BRUKER

Product Overview

- Life Science Mass Spectrometry

Innovation with Integrity

Mass Spectrometry

Empowering Science with Innovation and Integrity

As one of the world's leading analytical instrumentation companies, Bruker offers a broad spectrum of advanced solutions in all fields of research and development. All our systems and instruments are designed to improve product safety, accelerate time-to-market, and support our customers in life science research and industries in successfully enhancing quality of life.

We have been driving innovation in analytical instrumentation for more than 50 years. Today, over 6,000 employees are working worldwide on this challenge in more than 70 locations across all continents.

High Performance, Easy-to-Use, Expertly Supported

Bruker has been committed to providing scientists with the very best in innovative mass spectrometry and analytical solutions. Bruker's systems are expertly designed for performance and utility, and feature a number of unique capabilities and technologies to enhance data quality and facilitate data mining. Bruker's systems are the highest performance instruments in their class. Recent advances in Bruker's mass spectrometry product lines make this analytical power more accessible than ever to both new and expert users.

Bruker's Sales, Service, and Applications teams will assemble your optimal instrument and software package, allowing you to smoothly go from ideas to results.

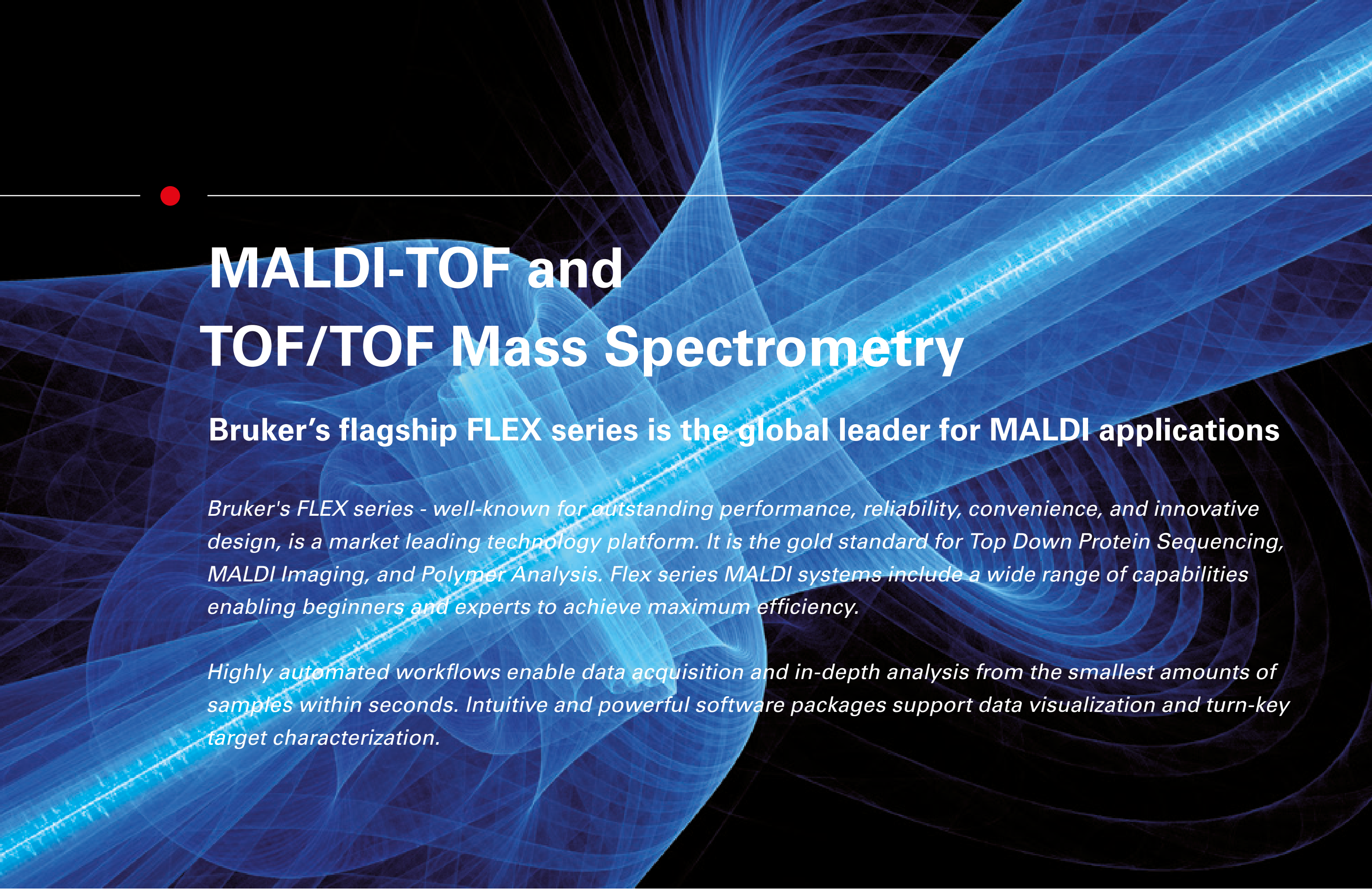
Highly Differentiated Mass Spectrometry Solutions

Bruker's unique mass spectrometry solutions are the measure of innovation. They deliver a standard of performance that sets the new standard. Aspire to tackle the most challenging problem and accelerate scientific discovery.

