAM) analyses. MAM peptide analysis as well as host cell protein (HCP) analyses can benefit from the use of CCS-enabled data analysis in terms of sequence coverage and dynamic range. Multi-Target-Screening workflows enable batchwise processing multiple samples. OligoQuest™ enables oligonucleotide sequence analysis using LC-UV-MS/MS including side product quantitation and identification or targeted analysis.

### OmniScape™

Field of Application: Top-Down protein sequencing

OmniScape™ offers unparalleled access to Top-Down mass spectrometry data of proteins. The OmniWave™ algorithm excels at detecting even low-abundance, highly charged fragment ion isotope patterns, seamlessly integrating them into further analysis workflows. Unknown proteins can be de novo sequenced and identified through homology-based database searches. Protein sequences, including their various proteoforms, can be confirmed and screened for PTMs. All results are validated peak by peak within an intuitive software interface.
Multiple datasets from different experimental conditions can be combined to achieve significantly larger sequence coverage and higher certainty in proteoform assessment. OmniScape™ supports data import from all Bruker instruments and third-party instruments via a generic profile data text format. The software is user-friendly and quick to learn, with algorithms that handle complex computational challenges at high speed.

### Bruker ProteoScape™

Field of Application: Proteomics

Run & Done with Bruker ProteoScape! A hardware and software solution, enabling integrated real-time CCS-enabled analysis of dda-PASEF, dia-PASEF and diagonal-PASEF data. Bruker ProteoScape (BPS) removes the data analysis bottleneck introduced by large sample cohorts allowing for greater throughput and more identifications seconds after a measurement is complete. BPS is smart, allowing for user-defined qualifications/parameters to seamlessly guide the progression of your sample queue, while checking suitability and saving precious samples, expensive consumables, and instrument time. Utilizing workflows integrated with powerful algorithms such as TIMSrescore, TIMS DIA-NN, Spectronaut and BPS Novor, Bruker ProteoScape streamlines your labs analysis pipeline from data to results as quickly as possible.

### Spectronaut®

Field of Application: Proteomics

Spectronaut® is Biognosys' flagship data analysis software for data-independent acquisition (DIA) mass spectrometry (MS) based proteomics.

The software employs advanced search and artificial intelligence (AI) algorithms to translate data into actionable insights for life science research. Spectronaut enables reproducible and precise quantification of thousands of proteins in a single experiment and provides multi-dimensional insights into protein expression, function, and structure across all major biological species and sample types.