Dig deeper into the proteome with PASEF on the timsTOF Pro. Even with fast nanoLC runs, you will obtain higher sensitivity and better quantification due to the advantages provided by Trapped Ion Mobility (TIMS).

Unleash the power of Isotopic Fine Structure and eXtreme Resolution across the acquired m/z range. With resolution of R > 20 million and parts per billion mass accuracy, scimaX™ MRMS will find your formula for success.

Screen > 1M compounds per week on the rapifleX MALDI PharmaPulse®. With false discovery rates < 1%, this unique lable-free approach to uHTS drug discovery, saves costs while radically improving productivity.



MALDI-TOF and TOF/TOF Mass Spectrometry

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

Bruker's FLEX series - well-known for outstanding performance, reliability, convenience, and innovative design, is a market leading technology platform. It is the gold standard for Top Down Protein Sequencing, MALDI Imaging, and Polymer Analysis. Flex series MALDI systems include a wide range of capabilities enabling beginners and experts to achieve maximum efficiency.

Highly automated workflows enable data acquisition and in-depth analysis from the smallest amounts of samples within seconds. Intuitive and powerful software packages support data visualization and turn-key target characterization.

microflex LRF series

From biomarker discovery to the analysis of oligonucleotides, small molecules, polymers and quality control screening, the bench-top microflex® LRF is the perfect choice. It is easy to use with intuitive operations that are ideal for non-expert users and busy multi-instrument labs. The oil free vacuum system is fully integrated and noise reduced. Stable ion generation is produced by a 60 Hz fiber-optic laser – this robust design guarantees reliable daily operation.

autoflex maX series

Innovative MALDI-TOF and TOF/TOF technology optimized for robustness enables reliable and detailed protein/peptide characterization, polymer analysis, MALDI tissue imaging, glycan analysis, and high-throughput biochemical screening. Its smartbeam™-II laser technology with up to 2,000 Hz repetition rate is a must for MALDI Imaging and delivers superior performance for proteomics studies. The field-upgradable autoflex® maX instruments are available as linear, high resolution reflectron or TOF/TOF versions. The TOF/TOF configurations enable fast and sensitive MS/MS experiments via LID and high energy CID.

	microflex LRF
resolution:	15,000
mass range:	up to 300,000
mass accuracy:	15 (int. calib.) [ppm]
laser:	Nitrogen
size [mm]:	530 x 680 x 1,350
laser frequency [Hz]:	60 (MS)

	autoflex maX [LIN, LRF and TOF/TOF]	
resolution:	26,000	
mass range:	up to 500,000	
mass accuracy:	2 (int. calib.) [ppm]	
laser:	smartbeam II	
size [mm]:	825 x 1,920 x 750	
laser frequency [Hz]:	**LRF**	**TOF/TOF**
	2,000 (MS)	2,000 (MS) 200 (TOF/TOF)

MALDI Solutions

rapifleX MALDI PhamaPulse

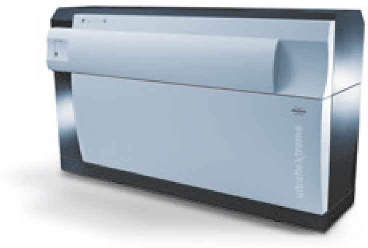
The rapifleX MALDI PharmaPulse (MPP) enhances label-free HTS, combining the mass detection of enzymes, substrates and products with the required speed to comb through compound libraries containing millions of substances. The use of mass spectrometry allows the measurement of unmodified substrates in 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.

rapifleX MALDI Tissue Imager

The newly developed smartbeam 3D laser fires at a repetition rate of up to 10 kHz and features a laser diameter of 5 µm. The laser can move independently from the (continuously moving) sample stage to scan the full area of each pixel and achieve high pixel rates. This produces truly square pixels, utilizing all of the available sample area for maximum sensitivity and pixel-to-pixel reproducibility.

ultrafleXtreme

With its further enhanced dynamic range and the patented smartbeam-II laser the ultrafleXtreme provides outstanding spectral quality in both MS and MS/MS modes empowering tissue imaging, intact protein analysis, glycoproteomics, biologics or oligo QC, and LC-MALDI workflows. Broadband mass resolving power up to 40,000 enables precision proteomics via Bruker's unique PAN™ technology for highest mass resolution across a very wide mass range. A very long MALDI laser lifetime in combination with automated laser based source cleaning in just minutes leads to high uptime and low maintenance costs.



ultrafleXtreme speed TOF/TOF	
resolution:	40,000
mass range:	up to 1,000,000
mass accuracy:	1.5 (int. calib.) [ppm]
laser:	smartbeam II
size [mm]:	784 x 1,332 x 2,300
laser frequency [Hz]:	2,000 (MS) / 1,000 (TOF/TOF)

rapifleX series

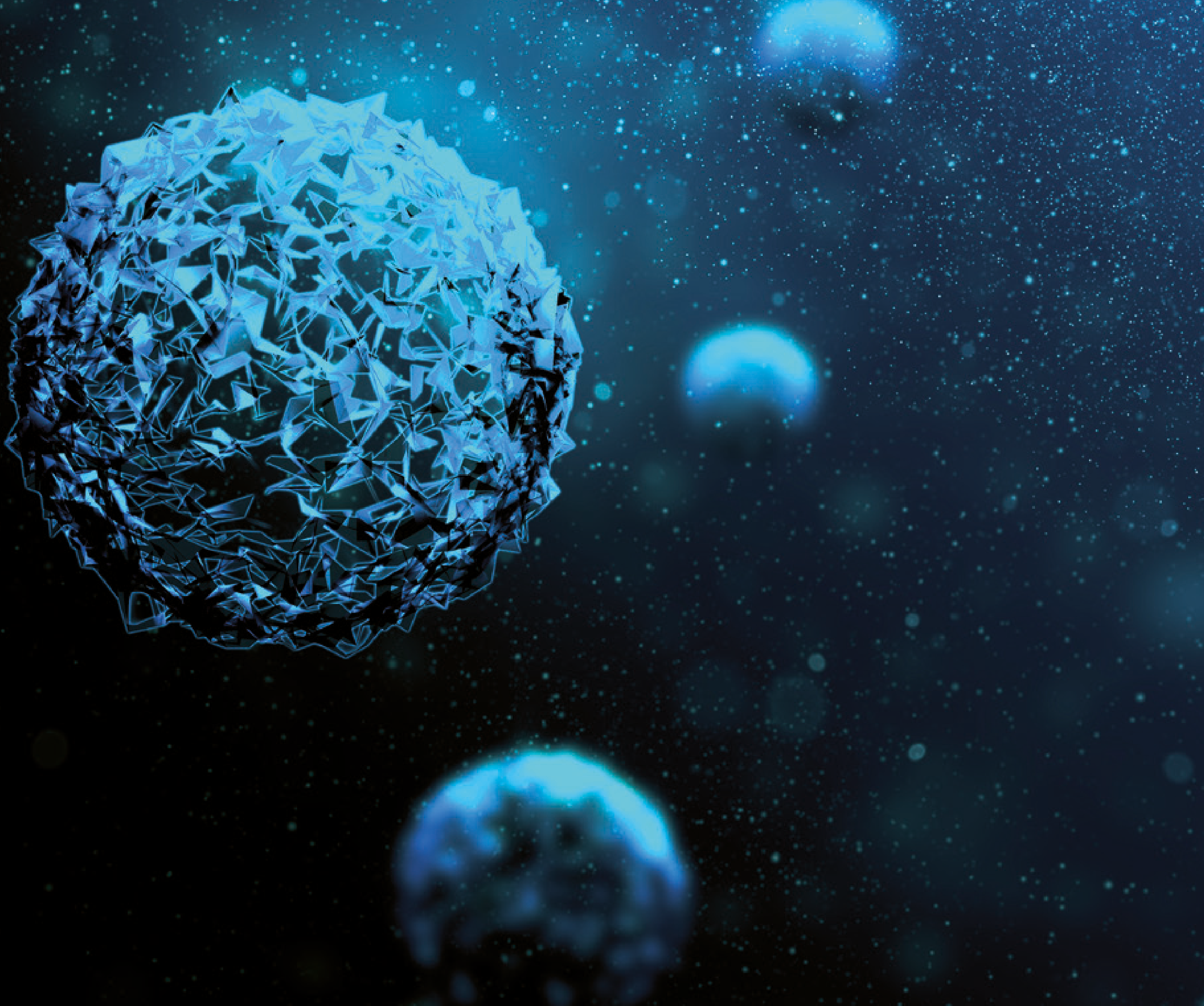
The rapifleX® series is the most advanced and adaptable MALDI TOF(/TOF) system available today. The 10 kHz smartbeam 3D technology allows for up to 20 times faster MALDI tissue imaging in MS and MS/MS modes. With its mass resolving power of up to 50,000 and increased dynamic range, applications such as ultra-high throughput biochemical screening, top-down sequencing (e.g. of biotherapeutics), glycan structure analysis or disulfide/scrambling/trisulfide bond determination are easily addressed. Adaptable ion optics allow for best sensitivity in MS and MS/MS modes.

rapifleX [LRF and TOF/TOF]		
resolution:	50,000	
mass range:	up to 1,000,000	
mass accuracy:	1 (int. calib.) [ppm]	
laser:	smartbeam 3D	
size [mm]:	950 x 800 x 2,970	
optional:	autoloader	
laser frequency [Hz]:	**Basic**	**TOF/TOF**
	10,000 (MS)	10,000 (MS)& (TOF/TOF)