| | | |
|---|---|---|
| BRUKER MetaboScape® | **MetaboScape®**<br><br>Field of Application: Metabolomics and Lipidomics | MetaboScape is the software for 4D-Metabolomics™ and 4D-Lipidomics™ to pinpoint and identify compounds that change because of perturbation or disease. T-ReX® 4D processing unlocks CCS values as additional criterion for the Annotation Quality Scoring (exact mass, retention time, isotopic pattern, MS/MS spectrum, CCS). MetaboScape supports spectral libraries like MetaboBASE®, HMDB, MetaboBASE Plant, as well as custom libraries, in-silico fragmentation and CCS-Predict Pro. A range of interactive tools for quality control, and data exploration help to bring analysis results into biological context. Using its REST-API, MetaboScape and many of its functions can also be integrated into custom bioinformatics pipelines. |
| BRUKER TASQ® | **TASQ®**<br><br>Field of Application: Screening and Quantitation | TASQ (Target Analysis for Screening and Quantitation) is Bruker's solution for screening, confirmation and quantitation of large sample batches, including hundreds of compounds per analysis. The CCS-enabled TASQ solution allows exploiting the ion mobility separation on timsTOF instruments for further confidence. TASQ takes advantage of both nominal and high resolution, accurate-mass data generated by Bruker's triple quadrupole and QTOF mass spectrometers. TargetScreener HR – driven by TASQ – allows report generation from 'vial to report' in seven clicks. TASQ includes now support of Audit Trail, User Action Rights and User Access Control. |
| SCiLS | **SCiLS™ Lab**<br><br>Field of Application: Imaging | SCiLS Lab is the worldwide leading software for analysis of mass spectrometry imaging data from all major MS vendors. Comparative analysis of multiple samples can be visualized in both 2D and 3D, enabling a multitude of applications in pharmaceutical drug development, in biomarker research, as well as in translational pathology research. The quantitation workflow enables to easily quantify target molecules directly from tissue. SCiLS Lab integrates with MetaboScape for confident Molecular Annotations and enables spatial multiomics with the Ion Image Mapper. For integration with histology, it provides an interface to the powerful open-source software QuPath widely used in digital pathology. Use the SCiLS Lab application programming interface (API) to directly interact with your data in Python or R, and use your own code to perform custom processing and reporting or to create unique visualizations based on your SCiLS Lab data. |
| SCiLS | **SCiLS™ Scope**<br><br>Field of Application: Imaging | SCiLS™ Scope lowers the barriers for sharing and viewing MALDI HiPLEX-IHC and MALDI Imaging data. With the easy-to-use, lightweight interface and data in the open OME-TIFF format, it is ideal for sharing data between collaborators who want to focus on examining images. Intuitive review of images within a pathological context provides more insight per pixel. |
| BRUKER MALDI PharmaPulse® | **MALDI PharmaPulse®**<br><br>Field of Application: High-Throughput Screening (HTS) | MALDI PharmaPulse allows data acquisition and analysis of high-throughput screening data acquired on the timsTOF MALDI PharmaPulse (with and without MALDI-2). The Screening software workflow module provides the tools required for seamless setup, execution and result visualization of HTS screens. The Synthesis Screening workflow allows flexible screening of many different target compounds per individual well. Data in timsON and timsOFF, MS and MS/MS and optionally MALDI-2 mode are supported. |
| BRUKER GlycoScape™ | **GlycoScape™**<br><br>Field of Application: Glyco-proteomics | Run & Done for glycopeptide analysis! GlycoScape is included with the Bruker ProteoScape package and extends the capabilities to include real-time glycopeptide analysis for glycobiologist. Powered by the Myriad workflow which effectively deconvolutes glycopeptide fragmentation spectra into peptide and glycan moiety spectra using common N-glycan fragments. Each moiety is then identified by a specialized real-time algorithm after which the glycopeptide is "reassembled". A significant advantage of the Myriad workflow is that it does not require any glycan database(s), enabling the identification of glycans not in the database(s) and minimizing false negatives. |
| | **Other solutions** | Bruker's data formats are open to all, including third-party software vendors by accessing our SDK via our website. We collaborate intensively and openly support various partners, including the Max-Planck-Institute for Biochemistry on MaxQuant, the University of Michigan on the FragPipe suite, the University of Washington on Skyline, and Ghent University on IonBot. We work closely with Protein Metrics on Byos® for biopharma related workflows, Finally we support various academic groups providing open source software to the community. |

# Service Agreements

Choose one of the following LabScape Maintenance Service Agreements available for selected MS, LC, GC, and SPR instruments:

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**LabScape Essential** – Ensure peak performance. A combination of remote support and regular annual maintenance helps you operate your instrument under its optimal conditions.

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**LabScape Complete** – All support you need. A comprehensive solution providing complete service coverage including spare and wear and tear parts which helps you avoid instrument failures, costly repairs and down time.

**LabScape Complete 48** – All the support you need within 48 hours. A VIP package including guaranteed on-site response within 2 business days to resolve the problem before it affects your business.

| | LabScape Connect | LabScape Essential | LabScape Access | LabScape Complete | LabScape Complete 48 |
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| Regular Maintenance Work and Parts | | ✓ | ✓ | ✓ | ✓ |
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| Wear and Tear Part Replacement | discount | discount | discount | ✓ | ✓ |
| Loaner Equipment* | | | | | ✓ |
| **Compliance Services** | | | | | |
| Operational Qualification / Perform. Validation | | | | | included |
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| On-site Response | | | 3-5 business days | 3-5 business days | 2nd business day |
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| Consumable Parts | discount | discount | discount | premium discount | premium discount |
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* if applicable to the respective MS or SPR product
** SCiLS Pro, MetaboScape, TASQ, Biopharma Compass

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