Ultra High Resolution QTOF Mass Spectrometry

Outstanding accurate mass capabilities now with TIMS

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, 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. From the trusted family of UHR QTOF systems to the revolutionary separations orthogonality advantage of the timsTOF systems, critical sample details are delivered with speed and sensitivity.



timsTOF Pro

With timsTOF, Bruker introduces the next generation of ion mobility mass spectrometry. MS-based proteomics has become a powerful technology for the identification and quantification of thousands of proteins, and the power of trapped ion mobility spectrometry (TIMS) unlocks an additional dimension of separation.
The timsTOF Pro with PASEF technology is the new standard for shotgun proteomics. The instrument delivers revolutionary improvements in scan speed, coupled with enhanced specificity and high sensitivity.

	timsTOF / timsTOF Pro	
resolution:	50,000	
scan speed:	**Basic**	**Pro**
	1-50 Hz (MS & MS/MS)	1-100 Hz (MS & PASEF)
fragmentation:	**Basic**	**Pro**
	CID	PASEF
size [mm]:	980 x 1400 x 2570	

ESI QTOF

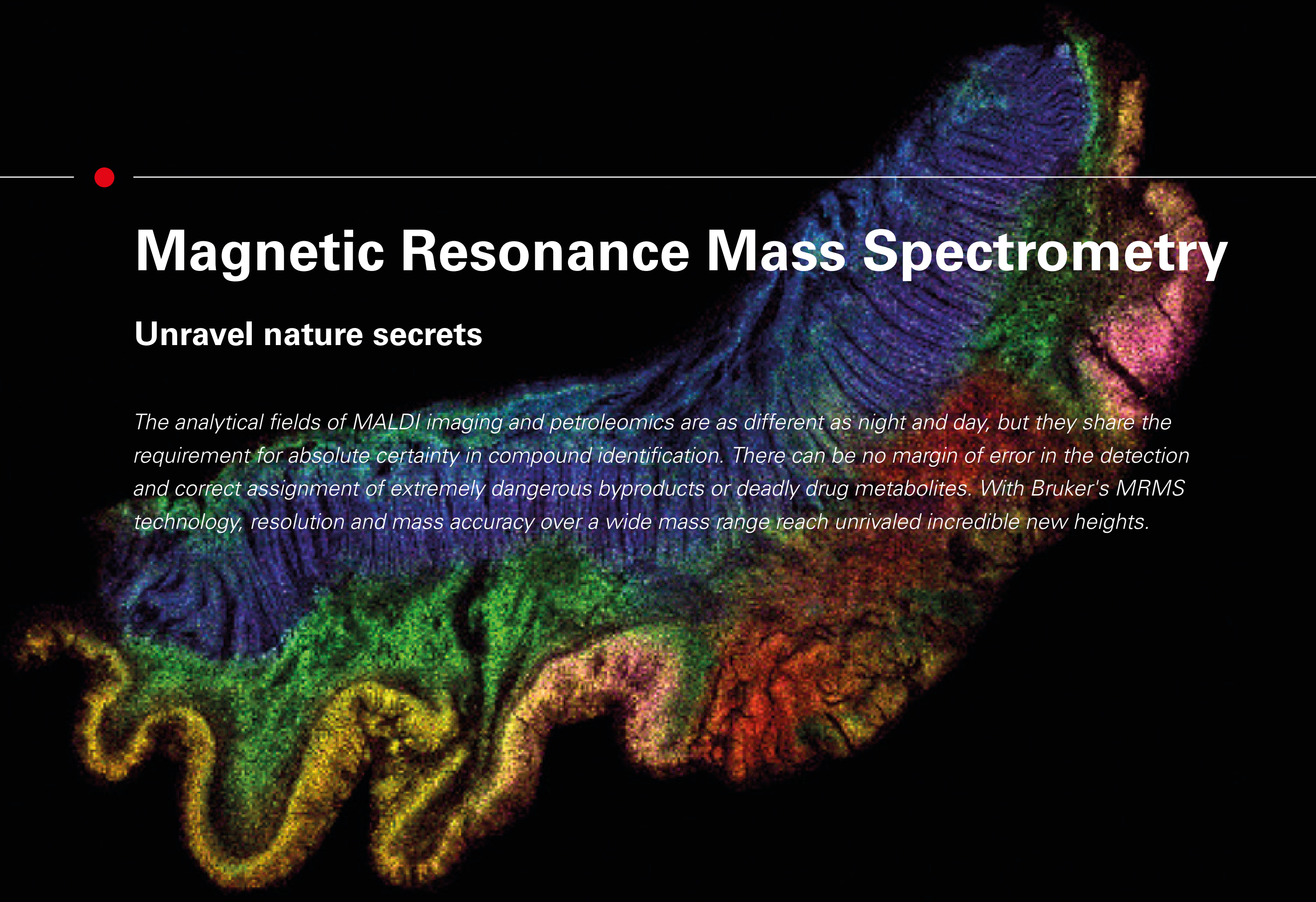
Our ESI QTOF mass spectrometers are the showcase instrument platform for life science research, drug discovery and development, and screening applications involving the analysis of both targeted and unknown compounds in complex matrices. The systems provide cutting edge performance in one-shot analysis 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	50,000	80,000
scan speed:	1-50 Hz (MS & MS/MS)	1-50 Hz (MS & MS/MS)	1-50 Hz (MS & MS/MS)
fragmentation:	CID	CID	CID, ETD
source:	All systems have ESI, APCI II, APPI II, ionBooster, GC APCI, DirectProbe DIP, CaptiveSpray		
size [mm]:	624 x 510 x 1240	700 x 600 x 1240	1320 x 800 x 2845

QTOF Solution

TargetScreener - Eliminate false positives and get the complete picture

Food, forensic or environmental laboratories are required to comprehensively screen and accurately report contaminants or toxicants in complex samples. Results need to meet legislative requirements or stand up to scrutiny in courts of law. TargetScreener contains highly curated databases which ensure false positives are minimized; a challenging task given the enormous number of analytes covered, their wide range of concentrations and the complexity of sample matrices tested. The power of the high resolution data ensures accurate quantitative results and allows retrospective analysis on previously analysed samples should new questions be posed. TargetScreener exceeds in this field of analysis.



Magnetic Resonance Mass Spectrometry

Unravel nature secrets

The analytical fields of MALDI imaging and petroleomics are as different as night and day, but they 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 scimaX MRMS system. This key innovation uses conduction-cooled 7T technology, which removes the requirement of liquid cryogen fills or quench ducts. 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 petroleomics and dissolved organic materials. 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

Ion Trap Mass Spectrometry

Rock solid performance

Bruker's legacy of innovation includes the amaZon family of ion trap mass spectrometers. Robust ETD technology provides unprecedented identification capabilities while advanced ion funnel technologies enable high analytical sensitivity. Detailed peptide and protein characterization are available via bottom-up CID or ETD and top-down ETD/PTR.

Ion Trap series

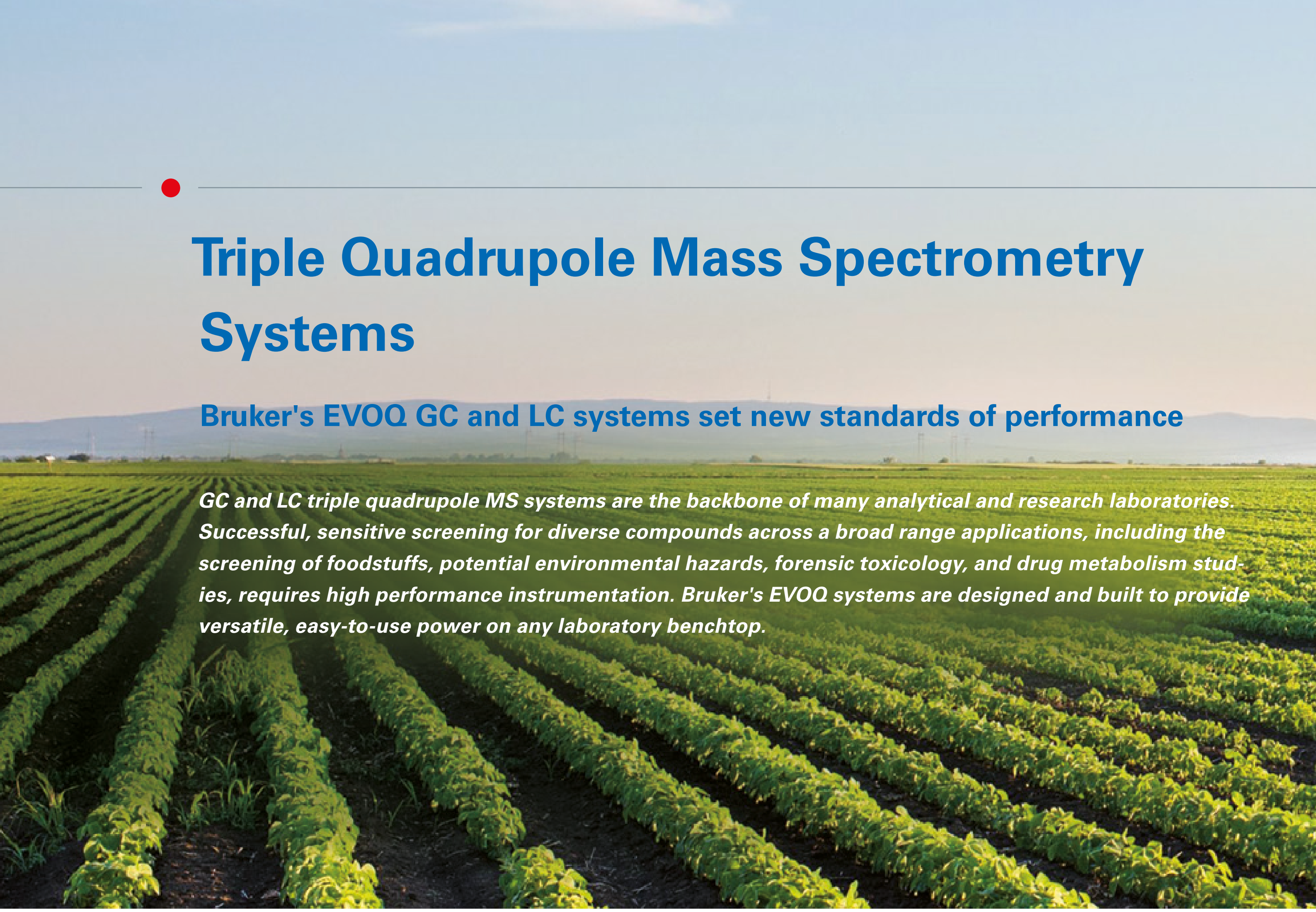
Modern ion trap systems offer reliably high performance in a rapidly changing world of mass spectrometry. Incredibly easy to use and with outstanding robustness, these systems deliver fastest MS^n results with high sensitivity. The class leader in ion trap technology, Bruker Daltonics offers a comprehensive series of ion trap systems meeting the needs of any user. Structural confirmation and screening applications in routine labs are well covered, as are protein ID and detailed target characterization.

	amaZon		
	speed	**speed ETD**	**SL**
mass range:	50 - 3,000	50 - 3,000	50 - 2,200
mass resolution:	0.3 u	0.3 u	0.35 u
scan rate u/sec:	52,000	52,000	52,000
size [cm]:	89 x 76 x 51	89 x 76 x 51	89 x 76 x 51
source:	ESI and APCI II source (Apollo); CaptiveSpray		
sensitivity:	250 fg reserpine: S/N > 500	250 fg reserpine: S/N > 500	250 fg reserpine: S/N > 50

Ion Trap Solution

Toxtyper

The Toxtyper® was developed by toxicologists for toxicologists. It delivers a very robust and highly automated screening solution for identifying potential toxicants within a few minutes. At the heart of the system is a highly curated library and together with the patented SmartFrag™ technology (which removes variability and eliminates the need for complicated, time-consuming MS/MS tuning) delivers accurate identification of drugs with complete transferability of results from lab to lab.



Triple Quadrupole Mass Spectrometry Systems

Bruker's EVOQ GC and LC systems set new standards of performance

GC and LC triple quadrupole MS systems are the backbone of many analytical and research laboratories. Successful, sensitive screening for diverse compounds across a broad range applications, including the screening of foodstuffs, potential environmental hazards, forensic toxicology, and drug metabolism studies, requires high performance instrumentation. Bruker's EVOQ systems are designed and built to provide versatile, easy-to-use power on any laboratory benchtop.

EVOQ Gas Chromatography - Triple Quadrupole Mass Spectrometry

EVOQ GC-TQ MS triple quadrupole systems set a new industry standard for GC-MS. With an innovative ‘lens-free’, elliptical ion path design, the EVOQ series delivers incredible sensitivity and high stability along with reduced chemical noise. This analytical power is simple to use and comes complete in a space-saving package that makes upgrading to new levels of robust and reliable performance strightfoward and cost-effective.

EVOQ GC-TQ

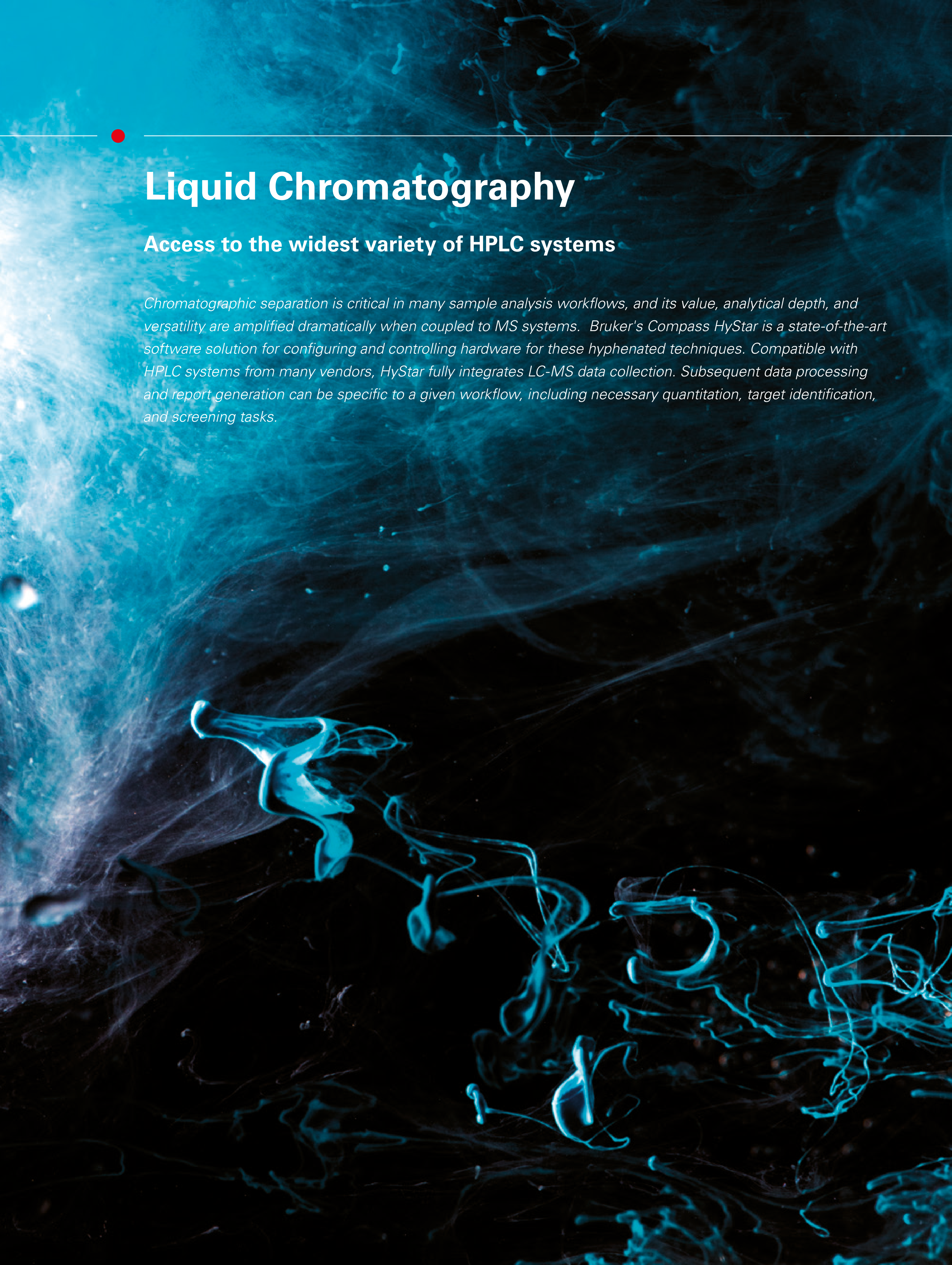
	Select	**Premium**	**Premium EI/CI**
mass range:	10 - 1,200	10 - 1,200	10 - 1,200
size [cm]:	45 x 28 x 57	45 x 28 x 57	45 x 28 x 57
mrm per second:	500	600	600
source:	EI	EI (CI optional)	EI/CI

EVOQ Liquid Chromatography - Triple Quadrupole Mass Spectrometry

EVOQ LC-TQ MS triple quadrupole systems provide analysts with a LC-MS platform designed for a singular purpose – to reliably quantify thousands of target analytes from real samples in the fastest sample-to-report time possible. These systems deliver exceptional sensitivity, precision, accuracy, linearity, and a wide dynamic range for your multiple reaction monitoring (MRM) assays. Innovations in software and atmospheric pressure ionization (API) technology make it a game changer for routine high-sensitivity, quantitative analysis. At Bruker today, we are pioneering the migration of technology from research to commerical laboratories. The EVOQ Elite and EVOQ Qube reflect this design philosophy and solve the hardware and software challenges faced by the quantitative analysis community.

EVOQ LC-TQ

	Cube	Elite	Elite ER
mass range:	10 - 1,250	10 - 1,250	10 - 2,000
size [cm]:	53 x 45 x 70	53 x 45 x 70	53 x 45 x 70
source:	HESI, ESI, APCI	HESI, ESI, APCI	HESI, ESI, APCI



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 – Simply Connect

The powerful and fully integrated nanoElute® (nanoflow UHPLC) system comes with unique valve design and software controlled flow path architecture for direct loading or pre-concentration of samples. Large volume, single stroke piston pumps deliver accurate gradients at pressures up to 1,000 bar to support a wide range of applications. Instant Expertise™ methods generate optimal separation gradients to suit proteomics samples. The system has a built-in scheduling of preventative maintenance and precise diagnostics to detect leaks and blockages. Additionally, the automated calibration feature monitors run-to-run consistency in a single mouse click.

	nanoElute
flow range:	50 - 2,000 nL
pressure limit:	1,000 bar
carryover:	0.003%
size [mm]:	790 × 490 × 900
additional information:	Trouble-free operation, ease-of-use along with top performance

Elute LC Series – Ultimate Precision

Elute 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.

	Elute LC			
	SP	**UHPLC**	**OLE**	**HT**
flow range:	1 - 5,000 µL	1 - 5,000 µL	1 - 5,000 µL	1 - 5,000 µL
pressure limit:	700 bar	1,300 bar	1,300 bar	1,300 bar
carryover:	0.001%	0.001%	0.001%	0.003%
size [mm]:	690 × 500 × 610	690 × 500 × 610	690 × 650 × 610	550 × 1,180 × 500
additional information:	Standard analytical LC for routine applications and moderate throughput	Faster and high resolution separations	Combine the advantages of UHPLC and online liquid exraction	UHPLC combined with PAL3 autosampler for high sample throughput

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™ nanoBooster**	The CaptiveSpray nanoBooster is the proteomics ion source that brings your MS to the next performance level, and its operation is just as easy as performing electrospray. The nanoBooster enhances glycoanalysis and supercharging and increases ID rates.
	**ionBooster**	The ionBooster offers a 5 – 100x gain in sensitivity for many compounds of interest in the fields of environmental analysis, food testing, and therapeutic drug monitoring research.
	**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.
	**VIP-HESI**	The VIP-HESI source used for the EVOQ LC-TQ Mass Spectrometers offers sustained sensitivity with minimal maintenance as well as capability to use higher flow rates, if necessary.

Software Solutions

Compass and Bioinformatics

Bruker Daltonics software solutions provide maximum information via streamlined, easy to use processes. They are closely integrated with our instruments, tailored for specific applications, and focused on reporting results clearly with the level of detail customized by each user.

Field of Application	Software Product	Description
BioPharma	**BioPharma Compass®**	Integrated biopharmaceutical workflows from acquisition to reporting for automated characterization, identity confirmation, attribute monitoring, and comparative quantitative assessments. Protein Screening, Top-Down Protein Sequencing and bottom-up workflows (Peptide Mapping / Screening) are supported within this full suite of ESI and MALDI data processing tools in addition to UV and FLD support.
BioPharma	**DisulfideDetect**	Based on LC-MALDI data, DisulfideDetect detects and evaluates disulfide bonds within therapeutic proteins, such as monoclonal antibodies. It provides an easy to understand, visual workspace for disulfide bond analysis for both native and non-native bonds as well as inter- and intra-chain disulfide bonds within the protein or antibody.
Proteomics, Glycomics	**ProteinScape®**	ProteinScape is a comprehensive platform for proteomics and glycomics workflows, including MS/MS-based protein and glycan database searches, glycopeptide analysis, and protein quantitation. Various interactive result viewers, powerful database queries and carefully organized result reports facilitate easy confirmation and communication of results. However, our data formats are open to third-party software suppliers, and we collaborate intensively with selected partners, e.g. Bioinformatics Solutions Inc. (PEAKS Studio) or the Max-Planck-Institute for Biochemistry (MaxQuant).
Metabolomics	**MetaboScape®**	Our software for discovery metabolomics pinpoints and identifies compounds that change as a result of perturbation or disease, and uses pathway mapping to establish them within a biological context. MetaboScape includes the T-ReX 3D algorithm for parameter-free retention time alignment and region-complete feature extraction for statistical confidence. It supports Bruker HMDB Metabolite Library, Bruker MetaboBASE Personal Library, Bruker MetaboBASE Plant Library, as well as custom libraries, and turns complementary data from Bruker's LC-QTOF-MS/MS, GC-APCI-QTOF-MS and MRMS into useful knowledge.
Screening, Quantitation	**TASQ®**	The TASQ (Target Analysis for Screening and Quantitation) software takes advantage of both nominal and high resolution, accurate-mass data generated by Bruker triple quadrupole and OTOF mass spectrometers. TASQ provides a turnkey solution for screening, confirmation and/or quantitation of large sample batches, including hundreds of compounds per analysis.. OTOF data can be retrospectively analysed as new compounds become of interest.
Imaging	**SCiLS™ Lab**	SCiLS Lab is the leading software for analysis of mass spectrometry imaging data and is an integral part of Bruker's MALDI molecular imager solution. Comparative analysis of multiple samples can be visualized in both 2D and 3D, enabling a multitude of applications in pharmaceutical, medical, and industrial research. The complete MALDI Molecular Imaging solution is comprised of the fully-automated ImagePrep station, MALDI-TOF mass spectrometer, data analysis via flexImaging and statistical evaluation with SCiLS lab.
Structure verification using HRAM-MS and NMR	**Bruker FUSION®-SV**	Bruker FUSION-SV integrates high resolution accurate mass (HRAM) mass spectrometry (MS) and complementary NMR data. The result is a significantly increased specificity for structure verification of small organic molecules. An automated result assessment leads to a meaningful and easily understandable report. Bruker FUSION-SV is tailored to the needs of the chemist in both academic and industrial laboratories.

A rapid MALDI-TOF mass spectrometry workflow for *Drosophila melanogasta* differential neuropeptidomics

Joseph P. Salisbury, Kristin J. Boggio, Yun-Wei A Hsu, Jeniffer Quijada, Anna Sivachenko, Gabriele Gloeckner, Paul J. Kowalski, Michael L. Easterling, Michael Rosbash, Jeffrey N. Agar

Dr. M. Rosbash. Winner of 2017 Nobel Prize in Medicine

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